

<110> Edwards, Jean-Baptiste Dumas Milne
Duclert, Aymeric
Bougueleret, Lydie
Jobert, Severin
Clusel, Catherine

<120> Complementary DNA's Encoding Proteins with Signal Peptides

<130> 56.US4.CIP

<140>

<141> 2001-10-15

<150> 60/066,677

<151> 1997-11-13

<150> 60/069,957

<151> 1997-12-17

<150> 60/074,121

<151> 1998-02-09

<150> 60/081,563

<151> 1998-04-13

<150> 60/096,116

<151> 1998-08-10

<150> 60/099,273

<151> 1998-09-04

<150> 09/191,997

<151> 1998-11-13

<150> 09/215,435

<151> 1998-12-17

<150> PCT/IB98/02122

<151> 1998-12-17

<150> 09/247,155

<151> 1999-02-09

<150> PCT/IB99/00282

<151> 1999-02-09

<150> 60/141,032

<151> 1999-06-25

<150> 09/469,099

<151> 1999-12-21

<150> 09/599,360

<151> 2000-06-21

<150> PCT/IB00/00951

<151> 2000-06-21

<150> 09/663,600

<151> 2000-09-15

09978360 101504

<160> 810

<170> Patent.pm

<210> 1

<211> 1450

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> 153..1127

<220>

<221> sig_peptide

<222> 153..230

<223> Von Heijne matrix

score 8.40

seq RLLRLLLSGLVLG/AA

<220>

<221> polyA_signal

<222> 1415..1420

<220>

<221> polyA_site

<222> 1434..1450

<220>

<221> misc_feature

<222> 88

<223> n=a, g, c or t

<400> 1

```
ctttcctctt cctcctcctc ctcccttgga tccgctctt cttcctcctg cgtcctcccc    60
cgctgcctcc gctgctcccg acgcggancc cggagcccg gccgagcccc tggcctcgcg    120
gtgccatgct gccccggcgg cggcgctgaa gg atg gcg acg ccg ctg cct ccg    173
                               Met Ala Thr Pro Leu Pro Pro
                               -25                               -20

ccc tcc ccg cgg cac ctg cgg ctg ctg cgg ctg ctg ctc tcc ggc ctc    221
Pro Ser Pro Arg His Leu Arg Leu Leu Arg Leu Leu Leu Ser Gly Leu
                               -15                               -10                               -5

gtc ctc ggc gcc gcc ctg cgt gga gcc gcc gcc ggc cac ccg gat gta    269
Val Leu Gly Ala Ala Leu Arg Gly Ala Ala Ala Gly His Pro Asp Val
                               1                               5                               10

gcc gcc tgt ccc ggg agc ctg gac tgt gcc ctg aag agg cgg gca agg    317
Ala Ala Cys Pro Gly Ser Leu Asp Cys Ala Leu Lys Arg Arg Ala Arg
                               15                               20                               25

tgt cct cct ggt gca cat gcc tgt ggg ccc tgc ctt cag ccc ttc cag    365
Cys Pro Pro Gly Ala His Ala Cys Gly Pro Cys Leu Gln Pro Phe Gln
30                               35                               40                               45

gag gac cag caa ggg ctc tgt gtg ccc agg atg cgc cgg cct cca ggc    413
Glu Asp Gln Gln Gly Leu Cys Val Pro Arg Met Arg Arg Pro Pro Gly
                               50                               55                               60

ggg ggc cgg ccc cag ccc aga ctg gaa gat gag att gac ttc ctg gcc    461
Gly Gly Arg Pro Gln Pro Arg Leu Glu Asp Glu Ile Asp Phe Leu Ala
65                               70                               75

cag gag ctt gcc cgg aag gag tct gga cac tca act ccg ccc cta ccc    509
Gln Glu Leu Ala Arg Lys Glu Ser Gly His Ser Thr Pro Pro Leu Pro
80                               85                               90

aag gac cga cag cgg ctc ccg gag cct gcc acc ctg ggc ttc tcg gca    557
Lys Asp Arg Gln Arg Leu Pro Glu Pro Ala Thr Leu Gly Phe Ser Ala
```

```

      95              100              105
cgg ggg cag ggg ctg gag ctg ggc ctc ccc tcc act cca gga acc ccc      605
Arg Gly Gln Gly Leu Glu Leu Gly Leu Pro Ser Thr Pro Gly Thr Pro
110              115              120              125
acg ccc acg ccc cac acc tcc ctg ggc tcc cct gtg tca tcc gac ccg      653
Thr Pro Thr Pro His Thr Ser Leu Gly Ser Pro Val Ser Ser Asp Pro
              130              135              140
gtg cac atg tcg ccc ctg gag ccc cgg gga ggg caa ggc gac ggc ctc      701
Val His Met Ser Pro Leu Glu Pro Arg Gly Gly Gln Gly Asp Gly Leu
              145              150              155
gcc ctt gtg ctg atc ctg gcg ttc tgt gtg gcc ggt gca gcc gcc ctc      749
Ala Leu Val Leu Ile Leu Ala Phe Cys Val Ala Gly Ala Ala Ala Leu
              160              165              170
tcc gta gcc tcc ctc tgc tgg tgc agg ctg cag cgt gag atc cgc ctg      797
Ser Val Ala Ser Leu Cys Trp Cys Arg Leu Gln Arg Glu Ile Arg Leu
              175              180              185
act cag aag gcc gac tac gcc act gcg aag gcc cct ggc tca cct gca      845
Thr Gln Lys Ala Asp Tyr Ala Thr Ala Lys Ala Pro Gly Ser Pro Ala
190              195              200              205
gct ccc cgg atc tcg cct ggg gac cag cgg ctg gca cag agc gcg gag      893
Ala Pro Arg Ile Ser Pro Gly Asp Gln Arg Leu Ala Gln Ser Ala Glu
              210              215              220
atg tac cac tac cag cac caa cgg caa cag atg ctg tgc ctg gag cgg      941
Met Tyr His Tyr Gln His Gln Arg Gln Gln Met Leu Cys Leu Glu Arg
              225              230              235
cat aaa gag cca ccc aag gag ctg gac acg gcc tcc tcg gat gag gag      989
His Lys Glu Pro Pro Lys Glu Leu Asp Thr Ala Ser Ser Asp Glu Glu
              240              245              250
aat gag gac gga gac ttc acg gtg tac gag tgc ccg ggc ctg gcc ccg      1037
Asn Glu Asp Gly Asp Phe Thr Val Tyr Glu Cys Pro Gly Leu Ala Pro
              255              260              265
acc ggg gaa atg gag gtg cgc aac cct ctg ttc gac cac gcc gca ctg      1085
Thr Gly Glu Met Glu Val Arg Asn Pro Leu Phe Asp His Ala Ala Leu
270              275              280              285
tcc gcg ccc ctg ccg gcc ccc agc tca ccg cct gca ctg cca      1127
Ser Ala Pro Leu Pro Ala Pro Ser Ser Pro Pro Ala Leu Pro
              290              295
tgacctggag gcagacagac gcccacctgc tccccgacct cgaggcccc ggggaggggc      1187
agggcctgga gcttcccact aaaaacatgt tttgatgctg tgtgcttttg gctgggcctt      1247
gggctccagg ccctgggacc ccttgccagg gagacccccg aacctttgtg ccaggacacc      1307
tcctggtccc ctgcacctct cctgtttggt ttagaccccc aaactggagg gggcatggag      1367
aaccgtagag cgcaggaacg ggtgggtaat tctagagaca aaagccaatt aaagtccatt      1427
tcagacaaaa aaaaaaaaaa aaa      1450

```

<210> 2
 <211> 1556
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 261..1166

<220>
 <221> sig_peptide
 <222> 261..314
 <223> Von Heijne matrix
 score 8.80
 seq RLVLIIILCSVVFS/AV

<220>

<221> polyA_site

<222> 1524..1556

<400> 2

cagcccagtc	ggcccggccc	ggggggccatg	gagctccgag	cggcgatcgc	gagcctcctg	60
cgaaccccag	cctgcacgcc	cggttagcat	tcggccggga	gatgcggcag	tggaatctgg	120
aagggcgggtg	aaaaacctac	gtcctgccct	cgccggcct	ctccattcgt	ccccgggta	180
gagaggtgcc	cggctcccac	cccttcccag	ccccagccct	ggagacagca	gcccctagac	240
tactgagggga	cagcgacagc	atg aag gct	ccg ggt cgg	ctc gtg ctc	atc atc	293
		Met Lys Ala	Pro Gly Arg	Leu Val Leu	Ile Ile	
		-15		-10		
ctg tgc tcc	gtg gtc ttc	tct gcc gtc	tac atc ctc	ctg tgc tgc	tgg	341
Leu Cys Ser	Val Val Phe	Ser Ala Val	Tyr Ile Leu	Leu Cys Cys	Trp	
	-5	1	5			
gcc ggc ctg	ccc ctc tgc	ctg gcc acc	tgc ctg gac	cac cac ttc	ccc	389
Ala Gly Leu	Pro Leu Cys	Leu Ala Thr	Cys Leu Asp	His His Phe	Pro	
10	15	20	25			
aca ggc tcc	agg ccc act	gtg ccg gga	ccc ctg cac	ttc agt gga	tat	437
Thr Gly Ser	Arg Pro Thr	Val Pro Gly	Pro Leu His	Phe Ser Gly	Tyr	
	30	35	40			
agc agt gtg	cca gat ggg	aag ccg ctg	gtc cgc gag	ccc tgc cgc	agc	485
Ser Ser Val	Pro Asp Gly	Lys Pro Leu	Val Arg Glu	Pro Cys Arg	Ser	
	45	50	55			
tgt gcc gtg	gtg tcc agc	tcc ggc caa	atg ctg ggc	tca ggc ctg	ggt	533
Cys Ala Val	Val Ser Ser	Ser Gly Gln	Met Leu Gly	Ser Gly Leu	Gly	
	60	65	70			
gct gag atc	gac agt gcc	gag tgc gtg	ttc cgc atg	aac cag gcg	ccc	581
Ala Glu Ile	Asp Ser Ala	Glu Cys Val	Phe Arg Met	Asn Gln Ala	Pro	
	75	80	85			
acc gtg ggc	ttt gag gcg	gat gtg ggc	cag cgc agc	acc ctg cgt	gtc	629
Thr Val Gly	Phe Glu Ala	Asp Val Gly	Gln Arg Ser	Thr Leu Arg	Val	
	90	95	100		105	
gtc tca cac	aca agc gtg	ccg ctg ctg	ctg cgc aac	tat tca cac	tac	677
Val Ser His	Thr Ser Val	Pro Leu Leu	Arg Asn Tyr	Ser His Tyr		
	110	115	120			
ttc cag aag	gcc cga gac	acg ctc tac	atg gtg tgg	ggc cag ggc	agg	725
Phe Gln Lys	Ala Arg Asp	Thr Leu Tyr	Met Val Trp	Gly Gln Gly	Arg	
	125	130	135			
cac atg gac	cgg gtg ctc	ggc ggc cgc	acc tac cgc	acg ctg ctg	cag	773
His Met Asp	Arg Val Leu	Gly Gly Arg	Thr Tyr Arg	Thr Leu Leu	Gln	
	140	145	150			
ctc acc agg	atg tac ccc	ggc ctg cag	gtg tac acc	ttc acg gag	cgc	821
Leu Thr Arg	Met Tyr Pro	Gly Leu Gln	Val Tyr Thr	Phe Thr Glu	Arg	
	155	160	165			
atg atg gcc	tac tgc gac	cag atc ttc	cag gac gag	acg ggc aag	aac	869
Met Met Ala	Tyr Cys Asp	Gln Ile Phe	Gln Asp Glu	Thr Gly Lys	Asn	
	170	175	180		185	
cgg agg cag	tcg ggc tcc	ttc ctc agc	acc ggc tgg	ttc acc atg	atc	917
Arg Arg Gln	Ser Gly Ser	Phe Leu Ser	Thr Gly Trp	Phe Thr Met	Ile	
	190	195	200			
ctc gcg ctg	gag ctg tgt	gag gag atc	gtg gtc tat	ggg atg gtc	agc	965
Leu Ala Leu	Glu Leu Cys	Glu Glu Ile	Val Val Tyr	Gly Met Val	Ser	
	205	210	215			
gac agc tac	tgc agg gag	aag agc cac	ccc tca gtg	cct tac cac	tac	1013
Asp Ser Tyr	Cys Arg Glu	Lys Ser His	Pro Ser Val	Pro Tyr His	Tyr	
	220	225	230			
ttt gag aag	ggc cgg cta	gat gag tgt	cag atg tac	ctg gca cac	gag	1061
Phe Glu Lys	Gly Arg Leu	Asp Glu Cys	Gln Met Tyr	Leu Ala His	Glu	
	235	240	245			
cag gcg ccc	cga agc gcc	cac cgc ttc	atc act gag	aag gcg gtc	ttc	1109
Gln Ala Pro	Arg Ser Ala	His Arg Phe	Ile Thr Glu	Lys Ala Val	Phe	
	250	255	260		265	

tcc cgc tgg gcc aag aag agg ccc atc gtg ttc gcc cat ccg tcc tgg	1157
Ser Arg Trp Ala Lys Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp	
270 275 280	
agg act gag tagcttccgt cgtcctgccca gccgccatgc cgttgcgagg	1206
Arg Thr Glu	
cctccgggat gtcccatccc aagccatcac actccactcc ctgagtaatt catggcattt	1266
gggggctcac cacctccagg tctgtcaagt ggcctttgtc cctggggctg atggcccca	1326
actcaccagc atcatgacct tgtgccagtc ctggctctcc ctcccagcc gccctacca	1386
ccttttggtg ccacacttct caggctggcc gccctggttg gggcagccga gagcctgggg	1446
ttcattggtg aaggggcctt ggagttgtga ctgccggggc cgtatcagga acgtacgggt	1506
aaacgtgtgt tttctggaaa aaaaaaaaaa aacaaaaaaaaa aaaaaaaaaa	1556

<210> 3
 <211> 1058
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 67..813

<220>
 <221> sig_peptide
 <222> 67..111
 <223> Von Heijne matrix
 score 5.20
 seq QLWKLVLGCVLT/GT

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1042..1058

<400> 3	
agcagactgt gcagtggggc aaggatttca tgagcatcct cctctaaacg cgtgacaaga	60
caaaaag atg ctt cag ctt tgg aaa ctt gtt ctc ctg tgc ggc gtg ctc	108
Met Leu Gln Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu	
-15 -10 -5	
act ggg acc tca gag tct ctt ctt gac aat ctt ggc aat gac cta agc	156
Thr Gly Thr Ser Glu Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser	
1 5 10 15	
aat gtc gtg gat aag ctg gaa cct gtt ctt cac gag gga ctt gag aca	204
Asn Val Val Asp Lys Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr	
20 25 30	
gtt gac aat act ctt aaa ggc atc ctt gag aaa ctg aag gtc gac cta	252
Val Asp Asn Thr Leu Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu	
35 40 45	
gga gtg ctt cag aaa tcc agt gct tgg caa ctg gcc aag cag aag gcc	300
Gly Val Leu Gln Lys Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala	
50 55 60	
cag gaa gct gag aaa ttg ctg aac aat gtc att tct aag ctg ctt cca	348
Gln Glu Ala Glu Lys Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro	
65 70 75	
act aac acg gac att ttt ggg ttg aaa atc agc aac tcc ctc atc ctg	396
Thr Asn Thr Asp Ile Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu	
80 85 90 95	
gat gtc aaa gct gaa ccg atc gat gat ggc aaa ggc ctt aac ctg agc	444
Asp Val Lys Ala Glu Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser	

Val Trp Gly Gln Cys Ser His Cys Phe His Met His Cys Ile Leu Lys	
50 55 60	
tgg ctg cac gca cag cag gtg cag cag cac tgc ccc atg tgc cgc cag	420
Trp Leu His Ala Gln Gln Val Gln Gln His Cys Pro Met Cys Arg Gln	
65 70 75	
gaa tgg aag ttc aag gag tgaggcccg cctggctctc gctggagggg	468
Glu Trp Lys Phe Lys Glu	
80	
catcctgaga ctcttctctc atgctggcgc cgatggctgc tggggacagc gcccctgagc	528
tgcaacaagg tggaaacaag ggctggagct gcgtttgttt tgccatcact atgttgacac	588
ttttatccaa taagtgaataa ctcattaaac tactcaaatac tcgaaaaaaaa aaaaaaaaaa	648

<210> 5
 <211> 2104
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 92..1753

<220>
 <221> sig_peptide
 <222> 92..130
 <223> Von Heijne matrix
 score 3.90
 seq MLYLQGWSMPAVA/EV

<220>
 <221> polyA_signal
 <222> 2070..2075

<220>
 <221> polyA_site
 <222> 2090..2104

<220>
 <221> misc_feature
 <222> 905
 <223> n=a, g, c or t

<220>
 <221> unsure
 <222> 259
 <223> Xaa = Asp,His,Asn,Tyr

<400> 5	
atagacttta tcatacttcg tagcatccag tatgttttct ttgctaagat tattgatttt	60
gtattgaagg gtcccatgtc catcgttttc a atg ctt tat ctc cag ggt tgg	112
Met Leu Tyr Leu Gln Gly Trp	
-10	
agc atg cct gct gtg gca gag gta aaa ctt cga gat gat caa tat aca	160
Ser Met Pro Ala Val Ala Glu Val Lys Leu Arg Asp Asp Gln Tyr Thr	
-5 1 5 10	
ctg gaa cac atg cat gct ttt gga atg tat aat tac ctg cac tgt gat	208
Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr Leu His Cys Asp	
15 20 25	
tca tgg tat caa gac agt gtc tac tat att gat acc ctt gga aga att	256
Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr Leu Gly Arg Ile	
30 35 40	
atg aat tta aca gta atg ctg gac act gcc tta gga aaa cca cga gag	304

Met	Asn	Leu	Thr	Val	Met	Leu	Asp	Thr	Ala	Leu	Gly	Lys	Pro	Arg	Glu	
	45						50					55				
gtg	ttt	cga	ctt	cct	aca	gat	ttg	aca	gca	tgt	gac	aac	cgt	ctt	tgt	352
Val	Phe	Arg	Leu	Pro	Thr	Asp	Leu	Thr	Ala	Cys	Asp	Asn	Arg	Leu	Cys	
	60					65					70					
gca	tct	atc	cat	ttc	tca	tct	tct	acc	tgg	gtt	acc	ttg	tca	gat	gga	400
Ala	Ser	Ile	His	Phe	Ser	Ser	Ser	Thr	Trp	Val	Thr	Leu	Ser	Asp	Gly	
75					80					85					90	
act	gga	aga	ttg	tat	gtc	att	gga	aca	ggg	gaa	cgt	gga	aat	agc	gct	448
Thr	Gly	Arg	Leu	Tyr	Val	Ile	Gly	Thr	Gly	Glu	Arg	Gly	Asn	Ser	Ala	
				95					100						105	
tct	gaa	aaa	tgg	gag	att	atg	ttt	aat	gaa	gaa	ctt	ggg	gat	cct	ttt	496
Ser	Glu	Lys	Trp	Glu	Ile	Met	Phe	Asn	Glu	Glu	Leu	Gly	Asp	Pro	Phe	
			110					115					120			
att	ata	att	cac	agt	atc	tca	ctg	cta	aat	gct	gaa	gaa	cat	tct	ata	544
Ile	Ile	Ile	His	Ser	Ile	Ser	Leu	Asn	Ala	Glu	Glu	His	Ser	Ile		
			125				130					135				
gct	acc	cta	ctt	ctt	cga	ata	gag	aaa	gag	gaa	ttg	gat	atg	aaa	gga	592
Ala	Thr	Leu	Leu	Leu	Arg	Ile	Glu	Lys	Glu	Glu	Leu	Asp	Met	Lys	Gly	
	140					145					150					
agt	ggg	ttc	tat	gtt	tct	ctg	gag	tgg	gtc	act	atc	agt	aag	aaa	aat	640
Ser	Gly	Phe	Tyr	Val	Ser	Leu	Glu	Trp	Val	Thr	Ile	Ser	Lys	Lys	Asn	
	155				160				165						170	
caa	gat	aat	aaa	aaa	tat	gaa	att	att	aag	cgt	gat	att	ctc	cgt	gga	688
Gln	Asp	Asn	Lys	Lys	Tyr	Glu	Ile	Ile	Lys	Arg	Asp	Ile	Leu	Arg	Gly	
				175					180					185		
aag	tca	gtg	cca	cat	tat	gct	gct	att	aag	cct	gat	gga	aat	ggg	cta	736
Lys	Ser	Val	Pro	His	Tyr	Ala	Ala	Ile	Lys	Pro	Asp	Gly	Asn	Gly	Leu	
			190				195						200			
atg	att	gta	tcc	tac	aag	tct	tta	aca	ttt	gtt	cag	gct	ggg	caa	gat	784
Met	Ile	Val	Ser	Tyr	Lys	Ser	Leu	Thr	Phe	Val	Gln	Ala	Gly	Gln	Asp	
	205						210					215				
ctt	gaa	gaa	aat	atg	gat	gaa	gac	ata	tca	gag	aaa	atc	aaa	gaa	cct	832
Leu	Glu	Glu	Asn	Met	Asp	Glu	Asp	Ile	Ser	Glu	Lys	Ile	Lys	Glu	Pro	
	220					225					230					
ctg	tat	tac	tgg	caa	cag	act	gaa	gat	gat	ttg	aca	gta	acc	ata	cgg	880
Leu	Tyr	Tyr	Trp	Gln	Gln	Thr	Glu	Asp	Asp	Leu	Thr	Val	Thr	Ile	Arg	
	235					240				245					250	
ctt	cca	gaa	gac	agt	act	aag	gag	nac	att	caa	ata	cag	ttt	ttg	cct	928
Leu	Pro	Glu	Asp	Ser	Thr	Lys	Glu	Xaa	Ile	Gln	Ile	Gln	Phe	Leu	Pro	
				255					260					265		
gat	cac	atc	aac	att	gta	ctg	aag	gat	cac	cag	ttt	tta	gaa	gga	aaa	976
Asp	His	Ile	Asn	Ile	Val	Leu	Lys	Asp	His	Gln	Phe	Leu	Glu	Gly	Lys	
			270					275					280			
ctc	tat	tca	tct	att	gat	cat	gaa	agc	agt	aca	tgg	ata	att	aaa	gag	1024
Leu	Tyr	Ser	Ser	Ile	Asp	His	Glu	Ser	Ser	Thr	Trp	Ile	Ile	Lys	Glu	
	285						290					295				
agt	aat	agc	ttg	gag	att	tcc	ttg	att	aag	aag	aat	gaa	gga	ctg	acc	1072
Ser	Asn	Ser	Leu	Glu	Ile	Ser	Leu	Ile	Lys	Lys	Asn	Glu	Gly	Leu	Thr	
	300					305					310					
tgg	cca	gag	cta	gta	att	gga	gat	aaa	caa	ggg	gaa	ctt	ata	aga	gat	1120
Trp	Pro	Glu	Leu	Val	Ile	Gly	Asp	Lys	Gln	Gly	Glu	Leu	Ile	Arg	Asp	
	315				320					325					330	
tca	gcc	cag	tgt	gct	gca	ata	gct	gaa	cgt	ttg	atg	cat	ttg	acc	tct	1168
Ser	Ala	Gln	Cys	Ala	Ala	Ile	Ala	Glu	Arg	Leu	Met	His	Leu	Thr	Ser	
				335					340					345		
gaa	gaa	ctg	aat	cca	aat	cca	gat	aaa	gaa	aaa	cca	cct	tgc	aat	gct	1216
Glu	Glu	Leu	Asn	Pro	Asn	Pro	Asp	Lys	Glu	Lys	Pro	Pro	Cys	Asn	Ala	
			350					355					360			
caa	gag	tta	gaa	gaa	tgt	gat	att	ttc	ttt	gaa	gag	agc	tcc	agt	tta	1264
Gln	Glu	Leu	Glu	Glu	Cys	Asp	Ile	Phe	Phe	Glu	Glu	Ser	Ser	Ser	Leu	

365	370	375	
tgc aga ttt gat ggc aat aca tta aaa act act cat gtg gtg aat ctt			1312
Cys Arg Phe Asp Gly Asn Thr Leu Lys Thr Thr His Val Val Asn Leu			
380	385	390	
gga agc aac cag tac ctt ttc tct gtc ata gtg gat cct aaa gaa atg			1360
Gly Ser Asn Gln Tyr Leu Phe Ser Val Ile Val Asp Pro Lys Glu Met			
395	400	405	410
ccc tgc ttc tgt ttg cgc cat gat gtt gat gcc cta ctc tgg caa cca			1408
Pro Cys Phe Cys Leu Arg His Asp Val Asp Ala Leu Leu Trp Gln Pro			
415	420	425	
cac tcc agc aaa caa gat gat atg tgg gag cac atc gca act ttc aat			1456
His Ser Ser Lys Gln Asp Asp Met Trp Glu His Ile Ala Thr Phe Asn			
430	435	440	
gct tta ggc tat gtc caa gca tca aag aga gac aaa aaa ttt ttt gcc			1504
Ala Leu Gly Tyr Val Gln Ala Ser Lys Arg Asp Lys Lys Phe Phe Ala			
445	450	455	
tgt gct cca aat tac tcg tat gca gcc ctt tgt gag tgc ctt cgt cga			1552
Cys Ala Pro Asn Tyr Ser Tyr Ala Ala Leu Cys Glu Cys Leu Arg Arg			
460	465	470	
gta ttc atc tat cgt cag cct gct ccc atg tcc act gta ctt tac aac			1600
Val Phe Ile Tyr Arg Gln Pro Ala Pro Met Ser Thr Val Leu Tyr Asn			
475	480	485	490
aga aag gaa ggc agg caa gta gga cag gtt gct aag cag caa gta gca			1648
Arg Lys Glu Gly Arg Gln Val Gly Gln Val Ala Lys Gln Gln Val Ala			
495	500	505	
agc cta gaa acc aat gat cct att tta gga ttt cag gca aca aat gag			1696
Ser Leu Glu Thr Asn Asp Pro Ile Leu Gly Phe Gln Ala Thr Asn Glu			
510	515	520	
aga tta ttt gtt ctt act acc aaa aac ctc ttt tta ata aaa gta aat			1744
Arg Leu Phe Val Leu Thr Thr Lys Asn Leu Phe Leu Ile Lys Val Asn			
525	530	535	
aca gag aat taattattct aacatattgg cctctttgta ctggaaaagt			1793
Thr Glu Asn			
540			
attcagtggg acctggagggt ctggacagtt atactgtaac ctcttaagtt ttaatgtgct			1853
aaatataatct tgtatgattt tttatttttt aataacattg gaaatataatt caagagatta			1913
tgattctgta aagctgtgga atgaagctgc agatttagag aacattggct tctgaaaaaa			1973
aaaaagagtg aagatagtag tagcaagtag acttattttt taaaacaggc tagaatctca			2033
tgttttatat gaaagatgta caattcagtg tttaaaaata aaaatattta ttgtgtaaaa			2093
aaaaaaaaaa a			2104

<210> 6
 <211> 515
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 144..440

<220>
 <221> sig_peptide
 <222> 144..287
 <223> Von Heijne matrix
 score 4.10
 seq VFMLIVSVLALIP/ET

<220>
 <221> polyA_signal
 <222> 457..462


```

tggccactat cctgtaggcc cttgattctg ccatctttca caaaaccagg gaatttagat 367
caaactgtga caccatgatg tgtccatgac tactgggttt tagcattttt ataggccagc 427
agactcttgt ggtctttaat ttaaagagct gagctgtagc cttctttaaa agagctcggg 487
ttttcacaaa aacaatgtag aagatatttt ctcacctcaa cgtgatgtcc agtgtgctca 547
tcagcacctg tttctccctc taatcataga ggatattctt attatttaga aaggcttcaa 607
gggaaacaac ttttggcacc taagtcgtgt cctaccttcg cttcagcttc gcatttccca 667
tttctgtgaa attcccaact ttagagaagc agatttgcca tggccttctg acaaccttgt 727
acatctctca cataaaccgc ataggcaggg cttactaca ggctggcccg agtctggact 787
gagtctgacc ctgaagttcc tttggaacag gagaggccat cttgtgatgg gctggaacaa 847
ggtaatttct catccacctc cctagtttca gttgagcaat ggaacttccc acctgagccc 907
ctaggggttca gctacagggt ataagactgc cgtcctgtgg tttagtgttg gttccttagc 967
agcagagtga tgccacctct gctgcccgtc atctgactcc tctggatggg tgttatcctg 1027
tggtcttaaga gctaacacca tgctgatctt gctttgctat atgtgtaact aataaactgc 1087
ctaatgcaa aaaaaaaaaa aaa 1110

```

```

<210> 10
<211> 623
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> CDS
<222> 49..447

<220>
<221> sig_peptide
<222> 49..111
<223> Von Heijne matrix
      score 5.00
      seq LIVIFFYCWLSSS/HE

```

```

<220>
<221> polyA_signal
<222> 579..584

```

```

<220>
<221> polyA_site
<222> 602..623

```

```

<400> 10
attagaattt tctttctcaa attaaagggt tgagaaattc gtgatgag atg tcc tgt 57
                                     Met Ser Cys
                                     -20
tcc cta aag ttt act ttg att gta att ttt ttt tac tgt tgg ctt tca 105
Ser Leu Lys Phe Thr Leu Ile Val Ile Phe Phe Tyr Cys Trp Leu Ser
                                     -15          -10          -5
tcc agc cat gag gag tta gaa ggt ggt aca tcg aag tct ttt gac ctc 153
Ser Ser His Glu Glu Leu Glu Gly Gly Thr Ser Lys Ser Phe Asp Leu
      1              5              10
cat aca gtg att atg ctt gtc atc gct ggt ggt atc ctg gcg gcc ttg 201
His Thr Val Ile Met Leu Val Ile Ala Gly Gly Ile Leu Ala Ala Leu
15              20              25              30
ctc ctg ctg ata gtt gtc gtg ctc tgt ctt tac ttc aaa ata cac aac 249
Leu Leu Leu Ile Val Val Val Leu Cys Leu Tyr Phe Lys Ile His Asn
                                     35          40          45
gcg cta aaa gct gca aag gaa cct gaa gct gtg gct gta aaa aat cac 297
Ala Leu Lys Ala Ala Lys Glu Pro Glu Ala Val Ala Val Lys Asn His
      50              55              60
aac cca gac aag gtg tgg tgg gcc aag aac agc cag gcc aaa acc att 345
Asn Pro Asp Lys Val Trp Trp Ala Lys Asn Ser Gln Ala Lys Thr Ile
      65              70              75

```

```

gcc acg gag tct tgt cct gcc ctg cag tgc tgt gaa gga tat aga atg      393
Ala Thr Glu Ser Cys Pro Ala Leu Gln Cys Cys Glu Gly Tyr Arg Met
      80                      85                      90
tgt gcc agt ttt gat tcc ctg cca cct tgc tgt tgc gac ata aat gag      441
Cys Ala Ser Phe Asp Ser Leu Pro Pro Cys Cys Cys Asp Ile Asn Glu
95                      100                      105                      110
ggc ctc tgagtttagga aagggtgggca caaaaatctt catgagcaat acttcttagt      497
Gly Leu
agattgtttt gttattcaaa tcaagttcta gtgtttttat gtgagattat ataatttaca      557
gtgttggttt atatactttt gaataaatgt acactattaa aaataaaaaa aaaaaaaaat      617
gccaaa                                              623

```

```

<210> 11
<211> 657
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> CDS
<222> 199..618

```

```

<220>
<221> sig_peptide
<222> 199..408
<223> Von Heijne matrix
      score 3.90
      seq FKVLTPQLSLLWG/CD

```

```

<220>
<221> polyA_signal
<222> 626..631

```

```

<220>
<221> polyA_site
<222> 643..657

```

```

<400> 11
aactggatag agtactgccc ccttcagccc atggagaaaag gcaaatgcct ccttcagagt      60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct      120
aaaataagga atgaaatggt ttccctgatat gattttttgt tttcatctga taataatttt      180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc      231
                        Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                        -70                      -65                      -60
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg      279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
                        -55                      -50                      -45
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac      327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
                        -40                      -35                      -30
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag      375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
                        -25                      -20                      -15
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct      423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
                        -10                      -5                      1                      5
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa      471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
                        10                      15                      20
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac      519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
                        25                      30                      35

```

```

cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc      567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      40      45      50
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata      615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
      55      60      65
tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa      657
Cys
70

<210> 12
<211> 1137
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 271..969

<220>
<221> sig_peptide
<222> 271..366
<223> Von Heijne matrix
      score 5.60
      seq WMGLACFRSLAAS/SP

<220>
<221> polyA_signal
<222> 1092..1097

<220>
<221> polyA_site
<222> 1123..1137

<400> 12
aaaaaccttt caagtgtccc ctccttttct taaagtcttt tataggggtc cccttcttgg      60
ccatctccat cctgtgagtc aggactgaaa gggcacagac aggtcactgc cagcattgtt      120
ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgtcccc      180
tctgaggggt acaggactta cccagtgagg aagcagctaa gcaggtctga ccagccgacc      240
tggacctggc caagggtcct gtcacccctc atg gcc acc ccg cca ttc cgg ctg      294
                                Met Ala Thr Pro Pro Phe Arg Leu
                                -30                                -25

ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc      342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
      -20      -15      -10
tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa      390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
      -5      1      5
cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa      438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
      10      15      20
att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc      486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
      25      30      35      40
cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa      534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
      45      50      55
gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa      582
Glu Glu Arg Pro Phe Trp Glu Glu Glu Lys Thr Phe Trp Lys Glu Glu
      60      65      70
aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act      630

```



```

-15          -10          -5
ttc gct gtg tat tct ctt tgg aaa acc gat gtg atc ctt gat cga aaa      326
Phe Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys
1          5          10          15
aaa aat cca gaa cct tgg gaa act gtg gac cct act gta cct caa aag      374
Lys Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys
          20          25          30
ctt ata aca atc aac caa caa tgg aaa ccc att gaa gag ttg caa aat      422
Leu Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn
          35          40          45
gtc caa agg gtg acc aaa tgacgagccc tcgcctcttt cttctgaaga      470
Val Gln Arg Val Thr Lys
50
gtactctata aatctagtgg aaacatttct gcacaaacta gattctggac accagtgtgc      530
ggaaatgctt ctgctacatt tttaggggtt gtctacattt tttgggtctt ggataaggaa      590
ttaaaggagt gcagcaataa ctgcactgtc caaaaaaaaa aaaaaa      636

<210> 14
<211> 818
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 59..703

<220>
<221> sig_peptide
<222> 59..181
<223> Von Heijne matrix
      score 6.80
      seq LVSCLSQSSALS/QS

<220>
<221> polyA_signal
<222> 783..788

<220>
<221> polyA_site
<222> 804..818

<400> 14
gacatcttga gctgaagcag ggttttgagc cactgctgct gctgctgccca ttgtcacc      58
atg gtc tca gct ctg cgg gga gca ccc ctg atc agg gtg cac tca agc      106
Met Val Ser Ala Leu Arg Gly Ala Pro Leu Ile Arg Val His Ser Ser
      -40          -35          -30
cct gtt tct tct cct tct gtg agt gga cca cgg agg ctg gtg agc tgc      154
Pro Val Ser Ser Pro Ser Val Ser Gly Pro Arg Arg Leu Val Ser Cys
      -25          -20          -15          -10
ctg tca tcc caa agc tca gct ctg agc cag agt ggt ggt ggc tcc acc      202
Leu Ser Ser Gln Ser Ser Ala Leu Ser Gln Ser Gly Gly Gly Ser Thr
          -5          1          5
tct gcc gcc ggc ata gaa gcc agg agc agg gct ctc aga agg cgg tgg      250
Ser Ala Ala Gly Ile Glu Ala Arg Ser Arg Ala Leu Arg Arg Arg Trp
          10          15          20
tgc cca gct ggg atc atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc      298
Cys Pro Ala Gly Ile Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys
          25          30          35
ctg cta ccc tcc agt gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc      346
Leu Leu Pro Ser Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala
40          45          50          55

```

```

aga gtg cta cat gac ttc ggg ctg gac gga tac cgg gga tac agc ctg      394
Arg Val Leu His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu
      60      65      70
gct gac tgg gtc tgc ctt gct tat ttc aca agc ggt ttc aac gca gct      442
Ala Asp Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala
      75      80      85
gct ttg gac tac gag gct gat ggg agc acc aac aac ggg atc ttc cag      490
Ala Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
      90      95      100
atc aac agc cgg agg tgg tgc agc aac ctc acc ccg aac gtc ccc aac      538
Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn
      105      110      115
gtg tgc cgg atg tac tgc tca gat ttg ttg aat cct aat ctc aag gat      586
Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp
      120      125      130      135
acc gtt atc tgt gcc atg aag ata acc caa gag cct cag ggt ctg ggt      634
Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly
      140      145      150
tac tgg gag gcc tgg agg cat cac tgc cag gga aaa gac ctc act gaa      682
Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys Asp Leu Thr Glu
      155      160      165
tgg gtg gat ggc tgt gac ttc taggatggac ggaacatgc acagcaggct      733
Trp Val Asp Gly Cys Asp Phe
      170
gggaaatgtg gtttggttcc tgacctaggc ttgggaagac aagccagcga ataaaggatg      793
gttgaacgtg aaaaaaaaaa aaaaa
      818

```

<210> 15
 <211> 1888
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 139..1389

 <220>
 <221> sig_peptide
 <222> 139..198
 <223> Von Heijne matrix
 score 5.00
 seq HLLAGFCVWVVLG/WV

<220>
 <221> polyA_signal
 <222> 1854..1859

<220>
 <221> polyA_site
 <222> 1873..1888

```

<400> 15
cccccccagc tggaaccaag aagggtgtgt ccccttctct ctgggtgtcc ttgtctcctg      60
ctatcagggc acagtcctca ggatgtttcg gggagaatag gagccagaac ctgagccctt      120
aagccattcc cctcacca atg atg ggg tcc cca gtg agt cat ctg ctg gcc      171
      Met Met Gly Ser Pro Val Ser His Leu Leu Ala
      -20      -15      -10
ggc ttc tgt gtg tgg gtc ttg ggc tgg gta ggg ggc tca gtc ccc      219
Gly Phe Cys Val Trp Val Val Leu Gly Trp Val Gly Gly Ser Val Pro
      -5      1      5
aac ctg ggc cct gct gag cag gag cag aac cat tac ctg gcc cag ctg      267

```

Asn	Leu	Gly	Pro	Ala	Glu	Gln	Glu	Gln	Asn	His	Tyr	Leu	Ala	Gln	Leu		
	10						15					20					
ttt	ggc	ctg	tac	ggc	gag	aat	ggg	acg	ctg	act	gca	ggg	ggc	ttg	gcg		315
Phe	Gly	Leu	Tyr	Gly	Glu	Asn	Gly	Thr	Leu	Thr	Ala	Gly	Gly	Leu	Ala		
	25					30					35						
cgg	ctt	ctc	cac	agc	ctg	ggg	cta	ggc	cga	gtt	cag	ggg	ctt	cgc	ctg		363
Arg	Leu	Leu	His	Ser	Leu	Gly	Leu	Gly	Arg	Val	Gln	Gly	Leu	Arg	Leu		
	40				45					50				55			
gga	cag	cat	ggg	cct	ctg	act	gga	cgg	gct	gca	tcc	cca	gct	gca	gac		411
Gly	Gln	His	Gly	Pro	Leu	Thr	Gly	Arg	Ala	Ala	Ser	Pro	Ala	Ala	Asp		
				60					65					70			
aat	tcc	aca	cac	agg	cca	cag	aac	cct	gag	ctg	agt	gtg	gat	gtc	tgg		459
Asn	Ser	Thr	His	Arg	Pro	Gln	Asn	Pro	Glu	Leu	Ser	Val	Asp	Val	Trp		
			75					80					85				
gca	ggg	atg	cct	ctg	ggt	ccc	tca	ggg	tgg	ggt	gac	ctg	gaa	gag	tca		507
Ala	Gly	Met	Pro	Leu	Gly	Pro	Ser	Gly	Trp	Gly	Asp	Leu	Glu	Glu	Ser		
		90				95						100					
aag	gcc	cct	cac	cta	ccc	cgt	ggg	cca	gcc	ccc	tcg	ggc	ctg	gac	ctc		555
Lys	Ala	Pro	His	Leu	Pro	Arg	Gly	Pro	Ala	Pro	Ser	Gly	Leu	Asp	Leu		
	105					110					115						
ctt	cac	agg	ctt	ctg	ttg	ctg	gac	cac	tca	ttg	gct	gac	cac	ctg	aat		603
Leu	His	Arg	Leu	Leu	Leu	Leu	Asp	His	Ser	Leu	Ala	Asp	His	Leu	Asn		
	120				125					130					135		
gag	gat	tgt	ctg	aac	ggc	tcc	cag	ctg	ctg	gtc	aat	ttt	ggc	ttg	agc		651
Glu	Asp	Cys	Leu	Asn	Gly	Ser	Gln	Leu	Leu	Val	Asn	Phe	Gly	Leu	Ser		
			140					145					150				
ccc	gct	gct	cct	ctg	acc	cct	cgt	cag	ttt	gct	ctg	ctg	tgc	cca	gcc		699
Pro	Ala	Ala	Pro	Leu	Thr	Pro	Arg	Gln	Phe	Ala	Leu	Leu	Cys	Pro	Ala		
			155				160						165				
ctg	ctt	tat	cag	atc	gac	agc	cgc	gtc	tgc	atc	ggc	gct	ccg	gcc	cct		747
Leu	Leu	Tyr	Gln	Ile	Asp	Ser	Arg	Val	Cys	Ile	Gly	Ala	Pro	Ala	Pro		
	170					175						180					
gca	ccc	cca	ggg	gat	cta	cta	tct	gcc	ctg	ctt	cag	agt	gcc	ctg	gca		795
Ala	Pro	Pro	Gly	Asp	Leu	Leu	Ser	Ala	Leu	Leu	Gln	Ser	Ala	Leu	Ala		
	185					190					195						
gtc	ctg	ttg	ctc	agc	ctc	cct	tct	ccc	cta	tcc	ctg	ctg	ctg	ctg	cgg		843
Val	Leu	Leu	Leu	Ser	Leu	Pro	Ser	Pro	Leu	Ser	Leu	Leu	Leu	Leu	Arg		
	200				205					210					215		
ctc	ctg	gga	cct	cgt	cta	cta	cgg	ccc	ttg	ctg	ggc	ttc	ctg	ggg	gcc		891
Leu	Leu	Gly	Pro	Arg	Leu	Leu	Arg	Pro	Leu	Leu	Gly	Phe	Leu	Gly	Ala		
			220						225				230				
ctg	gcg	gtg	ggc	act	ctt	tgt	ggg	gat	gca	ctg	cta	cat	ctg	cta	ccg		939
Leu	Ala	Val	Gly	Thr	Leu	Cys	Gly	Asp	Ala	Leu	Leu	His	Leu	Leu	Pro		
			235				240					245					
cat	gca	caa	gaa	ggg	cgg	cac	gca	gga	cct	ggc	gga	cta	cca	gag	aag		987
His	Ala	Gln	Glu	Gly	Arg	His	Ala	Gly	Pro	Gly	Gly	Leu	Pro	Glu	Lys		
	250					255						260					
gac	ctg	ggc	ccg	ggg	ctg	tca	gtg	ctc	gga	ggc	ctc	ttc	ctg	ctc	ttt		1035
Asp	Leu	Gly	Pro	Gly	Leu	Ser	Val	Leu	Gly	Gly	Leu	Phe	Leu	Leu	Phe		
	265					270					275						
gtg	ctg	gag	aac	atg	ctg	ggg	ctt	ttg	cgg	cac	cga	ggg	ctc	agg	cca		1083
Val	Leu	Glu	Asn	Met	Leu	Gly	Leu	Leu	Arg	His	Arg	Gly	Leu	Arg	Pro		
	280				285					290					295		
aga	tgc	tgc	agg	cga	aaa	cga	agg	aat	ctc	gaa	aca	cgc	aac	ttg	gat		1131
Arg	Cys	Cys	Arg	Arg	Lys	Arg	Arg	Asn	Leu	Glu	Thr	Arg	Asn	Leu	Asp		
			300					305					310				
ccg	gag	aat	ggc	agt	ggg	atg	gcc	ctt	cag	ccc	cta	cag	gca	gct	cca		1179
Pro	Glu	Asn	Gly	Ser	Gly	Met	Ala	Leu	Gln	Pro	Leu	Gln	Ala	Ala	Pro		
			315					320					325				
gag	cca	ggg	gct	cag	ggc	cag	agg	gag	aag	aac	agc	cag	cac	cca	cca		1227
Glu	Pro	Gly	Ala	Gln	Gly	Gln	Arg	Glu	Lys	Asn	Ser	Gln	His	Pro	Pro		

330	335	340	
gct ctg gcc cct cct ggg cac caa ggc cac agt cat ggg cac cag ggt			1275
Ala Leu Ala Pro Pro Gly His Gln Gly His Ser His Gly His Gln Gly			
345	350	355	
ggc act gat atc acg tgg atg gtc ctc ctg gga gat ggt cta cac aac			1323
Gly Thr Asp Ile Thr Trp Met Val Leu Leu Gly Asp Gly Leu His Asn			
360	365	370	375
ctc act gat ggg ctg gcc ata ggt gct gcc ttc tct gat ggc ttc tcc			1371
Leu Thr Asp Gly Leu Ala Ile Gly Ala Ala Phe Ser Asp Gly Phe Ser			
380	385	390	
gcg gcc tca gta cca cct tagcgggtctt ctgccatgag ctgccccacg			1419
Ala Ala Ser Val Pro Pro			
395			
aactgggtga ctttgccatg ctgctccagt cagggctgtc ctttcggcgg ctgctgctgc			1479
tgagcctcgt gtctggagcc ctgggattgg ggggtgcagt cctgggggtg gggctcagcc			1539
tgggccctgt cccctcact ccctgggtgt ttggggtcac tgctgggggtc ttcctctatg			1599
tggcccttgt ggacatgcta ccagccctgc ttcgtcctcc ggagcccctg cctacgcccc			1659
atgtgtcctt gcaggggctg gggctgctgc tggggggcgg cctcatgctt gccataaccc			1719
tgctggagga gcggctactg cccgtgacca ctgagggctg atggggccag tggaaagggg			1779
tcgggttgcc cttccttccc cccaaccaca ggaatggagg cgggacacag ggccagtagg			1839
agcaatagga ttttaataaa cagaacccat cccaaaaaaa aaaaaaaaaa			1888
<210> 16			
<211> 1894			
<212> DNA			
<213> Homo Sapiens			
<220>			
<221> CDS			
<222> 21..1118			
<220>			
<221> sig_peptide			
<222> 21..89			
<223> Von Heijne matrix			
score 10.80			
seq ALALLSAFSATQA/RK			
<220>			
<221> polyA_signal			
<222> 1858..1863			
<220>			
<221> polyA_site			
<222> 1879..1894			
<220>			
<221> misc_feature			
<222> 1695			
<223> n=a, g, c or t			
<400> 16			
agacgtgagc agagcagata atg gca agc atg gct gcc gtg ctc acc tgg gct			53
Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala			
-20	-15		
ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc			101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe			
-10	-5	1	
tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag			149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln			
5	10	15	20

atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc	197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser	
25 30 35	
ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg	245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg	
40 45 50	
cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccg gtg ggc	293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly	
55 60 65	
atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc	341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu	
70 75 80	
cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag	389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu	
85 90 95 100	
ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag	437
Gly Leu Arg Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln	
105 110 115	
gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg	485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly	
120 125 130	
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct	533
Glu Asp Thr Lys Ala Gln Leu Gly Gly Val Asp Glu Ala Trp Ala	
135 140 145	
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc	581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe	
150 155 160	
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg	629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly	
165 170 175 180	
cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc	677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala	
185 190 195	
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc	725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu	
200 205 210	
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac	773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp	
215 220 225	
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag	821
Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu	
230 235 240	
gaa ggg gcc ggc ccg gac ccc cag atg ctc tcc gag gag gtg cgc cag	869
Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln	
245 250 255 260	
cga ctt cag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc	917
Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe	
265 270 275	
act cgc gcc atc gac cag gag act gag gag gtc cag cag cag ctg gcg	965
Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala	
280 285 290	
cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca	1013
Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr	
295 300 305	
gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg	1061
Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu	
310 315 320	
tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg	1109
Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu	
325 330 335 340	
ggg gac ccc tgaggatcta cctgcccagg cccattccca gctccttgctc	1158

Gly Asp Pro
 tgggggagcct tggctctgag cctctagcat ggttcagtc ttgaaagtgg cctggtgggt 1218
 ggaggggtgga aggtcctgtg caggacaggg aggccaccaa aggggctgct gtctcctgca 1278
 tatccagcct cctgcgactc cccaatctgg atgcattaca ttcaccaggc ttgcaaacc 1338
 cagcctccca gtgtcattt gggaatgctc atgagttact ccattcaagg gtgagggagt 1398
 agggagggag aggcaccatg catgtgggtg attatctgca agcctgtttg ccgtgatgct 1458
 ggaagcctgt gccactacat cctggagttt ggctctagtc acttctggct gcctgggtggc 1518
 cactgctaca gctggtccac agagaggagc acttgtctcc ccagggtgct catggcagct 1578
 atcaggggaa tagaaggag aaagagaata tcatggggag aacatgtgat ggtgtgtgaa 1638
 tatccctgct ggctctgatg ctgggtgggt cgaaggtgt gggctgtgat aggaganggc 1698
 agagcccatg tttcctgaca tagctctaca cctaaataag ggactgaacc ctcccaactg 1758
 tgggagctcc ttaaaccctc tggggagcat actgtgtgct ctccccatct ccagcccctc 1818
 cctctgggtt cccaagttga agcctagact tctggctcaa atgaaataga tgtttatgat 1878
 aaaaaaaaa aaaaaa 1894

<210> 17
 <211> 1913
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 143..592

<220>
 <221> sig_peptide
 <222> 143..277
 <223> Von Heijne matrix
 score 5.90
 seq VLVDLAILGQAYA/FA

<220>
 <221> polyA_signal
 <222> 1877..1882

<220>
 <221> polyA_site
 <222> 1899..1913

<400> 17
 atttttttgt gcctaagatg cccagtgcgt tgctgggttt ttctgctgtc ctggggctct 60
 ggacatgagg ccagaccttg tgaccttgtt ggcagtgggc agtggttga tgtgaggtcc 120
 cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
 Met Val Leu Met Trp Thr Ser Gly Asp Ala
 -45 -40
 ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220
 Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
 -35 -30 -25 -20
 gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268
 Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
 -15 -10 -5
 gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca 316
 Ala Tyr Ala Phe Ala Pro Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala
 1 5 10
 ccc cac tgg cac caa ggc cct ctg aca gtg ggg agg acg agg atg tgg 364
 Pro His Trp His Gln Gly Pro Leu Thr Val Gly Arg Thr Arg Met Trp
 15 20 25
 gac cgc cag ccg cgg gca ctg gtg ggc cct gac ctc ccc gcg ggg agg 412
 Asp Arg Gln Pro Arg Ala Leu Val Gly Pro Asp Leu Pro Ala Gly Arg
 30 35 40 45
 gtg ggt gcc gtg gcc cct gca ggt gtg gca gag atg ggg cac ggg cat 460

09578360.101501

Val	Gly	Ala	Val	Ala	Pro	Ala	Gly	Val	Ala	Glu	Met	Gly	His	Gly	His	
			50						55					60		
tgg	ggt	ctc	cat	cag	cct	ctg	tgg	ggt	gtc	tca	ggg	tgg	gca	gtg	ggg	508
Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly	
		65						70					75			
gtg	ggg	ctg	gga	cgc	tgt	ttg	tgc	tca	gcg	ggg	aca	gcc	agg	gtt	gat	556
Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp	
		80					85					90				
ctg	gcc	ccg	agg	gtt	ttg	gat	gtt	ttt	agg	atg	aca	taaaaagcaa				602
Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr					
	95						100				105					
gtgtttttccc	catttccctct	tatgaaacac	cgtctgagcc	caaggtacac	attgggcggc											662
ctgcaggaac	ctgctccagg	tggacacacg	ggccagcagc	cgcgaaacctt	gaagctgggg											722
tgaccgcagg	agaccctgta	aggcctgtga	gcggagccct	cgaccccgtg	acaccctggc											782
cagacaccct	gcttggactg	gggtggcctc	tgctaccag	gggtctggca	cgggggaggg											842
ctggggcttt	ctctgcctgg	tacacacgga	aaggcggctg	tgcgagcgc	gggtcaccgt											902
gctccgggtt	ttctgacagt	cggtgtttcc	tgggcctttg	gagtggctgc	gaggcctgaa											962
cgcttctgtg	atccgctgtg	tccagcccgg	ctgagcatcg	ccagggctag	ctcatgctgc											1022
tcttgtcagc	ctctggttct	cctcgagtcc	ttggggacgt	ggcagatgcc	agcgaccatc											1082
agacaacgtg	gaggccctca	tgggcaatgg	ctgagggggc	cgggctgagg	ctgtgcacat											1142
gcagtctgca	cgccactcct	gggctctgct	ggcggagatc	cccttctctc	tgggtgcaga											1202
ctgcacctcc	ggatgcagtt	ttgatgtcca	tcttccagga	gagagacggt	ctcgggtcca											1262
gggagtgagg	ggggctgccc	ctgccgtgca	ggtcctggcc	gatggcgctt	taccctgctg											1322
ccctgggctt	ttggcctgaa	gcaaattcct	gagtgggggg	tactggggcc	tgccgcctcc											1382
tgtctgtgct	actgcccacc	cccgtgtgct	ggctccctca	cttctggctg	cagtgggagc											1442
cgccagtctg	acccttgtca	cgcacgctc	tgccccacc	ccgttgcaag	aggtcacacc											1502
atgtcagcag	ccttgcactg	accgcagccg	gccccaggc	ctcagagttc	tggatgcttc											1562
cgtgcggctc	caacaggcat	cgtcttccct	tccgcagggtg	gaggggcccgc	ttcccgcagg											1622
catctgagct	ctgtgccggg	gccgtggcca	tgggaagatg	ttccacgctg	cctcctcctc											1682
gagtttttcc	cggaacact	cttgaatgtc	tgagtggagg	tcttgcttag	ctctttggcc											1742
tgtgagatgc	tttgaaaatt	tttatttttt	taagatgaag	caagatgtct	gtagcggtaa											1802
ttgcctcaca	ttaaactgtc	gccgactgca	ggcgcagtga	ctgctgaatg	taccctgtgt											1862
ggcgacttgg	aatcaataaa	ccatttgtgg	atcctaataaa	aaaaaaaaaa	a											1913

```

<210> 18
<211> 1744
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 76..999

<220>
<221> sig_peptide
<222> 76..279
<223> Von Heijne matrix
      score 5.10
      seq LSLPVCTVSLVSS/VS

<220>
<221> polyA_signal
<222> 1711..1716

<220>
<221> polyA_site
<222> 1729..1744

<220>
<221> misc_feature
<222> 336

```

<223> n=a, g, c or t

<400> 18

```
aagttgagggc caccctgggtg gcaccaaagc cctctcaggc aggcagaccc agggcctccc      60
cgccacacct tgttc atg gat ttt gtc gct gga gcc atc gga ggc gtc tgc      111
          Met Asp Phe Val Ala Gly Ala Ile Gly Gly Val Cys
                    -65                                -60
ggt gtt gct gtg ggc tac ccc ctg gac acg gtg aag gtc agg atc cag      159
Gly Val Ala Val Gly Tyr Pro Leu Asp Thr Val Lys Val Arg Ile Gln
          -55                                -50                                -45
acg gag cca aag tac aca ggc atc tgg cac tgc gtc cgg gat acg tat      207
Thr Glu Pro Lys Tyr Thr Gly Ile Trp His Cys Val Arg Asp Thr Tyr
          -40                                -35                                -30                                -25
cac cga gag cgc gtg tgg ggc ttc tac cgg ggc ctc tcg ctg ccc gtg      255
His Arg Glu Arg Val Trp Gly Phe Tyr Arg Gly Leu Ser Leu Pro Val
                    -20                                -15                                -10
tgc acg gtg tcc ctg gta tct tcc gtg tct ttt ggc acc tac cgc cac      303
Cys Thr Val Ser Leu Val Ser Ser Val Ser Phe Gly Thr Tyr Arg His
                    -5                                1                                5
tgc ctg gcg cac atc tgc cgg ctc cgg tac ggn aac cct gac gcc aag      351
Cys Leu Ala His Ile Cys Arg Leu Arg Tyr Gly Asn Pro Asp Ala Lys
          10                                15                                20
ccc acc aag gcc gac atc acg ctc tcg gga tgc gcc tcc ggc ctc gtc      399
Pro Thr Lys Ala Asp Ile Thr Leu Ser Gly Cys Ala Ser Gly Leu Val
          25                                30                                35                                40
cgc gtg ttc ctg acg tcg ccc act gag gtg gcc aaa gtc cgc ttg cag      447
Arg Val Phe Leu Thr Ser Pro Thr Glu Val Ala Lys Val Arg Leu Gln
                    45                                50                                55
acg cag aca cag gcg cag aag cag cag cgg ctg ctt tcg gcc tcg ggg      495
Thr Gln Thr Gln Ala Gln Lys Gln Gln Arg Leu Leu Ser Ala Ser Gly
                    60                                65                                70
ccg ttg gct gtg ccc ccc atg tgt cct gtg ccc cca gcc tgc cca gag      543
Pro Leu Ala Val Pro Pro Met Cys Pro Val Pro Pro Ala Cys Pro Glu
                    75                                80                                85
ccc aag tac cgc ggg cca ctg cac tgc ctg gcc acg gta gcc cgt gag      591
Pro Lys Tyr Arg Gly Pro Leu His Cys Leu Ala Thr Val Ala Arg Glu
          90                                95                                100
gag ggg ctg tgc ggc ctc tac aag ggc agc tcg gcc ctg gtc tta cgg      639
Glu Gly Leu Cys Gly Leu Tyr Lys Gly Ser Ser Ala Leu Val Leu Arg
          105                                110                                115
gac ggc cac tcc ttt gcc acc tac ttc ctt tcc tac gcg gtc ctc tgc      687
Asp Gly His Ser Phe Ala Thr Tyr Phe Leu Ser Tyr Ala Val Leu Cys
                    125                                130                                135
gag tgg ctc agc ccc gct ggc cac agc cgg cca gat gtc ccg ggc gtg      735
Glu Trp Leu Ser Pro Ala Gly His Ser Arg Pro Asp Val Pro Gly Val
                    140                                145                                150
ctg gtg gcc ggg ggc tgt gca gga gtc ctg gcc tgg gct gtg gcc acc      783
Leu Val Ala Gly Gly Cys Ala Gly Val Leu Ala Trp Ala Val Ala Thr
                    155                                160                                165
ccc atg gac gtg atc aag tcg aga ctg cag gca gac ggg cag ggc cag      831
Pro Met Asp Val Ile Lys Ser Arg Leu Gln Ala Asp Gly Gln Gly Gln
          170                                175                                180
agg cgc tac cgg ggt ctc ctg cac tgt atg gtg acc agc gtt cga gag      879
Arg Arg Tyr Arg Gly Leu Leu His Cys Met Val Thr Ser Val Arg Glu
          185                                190                                195                                200
gag gga ccc cgg gtc ctt ttc aag ggg ctg gta ctc aat tgc tgc cgc      927
Glu Gly Pro Arg Val Leu Phe Lys Gly Leu Val Leu Asn Cys Cys Arg
                    205                                210                                215
gcc ttc cct gtc aac atg gtg gtc ttc gtc gcc tat gag gca gtg ctg      975
Ala Phe Pro Val Asn Met Val Val Phe Val Ala Tyr Glu Ala Val Leu
                    220                                225                                230
```

09978360 "101501

```

agg ctc gcc cgg ggt ctg ctc aca tagccggtcc ccacgcccag cggcccaccc 1029
Arg Leu Ala Arg Gly Leu Leu Thr
      235      240
accagcagct gctggaggctc gtagtggctg gaggaggcaa ggggtagtgt ggctggggttc 1089
gggaccccac agggccattg cccaggagaa tgaggagcct ccctgcagtg ttgtcggccg 1149
aggcctaagc tcgccctgcc cagctactga cctcaggtcg aggggcccgc cagccatcag 1209
ccagggttg cctagggttg caggagccag ggaggagtgg gcctctttga tgagagcggt 1269
gagttgcatg gagtcgggtg ttcattcccag cctccccatg gccctcgccct cccatgtctt 1329
tgaagcacc ctcaggaggag tcaggtgtgt gctcagccac cctctgcccc attcctagac 1389
cctcaccccc accactgttc ctgtgtcttc atgagctgtc ccttacaggc aggggcttcc 1449
cacaggctgg gggcctcggg gcggggagca tgagctgggc tggcaccacg actgagggct 1509
cccggccccg cttcttcccc acagcaggct gctcagaggg ggtgctgccg ggactgccat 1569
gcccacctga gaggggcctg ggggtggcct cctcggcccg ttaggggaatt tggggtgagg 1629
ttcctcagga gccctcactc tgccctgtgga cgctgcacct gccacttaaa gaccccaaag 1689
actctgttgg gaactgttgt caataaaatg tttctgagga aaaaaaaaaa aaaaa 1744

```

```

<210> 19
<211> 946
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> CDS
<222> 123..464

<220>
<221> sig_peptide
<222> 123..269
<223> Von Heijne matrix
      score 4.90
      seq PSLAAGLLFGSLA/GL

```

```

<220>
<221> polyA_signal
<222> 908..913

```

```

<220>
<221> polyA_site
<222> 931..946

```

```

<400> 19
aaatcgcggt tccggagaga cctggctgct gtgtcccgcg gcttgcgctc cgtagtggac 60
tccgcggggc ttcggcagat gcaggcctgg ggtagtctcc tttctggact gagaagagaa 120
ga atg gag aag ccc ctc ttc cca tta gtg cct ttg cat tgg ttt ggc 167
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
      -45      -40      -35
ttt ggc tac aca gca ctg gtt gtt tct ggt ggg atc gtt ggc tat gta 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
      -30      -25      -20
aaa aca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttc ggc agt 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
      -15      -10      -5
cta gcc ggc ctg ggt gct tac cag ctg tat cag gat cca agg aac gtt 311
Leu Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
      1      5      10
tgg ggt ttc cta gcc gct aca tct gtt act ttt gtt ggt gtt atg gga 359
Trp Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly
15      20      25      30
atg aga tcc tac tac tat gga aaa ttc atg cct gta ggt tta att gca 407
Met Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala
      35      40      45

```

ggt gcc agt ttg ctg atg gcc gcc aaa gtt gga gtt cgt atg ttg atg 455
 Gly Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met
 50 55 60
 aca tct gat tagcagaagt catgttccag cttggactca tgaaggatta 504
 Thr Ser Asp
 65
 aaaatctgca tcttccacta ttttcaatgt attaagagaa ataagtgcag cattttttgca 564
 tctgacattt tacctaaaaa aaaaaagaca ccaaatttgg cggaggggtg gaaaatcagt 624
 tgttaccatt ataaccctac agaggtggtg agcatgtaac atgagcttat tgagaccatc 684
 atagagatcg attcttgtat attgatttta tctctttctg tatctatagg taaatctcaa 744
 gggtaaaatg ttaggtgttg acattgagaa ccctgaaacc ccattccctg ctcagaggaa 804
 cagtgtgaaa aaaaatctct tgagagattt agaatatctt ttcttttgct catcttagac 864
 cacagactga ctttgaaatt atgttaagtg aaatatcaat gaaaataaag tttactataa 924
 ataattaaaa aaaaaaaaaa aa 946

<210> 20
 <211> 1622
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 85..1230

<220>
 <221> sig_peptide
 <222> 85..129
 <223> Von Heijne matrix
 score 10.10
 seq LLLPLALCILVLC/CG

<220>
 <221> polyA_signal
 <222> 1589..1594

<220>
 <221> polyA_site
 <222> 1607..1622

<400> 20
 aaagtctgcc ttaaagagcc ttacaagcca gccagtcctt gcagctccac aaactgaccc 60
 atcctggggc ttgttctcca caga atg ggt ctg ctc ctt ccc ctg gca ctc 111
 Met Gly Leu Leu Leu Pro Leu Ala Leu
 -15 -10
 tgc atc cta gtc ctg tgc tgc gga gca atg tct cca ccc cag ctg gcc 159
 Cys Ile Leu Val Leu Cys Cys Gly Ala Met Ser Pro Pro Gln Leu Ala
 -5 1 5 10
 ctc aac ccc tcg gct ctg ctc tcc cgg ggc tgc aat gac tca gat gtg 207
 Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp Ser Asp Val
 15 20 25
 ctg gca gtt gca ggc ttt gcc ctg cgg gat att aac aaa gac aga aag 255
 Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys Asp Arg Lys
 30 35 40
 gat ggc tat gtg ctg aga ctc aac cga gtg aac gac gcc cag gaa tac 303
 Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala Gln Glu Tyr
 45 50 55
 aga cgg ggt ggc ctg gga tct ctg ttc tat ctt aca ctg gat gtg cta 351
 Arg Arg Gly Gly Leu Gly Ser Leu Phe Tyr Leu Thr Leu Asp Val Leu
 60 65 70
 gag act gac tgc cat gtg ctc aga aag aag gca tgg caa gac tgt gga 399
 Glu Thr Asp Cys His Val Leu Arg Lys Lys Ala Trp Gln Asp Cys Gly

75	80	85	90	
atg agg ata ttt ttt gaa tca gtt tat ggt caa tgc aaa gca ata ttt				447
Met Arg Ile Phe Phe Glu Ser Val Tyr Gly Gln Cys Lys Ala Ile Phe				
	95	100	105	
tat atg aac aac cca agt aga gtt ctc tat tta gct gct tat aac tgt				495
Tyr Met Asn Asn Pro Ser Arg Val Leu Tyr Leu Ala Ala Tyr Asn Cys				
	110	115	120	
act ctt cgc cca gtt tca aaa aaa aag att tac atg acg tgc cct gac				543
Thr Leu Arg Pro Val Ser Lys Lys Lys Ile Tyr Met Thr Cys Pro Asp				
	125	130	135	
tgc cca agc tcc ata ccc act gac tct tcc aat cac caa gtg ctg gag				591
Cys Pro Ser Ser Ile Pro Thr Asp Ser Ser Asn His Gln Val Leu Glu				
	140	145	150	
gct gcc acc gag tct ctt gcg aaa tac aac aat gag aac aca tcc aag				639
Ala Ala Thr Glu Ser Leu Ala Lys Tyr Asn Asn Glu Asn Thr Ser Lys				
	155	160	165	170
cag tat tct ctc ttc aaa gtc acc agg gct tct agc cag tgg gtg gtc				687
Gln Tyr Ser Leu Phe Lys Val Thr Arg Ala Ser Ser Gln Trp Val Val				
	175	180	185	
ggc cct tct tac ttt gtg gaa tac tta att aaa gaa tca cca tgt act				735
Gly Pro Ser Tyr Phe Val Glu Tyr Leu Ile Lys Glu Ser Pro Cys Thr				
	190	195	200	
aaa tcc cag gcc agc agc tgt tca ctt cag tcc tcc gac tct gtg cct				783
Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp Ser Val Pro				
	205	210	215	
gtt ggt ctt tgc aaa ggt tct ctg act cga aca cac tgg gaa aag ttt				831
Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp Glu Lys Phe				
	220	225	230	
gtc tct gtg act tgt gac ttc ttt gaa tca cag gct cca gcc act gga				879
Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro Ala Thr Gly				
	235	240	245	250
agt gaa aac tct gct gtt aac cag aaa cct aca aac ctt ccc aag gtg				927
Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu Pro Lys Val				
	255	260	265	
gaa gaa tcc cag cag aaa aac acc ccc cca aca gac tcc ccc tcc aaa				975
Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser Pro Ser Lys				
	270	275	280	
gct ggg cca aga gga tct gtc caa tat ctt cct gac ttg gat gat aaa				1023
Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu Asp Asp Lys				
	285	290	295	
aat tcc cag gaa aag ggc cct cag gag gcc ttt cct gtg cat ctg gac				1071
Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val His Leu Asp				
	300	305	310	
cta acc acg aat ccc cag gga gaa acc ctg gat att tcc ttc ctc ttc				1119
Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser Phe Leu Phe				
	315	320	325	330
ctg gag cct atg gag gag aag ctg gtg gtc ctg cct ttc ccc aaa gaa				1167
Leu Glu Pro Met Glu Glu Lys Leu Val Leu Pro Phe Pro Lys Glu				
	335	340	345	
aaa gca cgc act gct gag tgc cca ggg cca gcc cag aat gcc agc cct				1215
Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn Ala Ser Pro				
	350	355	360	
ctt gtc ctt ccg cca tgagaatcac acagagtctt ctgtaggggt atgggtgcgc				1270
Leu Val Leu Pro Pro				
	365			
gcatgacatg ggaggcgatg gggacgatgg acagagacag agcgtgcaca cgtagagtgg				1330
ctagtgaagg acgcctttttt gactcttctt ggtctcagca tgttgactgg gattggaaat				1390
aatgagactg agccctcggc ttgggctgca ctctaccctg tacactgcct tgtaccctga				1450
gctgcatcac ctccataaact gagcagtctc ataccatgga gagatgcctc tcttatgtct				1510
tcagccactc acttataaag atacttatct ttccagcagt atatatgtgc tgaaatctca				1570
gcatgaaagc attgcatgag taaagatact ttccctaaaa aaaaaaaaaa aa				1622

<210> 21
 <211> 715
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 29..664

<220>
 <221> sig_peptide
 <222> 29..619
 <223> Von Heijne matrix
 score 4.80
 seq SFFGASFLMGS LG/GM

<220>
 <221> polyA_signal
 <222> 657..662

<220>
 <221> polyA_site
 <222> 699..715

<220>
 <221> misc_feature
 <222> 295,357
 <223> n=a, g, c or t

<220>
 <221> unsure
 <222> -88
 <223> Xaa = Ala,Asp,Gly,Val

<220>
 <221> unsure
 <222> -109
 <223> Xaa = Asp,Glu

<400> 21
 cttttcctgc ctctgattcc gggctgtc atg gcg acc ccc aac aat ctg acc 52
 Met Ala Thr Pro Asn Asn Leu Thr
 -195 -190
 ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg 100
 Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala
 -185 -180 -175
 gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc 148
 Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala
 -170 -165 -160
 cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc 196
 His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe
 -155 -150 -145
 agc tcg cag aag gcc aag atc ttg gag cat gat gat gtg agc tac ctg 244
 Ser Ser Gln Lys Ala Lys Ile Leu Glu His Asp Asp Val Ser Tyr Leu
 -140 -135 -130
 aag aag atc ctc ggg gaa ctg gcc atg gtg ctg gac cag att gag gcg 292
 Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln Ile Glu Ala
 -125 -120 -115 -110
 gan ctg gag aag agg aag ctg gag aac gag ggg cag aaa tgc gag ctg 340
 Xaa Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu

0998360-101601

	-105	-100	-95	
tgg ctc tgt ggc tgt gnc ttc acc ctc gct gat gtc ctc ctg gga gcc				388
Trp Leu Cys Gly Cys Xaa Phe Thr Leu Ala Asp Val Leu Leu Gly Ala				
	-90	-85	-80	
acc ctg cac cgc ctc aag ttc ctg gga ctg tcc aag aaa tac tgg gaa				436
Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu				
	-75	-70	-65	
gat ggc agc cgg ccc aac ctg cag tcc ttc ttt gag agg gtc cag aga				484
Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg Val Gln Arg				
	-60	-55	-50	
cgc ttt gcc ttc cgg aaa gtc ctg ggt gac atc cac acc acc ctg ctg				532
Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr Thr Leu Leu				
	-45	-40	-35	-30
tcg gcc gtc atc ccc aat gct ttc cgg ctg gtc aag agg aaa ccc cca				580
Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg Lys Pro Pro				
	-25	-20	-15	
tcc ttc ttc ggg gcg tcc ttc ctc atg ggc tcc ctg ggt ggg atg ggc				628
Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly Gly Met Gly				
	-10	-5	1	
tac ttt gcc tac tgg tac ctc aag aaa aaa tac atc tagggccagg				674
Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile				
	5	10	15	
cctggggcctt ggtgtctgac tgccaaaaaa aaaaaaaaaa a				715

<210> 22
 <211> 1549
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 18..878

<220>
 <221> sig_peptide
 <222> 18..95
 <223> Von Heijne matrix
 score 6.30
 seq GVGLVTLGLAVG/SY

<220>
 <221> polyA_signal
 <222> 1500..1505

<220>
 <221> polyA_site
 <222> 1533..1549

<220>
 <221> misc_feature
 <222> 944
 <223> n=a, g, c or t

<400> 22	
ggaaaaaggcg ctccgctc atg ggg atc cag acg agc ccc gtc ctg ctg gcc	50
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala	
	-25
tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc	98
Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser	
	-15
tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc	146

Tyr	Leu	Val	Arg	Arg	Ser	Arg	Arg	Pro	Gln	Val	Thr	Leu	Leu	Asp	Pro	
			5					10					15			
aat	gaa	aag	tac	ctg	cta	cga	ctg	cta	gac	aag	acg	ctc	tct	gca	cgg	194
Asn	Glu	Lys	Tyr	Leu	Leu	Arg	Leu	Leu	Asp	Lys	Thr	Leu	Ser	Ala	Arg	
		20					25					30				
tcc	cca	ggc	aaa	cat	atc	tac	ctc	tcc	acc	cga	att	gat	ggc	agc	ctg	242
Ser	Pro	Gly	Lys	His	Ile	Tyr	Leu	Ser	Thr	Arg	Ile	Asp	Gly	Ser	Leu	
		35				40					45					
gtc	atc	agg	cca	tac	act	cct	gtc	acc	agt	gat	gag	gat	caa	ggc	tat	290
Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr	
50					55					60					65	
gtg	gat	ctt	gtc	atc	aag	gtc	tac	ctg	aag	ggg	gtg	cac	ccc	aaa	ttt	338
Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe	
				70					75					80		
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	ggt	ggg	386
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly	
			85					90					95			
gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga	434
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly	
		100					105						110			
aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc	482
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro	
		115				120					125					
cga	gtg	gcg	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	atc	acc	530
Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr	
					135					140					145	
cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca	578
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro	
				150					155						160	
acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc	626
Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile	
			165					170					175			
ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	cgc	ttt	674
Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe	
		180					185					190				
aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc	722
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser	
		195				200					205					
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac</					

<210> 23
 <211> 1328
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 73..1008

<220>
 <221> sig_peptide
 <222> 73..147
 <223> Von Heijne matrix
 score 14.10
 seq LTL L L L L L T L L A F A / G Y

<220>
 <221> polyA_signal
 <222> 1286..1291

<220>
 <221> polyA_site
 <222> 1312..1328

<400> 23
 actgcgcgga tcggcggtccg cagcggggcgg ctgctgagct gccttgaggt gcagtgttgg 60
 ggatccagag cc atg tcg gac ctg cta cta ctg ggc ctg att ggg ggc ctg 111
 Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
 -25 -20 -15
 act ctc tta ctg ctg ctg acg ctg cta gcc ttt gcc ggg tac tca ggg 159
 Thr Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
 -10 -5 1
 cta ctg gct ggg gtg gaa gtg agt gct ggg tca ccc ccc atc cgc aac 207
 Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 5 10 15 20
 gtc act gtg gcc tac aag ttc cac atg ggg ctc tat ggt gag act ggg 255
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
 25 30 35
 cgg ctt ttc act gag agc tgc atc tct ccc aag ctc cgc tcc atc gct 303
 Arg Leu Phe Thr Glu Ser Cys Ile Ser Pro Lys Leu Arg Ser Ile Ala
 40 45 50
 gtc tac tat gac aac ccc cac atg gtg ccc cct gat aag tgc cga tgt 351
 Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys
 55 60 65
 gcc gtg ggc agc atc ctg agt gaa ggt gag gaa tcg ccc tcc cct gag 399
 Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu Ser Pro Ser Pro Glu
 70 75 80
 ctc atc gac ctc tac cag aaa ttt ggc ttc aag gtg ttc tcc ttc ccg 447
 Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe Lys Val Phe Ser Phe Pro
 85 90 95 100
 gca ccc agc cat gtg gtg aca gcc acc ttc ccc tac acc acc att ctg 495
 Ala Pro Ser His Val Val Thr Ala Thr Phe Pro Tyr Thr Thr Ile Leu
 105 110 115
 tcc atc tgg ctg gct acc cgc cgt gtc cat cct gcc ttg gac acc tac 543
 Ser Ile Trp Leu Ala Thr Arg Arg Val His Pro Ala Leu Asp Thr Tyr
 120 125 130
 atc aag gag cgg aag ctg tgt gcc tat cct cgg ctg gag atc tac cag 591
 Ile Lys Glu Arg Lys Leu Cys Ala Tyr Pro Arg Leu Glu Ile Tyr Gln
 135 140 145
 gaa gac cag atc cat ttc atg tgc cca ctg gca cgg cag gga gac ttc 639

FASTA "09EB2660"

Glu Asp Gln Ile His Phe Met Cys Pro Leu Ala Arg Gln Gly Asp Phe	
150 155 160	
tat gtg cct gag atg aag gag aca gag tgg aaa tgg cgg ggg ctt gtg	687
Tyr Val Pro Glu Met Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val	
165 170 175 180	
gag gcc att gac acc cag gtg gat ggc aca gga gct gac aca atg agt	735
Glu Ala Ile Asp Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser	
185 190 195	
gac acg agt tct gta agc ttg gaa gtg agc cct ggc agc cgg gag act	783
Asp Thr Ser Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr	
200 205 210	
tca gct gcc aca ctg tca cct ggg gcg agc agc cgt ggc tgg gat gac	831
Ser Ala Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp	
215 220 225	
ggg gac acc cgc agc gag cac agc tac agc gag tca ggt gcc agc ggc	879
Gly Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly	
230 235 240	
tcc tct ttt gag gag ctg gac ttg gag ggc gag ggg ccc tta ggg gag	927
Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly Glu	
245 250 255 260	
tca cgg ctg gac cct ggg act gag ccc ctg ggg act acc aag tgg ctc	975
Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys Trp Leu	
265 270 275	
tgg gag ccc act gcc cct gag aag ggc aag gag taacccatgg cctgcaccct	1028
Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu	
280 285	
cctgcagtgc agttgctgag gaactgagca gactctccag cagactctcc agccctcttc	1088
ctccttctctc tggggggagga ggggttctctg agggacctga cttcccctgc tccaggcctc	1148
ttgctaagcc ttctcctcac tgcccttttag gctcccaggg ccagaggagc cagggactat	1208
tttctgcacc agcccccagg gctgccaccc ctgttgtgtc tttttttcag actcacagtg	1268
gagcttccag gaccacagaat aaagccaatg atttacttgt ttcaaaaaaa aaaaaaaaaa	1328
<210> 24	
<211> 1515	
<212> DNA	
<213> Homo Sapiens	
<220>	
<221> CDS	
<222> 165..842	
<220>	
<221> sig_peptide	
<222> 165..251	
<223> Von Heijne matrix	
score 7.00	
seq LASFAALVLVCRQ/RV	
<220>	
<221> polyA_signal	
<222> 1474..1479	
<220>	
<221> polyA_site	
<222> 1500..1515	
<400> 24	
agtcgcggga tgcgcccggg agccacagcc tgaggccctc aggtctctgc aggtgtcgtg	60
gaggaacctg gcacctgcca tctcttctcc caatttgcca cttccagcag ctttagccca	120
tgaggaggat gtgaccggga ctgagtcagg agccctctgg aagc atg gag act gtg	176
Met Glu Thr Val	

gtg Val -25	att Ile	gtt Val	gcc Ala	ata Ile	ggt Gly -20	gtg Val	ctg Leu	gcc Ala	acc Thr	atc Ile -15	ttt Phe	ctg Leu	gct Ala	tcg Ser	ttt Phe -10	224	
gca Ala	gcc Ala	ttg Leu	gtg Val	ctg Leu -5	gtt Val	tgc Cys	agg Arg	cag Gln	cgc Arg	tac Tyr	tgc Cys	cgg Arg	ccg Pro	cga Arg	gac Asp	272	
ctg Leu	ctg Leu	cag Gln	cgc Arg	tat Tyr	gat Asp	tct Ser	aag Lys	ccc Pro	att Ile	gtg Val	gac Asp	ctc Leu	att Ile	ggt Gly	gcc Ala	320	
atg Met	gag Glu	acc Thr	cag Gln	tct Ser	gag Glu	ccc Pro	tct Ser	gag Glu	tta Leu	gaa Glu	ctg Leu	gac Asp	gat Asp	gtc Val	gtt Val	368	
atc Ile 40	acc Thr	aac Asn	ccc Pro	cac His	att Ile 45	gag Glu	gcc Ala	att Ile	ctg Leu	gag Glu	aat Asn	gaa Glu	gac Asp	tgg Trp	atc Ile 55	416	
gaa Glu	gat Asp	gcc Ala	tcg Ser	ggt Gly 60	ctc Leu	atg Met	tcc Ser	cac His	tgc Cys	att Ile	gcc Ala	atc Ile	ttg Leu	aag Lys	att Ile	464	
tgt Cys	cac His	act Thr	ctg Leu	aca Thr	gag Glu	aag Lys	ctt Leu	gtt Val	gcc Ala	atg Met	aca Thr	atg Met	ggc Gly	tct Ser	ggg Gly	512	
gcc Ala	aag Lys	atg Met	aag Lys	act Thr	tca Ser	gcc Ala	agt Ser	gtc Val	agc Ser	gac Asp	atc Ile	att Ile	gtg Val	gtg Val	gcc Ala	560	
aag Lys	cgg Arg	atc Ile	agc Ser	ccc Pro	agg Arg	gtg Val	gat Asp	gat Asp	gtt Val	gtg Val	aag Lys	tcg Ser	atg Met	tac Tyr	cct Pro	608	
ccg Pro	ttg Leu	gac Asp	ccc Pro	aaa Lys	ctc Leu	ctg Leu	gac Asp	gca Ala	cgg Arg	acg Thr	act Thr	gcc Ala	ctg Leu	ctc Leu	ctg Leu	656	
tct Ser	gtc Val	agt Ser	cac His	ctg Leu	gtg Val	ctg Leu	gtg Val	aca Thr	agg Arg	aat Asn	gcc Ala	tgc Cys	cat His	ctg Leu	acg Thr	704	
gga Gly	ggc Gly	ctg Leu	gac Asp	tgg Trp	att Ile	gac Asp	cag Gln	tct Ser	ctg Leu	tcg Ser	gct Ala	gct Ala	gag Glu	gag Glu	cat His	752	
ttg Leu	gaa Glu	gtc Val	ctt Leu	cga Arg	gaa Glu	gca Ala	gcc Ala	cta Leu	gct Ala	tct Ser	gag Glu	cca Pro	gat Asp	aaa Lys	ggc Gly	800	
ctc Leu	cca Pro	ggc Gly	cct Pro	gaa Glu	ggc Gly	ttc Phe	ctg Leu	cag Gln	gag Glu	cag Gln	tct Ser	gca Ala	att Ile			842	
tagtgcctac	gcttagcctt	gtgtgtgcat	gtgtggctggt	agaggagtat	aaaattgagc	tctctcgatc	attgaaacta	ttcattttatt	aggtttgggt	tgcaattttta	aaaaaaaaa	aggccagcag	ctagccatga	aggcccctgc	cgccatccct	ggatggctca	902
gcttagcctt	ctacttttct	ctatatagatt	agttgtttctc	cacggtctgga	gagttcagct	gtgtgtgcat	agtaaacgag	gagatccccg	tcaagtttatg	cctctttttgc	agttgcaaac	1022					
gtgtgtgcat	agtaaacgag	gagatccccg	tcaagtttatg	cctctttttgc	agttgcaaac	1082											
gtgtggctggt	gagtggcagt	ctaatactac	agttaggggga	gatgccattc	actctctgca	1142											
agaggagtat	tgaaaactgg	tggactgtca	gctttatttta	gctcacctag	tgttttcaag	1202											
aaaattgagc	caccgtctaa	gaaatcaaga	ggtttcacat	taaaattaga	atctctggcc	1262											
tctctcgatc	ggtcagaatg	tgttgcaaat	ctgatctgca	ttttcagaag	aggacaatca	1322											
attgaaacta	agtagggggt	tcttctttttg	gcaagacttg	tactctctca	cctggcctgt	1382											
ttcattttatt	tgtattatct	gcctgggtccc	tgaggcgctct	gggtctctctc	tctcccttgc	1442											
aggtttgggt	tctgaagctga	ggaactacaa	agttgatgat	ttcttttttta	tcttttatgcc	1502											
tgcaattttta	cctagctacc	actaggtgga	tagtaaaattt	atacttatgt	ttcccccaaa	1511											

<210> 25

<211> 1622

<212> DNA

<213> Homo Sapiens

 $\langle 220 \rangle$

<221> CDS
<222> 31..1248

<220>
<221> sig_peptide
<222> 31..135
<223> Von Heijne matrix
score 6.30
seq TLLLFAAPFGLLG/EK

<220>
<221> polyA_signal
<222> 1580..1585

<220>
<221> polyA_site
<222> 1607..1622

<400> 25
aacctcttcc gtcggctgaa ttgcggccgt atg cgc ggc tct gtg gag tgc acc 54
Met Arg Gly Ser Val Glu Cys Thr
-35 -30
tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta 102
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Trp Thr Leu
-25 -20 -15
ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag 150
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln
-10 -5 1 5
gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg 198
Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu
10 15 20
ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg 246
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp
25 30 35
agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc 294
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro
40 45 50
cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc 342
His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Ser Pro Glu Pro
55 60 65
gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct 390
Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser
70 75 80 85
gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc 438
Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser
90 95 100
gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg 486
Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu
105 110 115
gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc 534
Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr
120 125 130
ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act 582
Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr
135 140 145
ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc 630
Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser
150 155 160 165
agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt 678
Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys
170 175 180

```

cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc      726
Gln Leu Glu Val Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser
      185      190      195
ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc      774
Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro
      200      205      210
tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc      822
Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val
      215      220      225
ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca      870
Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala
      230      235      240      245
cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca      918
Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser
      250      255      260
gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct      966
Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser
      265      270      275
ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac      1014
Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn
      280      285      290
ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat      1062
Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr
      295      300      305
tgg gac caa cac tac ctc agc tgg tgc atg ctc ctg ggt gtg ggc ttc      1110
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe
      310      315      320      325
cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg      1158
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val
      330      335      340
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg      1206
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu
      345      350      355
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat      1248
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn
      360      365      370
taaggccgcg tctctggagg gaaggacatt actgaacctg tcttgctgtg cctcgaaact      1308
ctggaggttg gagcatcaag ttccagcccc cttcactccc ccatcttgct tttctgtgga      1368
acctcagagg ccagcctcga cttcctggag acccccaggt ggggcttcct tcatactttg      1428
ttgggggact ttggaggcgg gcaggggaca gggctattga taagggtcccc ttggtgttgc      1488
cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt      1548
ctgactgggt ggctgccctg gaaggcaaga aaatagattt attttttttt cacagggcaa      1608
aaaaaaaaaa aaaa      1622

```

<210> 26
 <211> 1448
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 131..490

<220>
 <221> sig_peptide
 <222> 131..301
 <223> Von Heijne matrix
 score 5.30
 seq AIALATVLFLIGA/FL

<220>

<221> polyA_signal
<222> 1411..1416

<220>
<221> polyA_site
<222> 1434..1448

<400> 26
ctgatcccgct ctggggccgg ctgagtggca cttaagcggg ccatgccatg caaccttggg 60
cgctgccaac cgtgggcgag ctctgggtgt gcgggcggcc tcgcgcggcg ctccgctgtg 120
tcagcgtgtt atg atg ccg tcc cgt acc aac ctg gct act gga atc ccc 169
Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro
-55 -50 -45
agt agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac 217
Ser Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr
-40 -35 -30
att gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc 265
Ile Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala
-25 -20 -15
atc gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att 313
Ile Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile
-10 -5 1
ata ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac 361
Ile Gly Ser Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp
5 10 15 20
cgg gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga 409
Arg Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly
25 30 35
ttt tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt 457
Phe Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly
40 45 50
tac tcc tat gat gac att cca gac ttt gat gac tagcaccac cccatagctg 510
Tyr Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp
55 60
aggaggagtc acagtggaac tgtcccagct ttaagatata tagcagaaac tatagctgag 570
gactaaggaa ttctgcagct tgcagatgtt taagaaaata atggccagat tttttgggtc 630
cttcccaaag atgttaagtg aacctacagt tagctaatta ggacaagctc tttttttcat 690
ccctgggccc tgacaagttt ttccacagga atatgtatca tggaagaata gaggttatcc 750
tgtaatggaa aagtgttgcc tgccaccacc ctctgtagag ctgagcattt ctttttaata 810
gtcttcattg ccaatttggt cttgtagcaa atggaacaat gtggtatggc taattttotta 870
ttattaagta atttatttta aaaatatctg agtatattat cctgtacact tatccctacc 930
ttcatgttcc agtgaagac cttagtaaaa tcaaagatca gtgagttcat ctgtaattatt 990
ttttttactt gctttcttac tgacagcaac caggaatttt tttatcctgc agagcaagtt 1050
ttcaaaatgt aaatacttcc tctgtttaac agtccttgga ccattctgat ccagttcacc 1110
agtaggttgg acagcatata atttgcata ttttgccttg tgtaaatcaa gatgttctgc 1170
agattattcc tttaacggcc ggacttttgg ctgtttccta atgaaacatg tagtggttat 1230
tatntagagt ttatagccgt attgctagca ccttgtagta tgatcatcatt ctgctcatga 1290
ttccaaggat cagcctggat gcctagagga ctagatcacc ttagtttgat tctatttttt 1350
agcttgcaaa aagtgactta tattccaaag aaattaaaat gttgaaatcc aaatcctaga 1410
aataaaatga gtttaacttca aacaaaaaaa aaaaaaaa 1448

<210> 27
<211> 894
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 61..690

<220>

<221> sig_peptide
 <222> 61..168
 <223> Von Heijne matrix
 score 4.60
 seq GTVVVLVAGTLCFA/WW

<220>
 <221> polyA_signal
 <222> 858..863

<220>
 <221> polyA_site
 <222> 879..894

<400> 27
 acaccttcac ctgcgcccag ctccctgcgc gcctggacag cgctgctgc ccgctccccg 60
 atg gcc ctg ccc cag atg tgt gac ggg agc cac ttg gcc tcc acc ctc 108
 Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu
 -35 -30 -25
 cgc tat tgc atg aca gtc agc ggc aca gtg gtt ctg gtg gcc ggg acg 156
 Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr
 -20 -15 -10 -5
 ctc tgc ttc gct tgg tgg agc gaa ggg gat gca acc gcc cag cct ggc 204
 Leu Cys Phe Ala Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly
 1 5 10
 cag ctg gcc cca ccc acg gag tat ccg gtg cct gag ggc ccc agc ccc 252
 Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro
 15 20 25
 ctg ctc agg tcc gtc agc ttc gtc tgc tgc ggt gca ggt ggc ctg ctg 300
 Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu
 30 35 40
 ctg ctc att ggc ctg ctg tgg tcc gtc aag gcc agc atc cca ggg cca 348
 Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro
 45 50 55 60
 cct cga tgg gac ccc tat cac ctc tcc aga gac ctg tac tac ctc act 396
 Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr
 65 70 75
 gtg gag tcc tca gag aag gag agc tgc agg acc ccc aaa gtg gtt gac 444
 Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp
 80 85 90
 atc ccc act tac gag gaa gcc gtg agc ttc cca gtg gcc gag ggg ccc 492
 Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro
 95 100 105
 cca aca cca cct gca tac cct acg gag gaa gcc ctg gag cca agt gga 540
 Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly
 110 115 120
 tcg agg gat gcc ctg ctc agc acc cag ccc gcc tgg cct cca ccc agc 588
 Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser
 125 130 135 140
 tat gag agc atc agc ctt gct ctt gat gcc gtt tct gca gag acg aca 636
 Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr
 145 150 155
 ccg agt gcc aca cgc tcc tgc tca ggc ctg gtt cag act gca cgg gga 684
 Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly
 160 165 170
 gga agt taaaggctcc tagcaggctcc tgaatccaga gacaaaaatg ctgtgccttc 740
 Gly Ser
 tccagagtct tatgcagtgc ctgggacaca gtaggcactc agcaaacggt cgttgttgaa 800
 ggctgttcta tttatctatt gctgtataac aaaccacccc agaatttagt ggcttaaaat 860
 aaatcccatt ttattacgaa aaaaaaaaaa aaaa 894

<210> 28
 <211> 1447
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 501..1253

<220>
 <221> sig_peptide
 <222> 501..1229
 <223> Von Heijne matrix
 score 4.10
 seq LPSLAHLLPALDC/LE

<220>
 <221> polyA_signal
 <222> 1392..1397

<220>
 <221> polyA_site
 <222> 1432..1447

<220>
 <221> misc_feature
 <222> 243,252,278,285,387,1429
 <223> n=a, g, c or t

<400> 28
 gtgagtcagg tgggtcctgg gcccaggaac cggcccggag ccgtggacgc cctacagctg 60
 agaaggggac ccaagggggtc ggccgcggcc aaggccccta ggaccgccgc cccagctcac 120
 gctgccgacg gcagctatag acattctgcg tcagggtccgg gctcctggac tttgcctttc 180
 ccgagccctg gaggtgggga gaaaagggttc accaattttt aaaatccaaa tatatctcat 240
 ggntacagtg gnaagaactg gccagagagt ctggaagntt tgggnttctg gtcctggctg 300
 tgccactgac tcaactgtgac cttgggatct tgtgctgtga agacatttcc caagtgtctc 360
 atgttagcca gcaaactctga cccacanggc ctggaaagag gtgattgtta ggttgcgag 420
 aggtgggtctt atccagctca gcttcccctg ggaccaccg tgggacctga ggcagaactg 480
 ggggtggactt ggccctcctcc atg gca cac cgg ctg cag ata cga ctg ctg acg 533
 Met Ala His Arg Leu Gln Ile Arg Leu Leu Thr
 -240 -235
 tgg gat gtg aag gac acg ctg ctc agg ctc cgc cac ccc tta ggg gag 581
 Trp Asp Val Lys Asp Thr Leu Leu Arg Leu Arg His Pro Leu Gly Glu
 -230 -225 -220
 gcc tat gcc acc aag gcc cgg gcc cat ggg ctg gag gtg gag ccc tca 629
 Ala Tyr Ala Thr Lys Ala Arg Ala His Gly Leu Glu Val Glu Pro Ser
 -215 -210 -205
 gcc ctg gaa caa ggc ttc agg cag gca tac agg gct cag agc cac agc 677
 Ala Leu Glu Gln Gly Phe Arg Gln Ala Tyr Arg Ala Gln Ser His Ser
 -200 -195 -190 -185
 ttc ccc aac tac ggc ctg agc cac ggc cta acc tcc cgc cag tgg tgg 725
 Phe Pro Asn Tyr Gly Leu Ser His Gly Leu Thr Ser Arg Gln Trp Trp
 -180 -175 -170
 ctg gat gtg gtc ctg cag acc ttc cac ctg gcg ggt gtc cag gat gct 773
 Leu Asp Val Val Leu Gln Thr Phe His Leu Ala Gly Val Gln Asp Ala
 -165 -160 -155
 cag gct gta gcc ccc atc gct gaa cag ctt tat aaa gac ttc agc cac 821
 Gln Ala Val Ala Pro Ile Ala Glu Gln Leu Tyr Lys Asp Phe Ser His
 -150 -145 -140
 ccc tgc acc tgg cag gtg ttg gat ggg gct gag gac acc ctg agg gag 869
 Pro Cys Thr Trp Gln Val Leu Asp Gly Ala Glu Asp Thr Leu Arg Glu

```

-135          -130          -125
tgc cgc aca cgg ggt ctg aga ctg gca gtg atc tcc aac ttt gac cga      917
Cys Arg Thr Arg Gly Leu Arg Leu Ala Val Ile Ser Asn Phe Asp Arg
-120          -115          -110          -105
cgg cta gag ggc atc ctg gag ggc ctt ggc ctg cgt gaa cac ttc gac      965
Arg Leu Glu Gly Ile Leu Glu Gly Leu Gly Leu Arg Glu His Phe Asp
          -100          -95          -90
ttt gtg ctg acc tcc gag gct gct ggc tgg ccc aag ccg gac ccc cgc      1013
Phe Val Leu Thr Ser Glu Ala Ala Gly Trp Pro Lys Pro Asp Pro Arg
          -85          -80          -75
att ttc cag gag gcc ttg cgg ctt gct cat atg gaa cca gta gtg gca      1061
Ile Phe Gln Glu Ala Leu Arg Leu Ala His Met Glu Pro Val Val Ala
          -70          -65          -60
gcc cat gtt ggg gat aat tac ctg tgc gat tac cag ggg cct cgg gct      1109
Ala His Val Gly Asp Asn Tyr Leu Cys Asp Tyr Gln Gly Pro Arg Ala
          -55          -50          -45
gtg ggc atg cac agc ttc ctg gtg gtt ggc cca cag gca ctg gac ccc      1157
Val Gly Met His Ser Phe Leu Val Val Gly Pro Gln Ala Leu Asp Pro
          -40          -35          -30          -25
gtg gtc agg gat tct gta cct aaa gaa cac atc ctg ccc tct ctg gcc      1205
Val Val Arg Asp Ser Val Pro Lys Glu His Ile Leu Pro Ser Leu Ala
          -20          -15          -10
cat ctg ctg cct gcc ctt gac tgc cta gag ggc tca act cca ggg ctt      1253
His Leu Leu Pro Ala Leu Asp Cys Leu Glu Gly Ser Thr Pro Gly Leu
          -5          1          5
tgaggccagt gaggaagtg gctgggccct aggccatgga gaaaacctta aacaaacctt      1313
ggagacaggg agcccccttct ttctccacag ctctggacct ttccccctct ccctgcggcc      1373
ttgtcacct actgtgataa taaagcagtg agtgctgagc tctcaccctt ccccnccaa      1433
aaaaaaaaaa aaaa      1447

```

<210> 29

<211> 1540

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> 25..402

<220>

<221> sig_peptide

<222> 25..96

<223> Von Heijne matrix

score 7.00

seq LLCCFRALSGSLs/MR

<220>

<221> polyA_signal

<222> 1500..1505

<220>

<221> polyA_site

<222> 1525..1540

<220>

<221> misc_feature

<222> 625,1411,1432,1440,1450,1506

<223> n=a, g, c or t

<400> 29

agcctggccc tccctctttc caaa atg gac aag tcc ctg ctg gaa ctg

51

```

Met Asp Lys Ser Leu Leu Leu Glu Leu
-20
ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg      99
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met
-15                               -10                               -5                               1
aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct      147
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro
5                               10                               15
gtg ata gaa att att cag tgt agg atg tgc cac ctc cag ttc cca gga      195
Val Ile Glu Ile Ile Gln Cys Arg Met Cys His Leu Gln Phe Pro Gly
20                               25                               30
gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag      243
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu
35                               40                               45
gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta      291
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu
50                               55                               60                               65
acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg      339
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg
70                               75                               80
tgg agt gtc tat ttg gtg aac ttc agg tgc tgc agg agc cat gac ctg      387
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Cys Arg Ser His Asp Leu
85                               90                               95
tgc aat gaa gac ctt tagaagttaa tgggtcttct gtgactccaa tttctgggtg      442
Cys Asn Glu Asp Leu
100
aggttgttgc ctcagcctct tcacaatgac tttctaaaaa aaatcacaca cacacacaca      502
cacactacag aagaggattg caaacacatg gctccatctt ctgcacacga aaggaaagtc      562
cctctccttt tctacagtct ctgtcacgcc ccttaaaata agtaaataaa taaccttgag      622
agnaaagaac aagatcaata tatcctgcag gttgctacaa acccttgtgc tttcactgta      682
tagccagttc attcagaaaa ggaggaaagg gtagtttaat ttcaaaaaag aatcccttcc      742
tctttcctct gctgctttcc ttccttctgt ggcagggtat tttaatatat ttttcaaatt      802
tttttccttt ctgtgttatc cttcttatcc cactccaaag aaagcacata actgtggcct      862
gaagggatgg ggagtagcaa cataaaaaaga agtggctcaa gtcttcttgg agtttggttca      922
tgaatgctga tcccagggtg aggagaagat tgggacatag aaaggaaact gcatcagaaa      982
catgaacaga gaaagattgt ctaccttcta gaatcagatc tgtttggggc tgggggttgg      1042
agaataaaaag caggagaagt ctatgggatt ctagaaatag tacctgcatc cagcttccct      1102
gccaaactca caaggagaca tcaacctcta gacagggaac agcttcagga tacttccagg      1162
agacagagcc accagcagca aaacaaatat tcccatgcct ggagcatggc atagaggaag      1222
ctgagaaatg tgggggtctga ggaagccatt tgagtctggc cactagacat ctcacagcc      1282
acttgtgtga agagatgcc catgaccca gatgcctctc ccacccttac ctccatctca      1342
cacacttgag cttgccactc tgtataattc taacatcctg gagaaaaatg gcagtttgac      1402
cgaacctgnt tcacaagggt agaggctgan ttctaacnga aacttgtnag aatgaagcct      1462
ggaaagagtg atgaattata ttatattata taaaaataat aatnaaaaaat ataaagaaag      1522
ctaaaaaaaa aaaaaaaaaa
1540

<210> 30
<211> 1643
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 280..678

<220>
<221> sig_peptide
<222> 280..411
<223> Von Heijne matrix
score 3.90
seq LSDSLWSPHCSWS/ER

```

<220>
 <221> polyA_signal
 <222> 1606..1611

<220>
 <221> polyA_site
 <222> 1628..1643

<400> 30
 cctaagtttt ctcaaaaatg tctttttaca gttagtttaa gtcaggatct aaacaaagtt 60
 catacattac atttgcttga tgtctctcaa ctgtcttata acctataaca attgctccca 120
 atccattttt catgccatta ctttatttaa aaacctgggc caaccagtt ctcaaaaggt 180
 attggacatc ctcagaaaag atgactgctc tatgttgaac caaacaactg attcttacag 240
 gtttcttctc cacttgctct ctggctgtgg cagccagat atg gac agg aga gct 294
 Met Asp Arg Arg Ala
 -40
 aca tcc ttc cct cca ctc cct gcc aaa gaa agg aga gct ggg ata agc 342
 Thr Ser Phe Pro Pro Leu Pro Ala Lys Glu Arg Arg Ala Gly Ile Ser
 -35 -30 -25
 agt gcc ctc ccc tgc cca ccc act atg tca ctt tct gac tcc ctt tgg 390
 Ser Ala Leu Pro Cys Pro Pro Thr Met Ser Leu Ser Asp Ser Leu Trp
 -20 -15 -10
 tcc cct cat tgc tct tgg agt gag aga cct cat tcc ttc tct cac tgg 438
 Ser Pro His Cys Ser Trp Ser Glu Arg Pro His Ser Phe Ser His Trp
 -5 1 5
 agg cag cca aga atg gga tcc tct ggt ggg tct ttg gat tat gta agt 486
 Arg Gln Pro Arg Met Gly Ser Ser Gly Gly Ser Leu Asp Tyr Val Ser
 10 15 20 25
 ttc aaa cac tgg ata cac agc tcc aga tct aaa ggc aag att gct gct 534
 Phe Lys His Trp Ile His Ser Ser Arg Ser Lys Gly Lys Ile Ala Ala
 30 35 40
 cta gag gca gga ctg ttc att tcc tgc ctt ggg gat gca ccc aga ggc 582
 Leu Glu Ala Gly Leu Phe Ile Ser Cys Leu Gly Asp Ala Pro Arg Gly
 45 50 55
 ctg aat gct tcc caa gga aac caa aga aag aac atg gtc tgt ttc aga 630
 Leu Asn Ala Ser Gln Gly Asn Gln Arg Lys Asn Met Val Cys Phe Arg
 60 65 70
 ggt gga gtg gcc agt cta gct ctg cca tct ctc act cct tcc tgc ctt 678
 Gly Gly Val Ala Ser Leu Ala Leu Pro Ser Leu Thr Pro Ser Cys Leu
 75 80 85
 tagggtacca ctgaggtgga aagcctgaac tgctgtctct gctctggctt gtgctcaagc 738
 tgtgtgtcct tggactggcc atctctctctc tgcaaccctc ggtcttctca tttgtaaaat 798
 ggaagtgatc ctctctgccc atacttctctt acagggtctg ttggagacaa tcaatcaaga 858
 tgagggaaat tgagattcta caaagagtgt gatgcctaca taacaaagta ttgtttttct 918
 cacagttggt ggtattttgag gagaaggtga agattttggt tggaagaggg accagcagac 978
 aaacttggtt tcttgtgtat aaaaagccat aacacgcccc acatccctca agctaggaag 1038
 aaacctgggc tggatggtga cccactggag aagctgtgac atcctagcat ggggaagagt 1098
 accaggatgc ccactcctct tccccaggaa ccaccaagga gcctggagcc tggctttatc 1158
 tcagccctga gtccccctct cccggtgcgc acaccctaa cttttttttt tttagatgga 1218
 atcttgctct gtcgcccagg ctggagtgca acggcagctc actgtaacct ccacctccca 1278
 gggtcaagcg attctcctgc ctcagcctcc cgagtagctg ggattacagg cgcgtgactc 1338
 catgcctggc taatttttgt attttttagta gaggtagggg ttcaccatgt tgaccagggg 1398
 ggtctggaac tcttgatctc aggtgatctg cctgcctcca cctcccaaag tgctggaatt 1458
 acaggtgtga gctaccgccc ccggccaatc tggggctcct agcttttggtg caccaactac 1518
 tcaaattcccc aacttctctc caagaggaat ttcaagaaac actgaccaat ctggttacag 1578
 aagctgaagg ggccccaacc aggctgcaat aaacctgctt tacccttcca aaaaaaaaaa 1638
 aaaaa 1643

<210> 31
 <211> 1314

<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 64..726

<220>
<221> sig_peptide
<222> 64..147
<223> Von Heijne matrix
score 3.70
seq VVFTLGMFSAGLS/DL

<220>
<221> polyA_signal
<222> 1279..1284

<220>
<221> polyA_site
<222> 1300..1314

<400> 31
agtaggtccc ggcaaccgca ggctcgcggc gggcgctggg cgcgggatcc gactctagtc 60
gta atg gag gcg ggc ggc ttt ctg gac tcg ctc att tac gga gca tgc 108
Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys
-25 -20 -15
gtg gtc ttc acc ctt ggc atg ttc tcc gcc ggc ctc tcg gac ctc agg 156
Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg
-10 -5 1
cac atg cga atg acc cgg agt gtg gac aac gtc cag ttc ctg ccc ttt 204
His Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe
5 10 15
ctc acc acg gaa gtc aac aac ctg ggc tgg ctg agt tat ggg gct ttg 252
Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu
20 25 30 35
aag gga gac ggg atc ctc atc gtc gtc aac aca gtg ggt gct gcg ctt 300
Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu
40 45 50
cag acc ctg tat atc ttg gca tat ctg cat tac tgc cct cgg aag cgt 348
Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg
55 60 65
gtt gtg ctc cta cag act gca acc ctg cta ggg gtc ctt ctc ctg ggt 396
Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly
70 75 80
tat ggc tac ttt tgg ctc ctg gta ccc aac cct gag gcc cgg ctt cag 444
Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln
85 90 95
cag ttg ggc ctc ttc tgc agt gtc ttc acc atc agc atg tac ctc tca 492
Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser
100 105 110 115
cca ctg gct gac ttg gct aag gtg att caa act aaa tca acc caa tgt 540
Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys
120 125 130
ctc tcc tac cca ctc acc att gct acc ctt ctc acc tct gcc tcc tgg 588
Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp
135 140 145
tgc ctc tat ggg ttt cga ctc aga gat ccc tat atc atg gtg tcc aac 636
Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn
150 155 160
ttt cca gga atc gtc acc agc ttt atc cgc ttc tgg ctt ttc tgg aag 684

0998360.101501

Phe	Pro	Gly	Ile	Val	Thr	Ser	Phe	Ile	Arg	Phe	Trp	Leu	Phe	Trp	Lys	
165						170					175					
tac	ccc	cag	gag	caa	gac	agg	aac	tac	tgg	ctc	ctg	caa	acc			726
Tyr	Pro	Gln	Glu	Gln	Asp	Arg	Asn	Tyr	Trp	Leu	Leu	Gln	Thr			
180					185					190						
tgag	gctgct	catctgacca	ctgggcacct	tagtgccaac	ctgaacccaaa	gagacctcct										786
tg	tttcagct	gggcctgctg	tccagcttcc	caggtgcagt	gggttggtggg	aacaagagat										846
gact	tttgagg	ataaaaaggac	caaagaaaaa	gctttactta	gatgattgat	tggggcctag										906
gagat	gaaat	cactttttat	tttttagaga	tttttttttt	tttaatttttg	aggttggggt										966
gcaat	cttta	gaatatgcct	taaaaggccg	ggcgcggtgg	ctcacgcctg	taatcccagc										1026
act	ttgggag	gccaaaggtgg	gcggatcgcc	tgaggtcagg	agttcaagac	caacctgact										1086
aacat	ggtga	aaccccatct	ctactaaaaa	tacaaaatta	gccaggcatg	atggcacatg										1146
cctg	taatcc	cagatacttg	ggaggctgag	gcaggagaat	tgcttgaacc	caggaggtgg										1206
aggt	gcagt	gagctgagat	cgtgccattg	tgatatgaat	atgccttata	tgctgatatg										1266
aatat	gcctt	aaaataaagt	gttccccacc	cctaaaaaaa	aaaaaaaaa											1314

<210> 32
 <211> 2356
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 42..1097

<220>
 <221> sig_peptide
 <222> 42..110
 <223> Von Heijne matrix
 score 4.40
 seq QFILLGTTSVVTA/AL

<220>
 <221> polyA_signal
 <222> 2323..2328

<220>
 <221> polyA_site
 <222> 2341..2356

<400> 32
 atccttggcg ccacagtcgg ccaccggggc tcgccgccgt c atg gag agc gga ggg 56
 Met Glu Ser Gly Gly
 -20
 cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg gtc 104
 Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val Val
 -15 -10 -5
 acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc caa 152
 Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser Gln
 1 5 10
 gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag agt 200
 Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys Ser
 15 20 25 30
 att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata gaa 248
 Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile Glu
 35 40 45
 gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg gaa 296
 Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val Glu
 50 55 60
 aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag atg 344
 Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys Met

	65					70					75					
gtg	tgg	aat	cga	acc	acc	cac	ctt	tgg	aat	gat	tgc	tca	aag	atc	att	392
Val	Trp	Asn	Arg	Thr	Thr	His	Leu	Trp	Asn	Asp	Cys	Ser	Lys	Ile	Ile	
	80					85					90					
cat	cag	agg	acc	aac	aca	gtg	ccc	ttt	gac	ctg	gtg	ccc	cac	gag	gat	440
His	Gln	Arg	Thr	Asn	Thr	Val	Pro	Phe	Asp	Leu	Val	Pro	His	Glu	Asp	
95					100					105					110	
ggc	gtg	gat	gtg	gct	gtg	cga	gtg	ctg	aag	ccc	ctg	gac	tca	gtg	gat	488
Gly	Val	Asp	Val	Ala	Val	Arg	Val	Leu	Lys	Pro	Leu	Asp	Ser	Val	Asp	
				115					120						125	
ctg	ggg	cta	gag	act	gtg	tat	gag	aag	ttc	cac	ccc	tgc	att	cag	tcc	536
Leu	Gly	Leu	Glu	Thr	Val	Tyr	Glu	Lys	Phe	His	Pro	Ser	Ile	Gln	Ser	
				130				135							140	
ttc	acc	gat	gtc	atc	ggc	cac	tac	atc	agc	ggg	gag	cgg	ccc	aaa	ggc	584
Phe	Thr	Asp	Val	Ile	Gly	His	Tyr	Ile	Ser	Gly	Glu	Arg	Pro	Lys	Gly	
				145			150					155				
atc	caa	gag	acc	gag	gag	atg	ctg	aag	gtg	ggg	gcc	acc	ctc	aca	ggg	632
Ile	Gln	Glu	Thr	Glu	Glu	Met	Leu	Lys	Val	Gly	Ala	Thr	Leu	Thr	Gly	
	160					165					170					
gtt	ggc	gaa	ctg	gtc	ctg	gac	aac	aac	tct	gtc	cgc	ctg	cag	ccg	ccc	680
Val	Gly	Glu	Leu	Val	Leu	Asp	Asn	Asn	Ser	Val	Arg	Leu	Gln	Pro	Pro	
175					180					185					190	
aaa	caa	ggc	atg	cag	tac	tat	cta	agc	agc	cag	gac	ttc	gac	agc	ctg	728
Lys	Gln	Gly	Met	Gln	Tyr	Tyr	Leu	Ser	Ser	Gln	Asp	Phe	Asp	Ser	Leu	
				195				200						205		
ctg	cag	agg	cag	gag	tgc	agc	gtc	agg	ctc	tgg	aag	gtg	ctg	gcg	ctg	776
Leu	Gln	Arg	Gln	Glu	Ser	Ser	Val	Arg	Leu	Trp	Lys	Val	Leu	Ala	Leu	
				210				215						220		
gtt	ttt	ggc	ttt	gcc	aca	tgt	gcc	acc	ctc	ttc	ttc	att	ctc	cgg	aag	824
Val	Phe	Gly	Phe	Ala	Thr	Cys	Ala	Thr	Leu	Phe	Phe	Ile	Leu	Arg	Lys	
		225					230					235				
cag	tat	ctg	cag	cgg	cag	gag	cgc	ctg	cgc	ctc	aag	cag	atg	cag	gag	872
Gln	Tyr	Leu	Gln	Arg	Gln	Glu	Arg	Leu	Arg	Leu	Lys	Gln	Met	Gln	Glu	
		240				245					250					
gag	ttc	cag	gag	cat	gag	gcc	cag	ctg	ctg	agc	cga	gcc	aag	cct	gag	920
Glu	Phe	Gln	Glu	His	Glu	Ala	Gln	Leu	Leu	Ser	Arg	Ala	Lys	Pro	Glu	
255					260					265					270	
gac	agg	gag	agt	ctg	aag	agc	gcc	tgt	gta	gtg	tgt	ctg	agc	agc	ttc	968
Asp	Arg	Glu	Ser	Leu	Lys	Ser	Ala	Cys	Val	Val	Cys	Leu	Ser	Ser	Phe	
				275				280						285		
aag	tcc	tgc	gtc	ttt	ctg</											


```

cacttgggag agctcggggg ggtccctggt tttccctcct ggagaatgag ggcgagaggc 1897
ctcgccctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc ctcacagctt 1957
ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata tgccctcttg 2017
gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg tcgcttctcc 2077
ttgtgttacc cctcccagc attaccattt gcccctcacc tgcccttggg gagcctttta 2137
gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc acatacacag 2197
ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc ctttgtgcag 2257
gcgaggaagg ggtgccctca ggggccgaca ctagtatgat gcagtgtcca gtgtgaacag 2317
cagaaattaa acatgttgca accaaaaaaa aaaaaaaaaa 2356

```

```

<210> 33
<211> 1701
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> CDS
<222> 245..1399

```

```

<220>
<221> sig_peptide
<222> 245..796
<223> Von Heijne matrix
      score 5.10
      seq GWLPLLLLSLLVA/TW

```

```

<220>
<221> polyA_signal
<222> 1669..1674

```

```

<220>
<221> polyA_site
<222> 1687..1701

```

```

<400> 33
atcccgcgca gtggcccggc gatgtcgctc gtgctgctaa gcctggccgc gctgtgcagg 60
agcgccgtac cccgagagcc gaccgttcaa tgtggctctg aaactgggcc atctccagag 120
tggatgctac aacatgatct aatcccggga gacttgaggg acctccgagt agaacctgtt 180
acaactagtg ttgcaacagg ggactattca attttgatga atgtaagctg ggtactccgg 240
gcag atg tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac aca 289
      Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr
              -180                      -175                      -170
gtc tat ttc att ggg gcc cat aaa att cct aat gca aat atg aat gaa 337
Val Tyr Phe Ile Gly Ala His Lys Ile Pro Asn Ala Asn Met Asn Glu
              -165                      -160                      -155
gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta gac 385
Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp
              -150                      -145                      -140
cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg tgg 433
His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp
              -135                      -130                      -125
gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa gtg 481
Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val
              -120                      -115                      -110
aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc caa 529
Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln
              -105                      -100                      -95                      -90
cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag aag 577
His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys
              -85                      -80                      -75
aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt gaa 625

```

Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu		
			-70					-65					-60				
ggt	gct	acg	gtg	cag	ctg	act	cca	tat	ttt	cct	act	tgt	ggc	agc	gac	673	
Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp		
		-55					-50					-45					
tgc	atc	cga	cat	aaa	gga	aca	gtt	gtg	ctc	tgc	cca	caa	aca	ggc	gtc	721	
Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val		
	-40					-35					-30						
cct	ttc	cct	ctg	gat	aac	aac	aaa	agc	aag	ccg	gga	ggc	tgg	ctg	cct	769	
Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro		
-25				-20					-15					-10			
ctc	ctc	ctg	ctg	tct	ctg	ctg	gtg	gcc	aca	tgg	gtg	ctg	gtg	gca	ggg	817	
Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	Val	Leu	Val	Ala	Gly		
			-5					1				5					
atc	tat	cta	atg	tgg	agg	cac	gaa	agg	atc	aag	aag	act	tcc	ttt	tct	865	
Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	Lys	Thr	Ser	Phe	Ser		
	10					15						20					
acc	acc	aca	cta	ctg	ccc	ccc	att	aag	gtt	ctt	gtg	gtt	tac	cca	tct	913	
Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val	Val	Tyr	Pro	Ser		
	25				30					35							
gaa	ata	tgt	ttc	cat	cac	aca	att	tgt	tac	ttc	act	gaa	ttt	ctt	caa	961	
Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr	Glu	Phe	Leu	Gln		
40				45				50						55			
aac	cat	tgc	aga	agt	gag	gtc	atc	ctt	gaa	aag	tgg	cag	aaa	aag	aaa	1009	
Asn	His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys		
			60					65					70				
ata	gca	gag	atg	ggt	cca	gtg	cag	tgg	ctt	gcc	act	caa	aag	aag	gca	1057	
Ile	Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	Gln	Lys	Lys	Ala		
		75				80						85					
gca	gac	aaa	gtc	gtc	ttc	ctt	ctt	tcc	aat	gac	gtc	aac	agt	gtg	tgc	1105	
Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	Asn	Ser	Val	Cys		
		90				95					100						
gat	ggt	acc	tgt	ggc	aag	agc	gag	ggc	agt	ccc	agt	gag	aac	tct	caa	1153	
Asp	Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser	Glu	Asn	Ser	Gln		
	105				110						115						
gac	ctc	ttc	ccc	ctt	gcc	ttt	aac	ctt	ttc	tgc	agt	gat	cta	aga	agc	1201	
Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	Asp	Leu	Arg	Ser		
	120				125					130					135		
cag	att	cat	ctg	cac	aaa	tac	gtg	gtg	gtc	tac	ttt	aga	gag	att	gat	1249	
Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	Arg	Glu	Ile	Asp		
			140					145						150			
aca	aaa	gac	gat	tac	aat	gct	ctc	agt	gtc	tgc	ccc	aag	tac	cac	ctc	1297	
Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	Lys	Tyr	His	Leu		
		155				160							165				
atg	aag	gat	gcc	act	gct	ttc	tgt	gca	gaa	ctt	ctc	cat	gtc	aag	cag	1345	
Met	Lys	Asp	Ala	Thr	Ala	Phe	Cys	Ala	Glu	Leu	Leu	His	Val	Lys	Gln		
	170				175							180					
cag	gtg	tca	gca	gga	aaa	aga	tca	caa	gcc	tgc	cac	gat	ggc	tgc	tgc	1393	
Gln	Val	Ser	Ala	Gly	Lys	Arg	Ser	Gln	Ala	Cys	His	Asp	Gly	Cys	Cys		
	185				190					195							
tcc	ttg	tagccccaccc	atgagaagca	agagacctta	aaggcttcct	atccccaccaa										1449	
Ser	Leu																
	200																
ttacagggaa	aaaacgtgtg	atgatacctga	agcttactat	gcagcctaca	aacagcctta											1509	
gtaattaaaa	catttttatac	caataaaatt	ttcaaattatt	gctaactaat	gtagcattaa											1569	
ctaacgattg	gaaactacat	ttacaacttc	aaagctgttt	tatacataga	aatcaattac											1629	
agtttttaatt	gaaaactata	accatttttga	taatgcaaca	ataaagcatc	ttcagccaaa											1689	
aaaaaaaaaa	aa															1701	

<210> 34
<211> 772

<222> 88..234
 <223> Von Heijne matrix
 score 4.70
 seq LLLVSTWSADLMS/YR

<220>
 <221> polyA_signal
 <222> 938..943

<220>
 <221> polyA_site
 <222> 964..987

<220>
 <221> misc_feature
 <222> 828,832
 <223> n=a, g, c or t

<400> 35
 ttttttcttt gacatgttca gatgttggca aggctgaaaa ctgcagggga tctggttggtg 60
 ataatccagg cctgaatata tacaaat atg aac aag acc cac aag gac tgc tca 114
 Met Asn Lys Thr His Lys Asp Cys Ser
 -45
 tca ccc cag tat tcc att tac aac atc ctg aat gaa ctc ccg acc agg 162
 Ser Pro Gln Tyr Ser Ile Tyr Asn Ile Leu Asn Glu Leu Pro Thr Arg
 -40 -35 -30 -25
 cct ata att ctc tct tgc agc caa ata tcc tgc tta ctc ctg gta tct 210
 Pro Ile Ile Leu Ser Cys Ser Gln Ile Ser Cys Leu Leu Leu Val Ser
 -20 -15 -10
 acc tgg tca gca gac ctc atg agt tat cgc cca gtg aca aaa cca tcc 258
 Thr Trp Ser Ala Asp Leu Met Ser Tyr Arg Pro Val Thr Lys Pro Ser
 -5 1 5
 caa aga tgc acc agt cca gca caa agt atg act gtc aat ctc aca aaa 306
 Gln Arg Cys Thr Ser Pro Ala Gln Ser Met Thr Val Asn Leu Thr Lys
 10 15 20
 gat gta ggg ttc tac gag gat act cag agt ata aga att acg cta agt 354
 Asp Val Gly Phe Tyr Glu Asp Thr Gln Ser Ile Arg Ile Thr Leu Ser
 25 30 35 40
 gaa ata agc caa gcc cag aaa gac aca tac ttt att att tca tgt atc 402
 Glu Ile Ser Gln Ala Gln Lys Asp Thr Tyr Phe Ile Ile Ser Cys Ile
 45 50 55
 tgt gga atc taaaagagtc aaattcatgg cagcagggag agggctgaag 451
 Cys Gly Ile
 aagggggaga tggtgatcaa agtttctatg tatacaaaga ccaaaccatc acattatgcc 511
 tcataaatat atacaattat tatttgctaa ttacaagtaa agcaatacaa gaagaaaaaa 571
 aggaatcata agtaaatcca tgacaagtga aaacgcaatg gagagaaggg aatcaatgat 631
 tgaagaagag aaaggacagt ggatttacia ctgcttcgaa agagtgattt gactggcaaaa 691
 ggactgggga gaggtccttt gggaaatgga caaaaccctc gaatggtag gaaagacaat 751
 ctctttataa atgcggggca taagctgagc acaaggtgaa gtttggcatg tactgccgtg 811
 ggatgttgta aaaattnatg ntcaaaagca aagcaattct tggttcatct gtgttcactg 871
 tgagactagc ctattattgg ggttaaaactt ataaacaaac ttctgttcat cttttttttt 931
 ctccaaaata aagtgatcaa attgtccac agaaaaaaaa aaaaaaaaaa aaaaaa 987

<210> 36
 <211> 1324
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 129..452

0993650101501

<220>
 <221> sig_peptide
 <222> 129..212
 <223> Von Heijne matrix
 score 5.20
 seq LDIVISFVGAVSS/ST

<220>
 <221> polyA_signal
 <222> 1290..1295

<220>
 <221> polyA_site
 <222> 1309..1324

<220>
 <221> misc_feature
 <222> 888,1080
 <223> n=a, g, c or t

<400> 36
 gatttttttc acaagcaata gtttagtagt tcaactttca ttaattattt ctagtaatta 60
 ctttcagtat tgaaaatact tactgttaat attcatgtaa gtaacaaaca tttaaataag 120
 aaaaataa atg tat ttt cat ttt cta ggt gcc gga gca att ctt att cct 170
 Met Tyr Phe His Phe Leu Gly Ala Gly Ala Ile Leu Ile Pro
 -25 -20 -15
 cgt tta gac att gtg att tcc ttc gtt gga gct gtg agc agc agc aca 218
 Arg Leu Asp Ile Val Ile Ser Phe Val Gly Ala Val Ser Ser Ser Thr
 -10 -5 1
 ttg gcc cta atc ctg cca cct ttg gtt gaa att ctt aca ttt tcg aag 266
 Leu Ala Leu Ile Leu Pro Pro Leu Val Glu Ile Leu Thr Phe Ser Lys
 5 10 15
 gaa cat tat aat ata tgg atg gtc ctg aaa aat att tct ata gca ttc 314
 Glu His Tyr Asn Ile Trp Met Val Leu Lys Asn Ile Ser Ile Ala Phe
 20 25 30
 act gga gtt gtt ggc ttc tta tta ggt aca tat ata act gtt gaa gaa 362
 Thr Gly Val Val Gly Phe Leu Leu Gly Thr Tyr Ile Thr Val Glu Glu
 35 40 45 50
 att att tat cct act ccc aaa gtt gta gct ggc act cca cag agt cct 410
 Ile Ile Tyr Pro Thr Pro Lys Val Val Ala Gly Thr Pro Gln Ser Pro
 55 60 65
 ttt cta aat ttg aat tca aca tgc tta aca tct ggt ttg aaa 452
 Phe Leu Asn Leu Asn Ser Thr Cys Leu Thr Ser Gly Leu Lys
 70 75 80
 tagtaaaagc agaatcatga gtcttctatt tttgtcccat ttctgaaaat tatcaagata 512
 actagtaaaa tacattgcta tatacataaa aatggtaaca aactctgttt tctttggcac 572
 gatattaata ttttggaagt aatcataact ctttaccagt agtggtaaac ctatgaaaaa 632
 tccttgcttt taagtgttag caatagttca aaaaattaag ttctgaaaat tgaaaaaatt 692
 aaaatgtaaa aaaattaaag aataaaaata cttctattat tcttttatct cagtaagaaa 752
 taccttaacc aagatatctc tcttttatgc tactcttttg ccactcactt gagaacagaa 812
 taggatttca acaataagag aataaaaata gaacatgtat aacaaaaagc tctctccaga 872
 tcatccctgt gaatgnccaa agtaaacctt atgtacagtg taacaaaaaa aaaatctcag 932
 ttatgttttt attagccaaa ttctaatagat tggctcctgg aagtatagaa aactcccatt 992
 aacataatat aagcatcaga aaattgcaaa cactagaatt aattttacac tctaattggt 1052
 gttgatcttc atagtcaaga ggcactgntc aagatcatga cttagtgttt caatgaaatt 1112
 tgacaaggga ctttaaaact tatccagtgc aactcccttg tttttcgtca gaggaaaagg 1172
 aggcctagaa aggttaagta acttggtcga gaccactcag ccttgagatc aagaaaacct 1232
 aatcttctga ctcccaggcc aggatgtttt atttctcaca tcatgtccaa gaaaaagaat 1292
 aaattatggt cagctcaaaa aaaaaaaaaa aa 1324

<210> 37
 <211> 1918
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 238..612

<220>
 <221> sig_peptide
 <222> 238..348
 <223> Von Heijne matrix
 score 9.40
 seq LLCCVLSASQLSS/QD

<220>
 <221> polyA_signal
 <222> 1885..1890

<220>
 <221> polyA_site
 <222> 1905..1918

<220>
 <221> misc_feature
 <222> 945,1624
 <223> n=a, g, c or t

<400> 37
 aaaaatctaa gcgacttcga tgccaaggaa gttgtgtaaa tgtgcacgcg ctacaccaca 60
 cccagggtgg aaaccacagt tgcagagtca ttaaacaatc aattgtttgt ttaacatctg 120
 tgataggcag ctttccttct tttcaacagt gatacctacg aaaatcaaaa taaatgcaag 180
 ctgagggttt gtgtcactg aaagggtgt caaccccaga aggccgacac aaaaaaaa 237
 atg gta tgt gaa gat gca ccg tct ttt caa atg gcc tgg gag agt caa 285
 Met Val Cys Glu Asp Ala Pro Ser Phe Gln Met Ala Trp Glu Ser Gln
 -35 -30 -25
 atg gcc tgg gag agg ggg cct gcc ctt ctc tgc tgt gtc ctt tcg gct 333
 Met Ala Trp Glu Arg Gly Pro Ala Leu Leu Cys Cys Val Leu Ser Ala
 -20 -15 -10
 tcc cag ttg agc tcc caa gac cag gac cca ctg ggg cat ata aaa tct 381
 Ser Gln Leu Ser Ser Gln Asp Gln Asp Pro Leu Gly His Ile Lys Ser
 -5 1 5 10
 ctg ctg tat cct ttc ggc ttc cca gtt gag ctc cca aga cca gga ccc 429
 Leu Leu Tyr Pro Phe Gly Phe Pro Val Glu Leu Pro Arg Pro Gly Pro
 15 20 25
 act ggg gca tat aaa aaa gtc aaa aat caa aat caa aca aca agt tct 477
 Thr Gly Ala Tyr Lys Lys Val Lys Asn Gln Asn Gln Thr Thr Ser Ser
 30 35 40
 gag tta ctt agg aaa cag act tcg cat ttc aat cag aga ggc cac aga 525
 Glu Leu Leu Arg Lys Gln Thr Ser His Phe Asn Gln Arg Gly His Arg
 45 50 55
 gca agg tct aaa ctt ctg gct tct aga caa att cct gat aga aca ttt 573
 Ala Arg Ser Lys Leu Leu Ala Ser Arg Gln Ile Pro Asp Arg Thr Phe
 60 65 70 75
 aaa tgt ggg aag tgg ctt ccc cag gtc cca tcc cct gtt tagggataga 622
 Lys Cys Gly Lys Trp Leu Pro Gln Val Pro Ser Pro Val
 80 85
 gttgatata tttttatagt tgccatgtat gcctctgcct gaattttttt aattgacttt 682
 tgagcttttg agattgcacg agggagaaca aggcctttgc tgttgtggat aggaaaagact 742
 taacctaaaa ttaaccagc aagaaagcat tagtaaaaat ctaacaatat gaagggtctt 802

0998360.101501

Val	Trp	His	Phe	Cys	Leu	Ser	His	Lys	Ser	Ser	Leu	Val	Ile	Val	Leu	
			-50					-45					-40			
aag	acg	gca	ggc	tgg	att	ccc	cag	gct	ggg	acc	ctt	atc	cct	ggt	tcc	272
Lys	Thr	Ala	Gly	Trp	Ile	Pro	Gln	Ala	Gly	Thr	Leu	Ile	Pro	Gly	Ser	
			-35					-30					-25			
aga	gag	gag	agc	aga	tct	gat	tca	caa	atg	att	atg	ctt	gtc	tgt	ttt	320
Arg	Glu	Glu	Ser	Arg	Ser	Asp	Ser	Gln	Met	Ile	Met	Leu	Val	Cys	Phe	
			-20				-15				-10					
aat	ctt	tcc	aga	ggc	tgt	ctg	aag	aag	gta	ttc	atc	atc	tct	gtt	tta	368
Asn	Leu	Ser	Arg	Gly	Cys	Leu	Lys	Lys	Val	Phe	Ile	Ile	Ser	Val	Leu	
			-5		1			5					10			
cct	gac	cca	gaa	acc	att	ctg	cta	gga	aaa	aca	gtg	ggc	att	gct		413
Pro	Asp	Pro	Glu	Thr	Ile	Leu	Leu	Gly	Lys	Thr	Val	Gly	Ile	Ala		
			15				20				25					
tgaaaaacagt	gttctgtggt	tgaaaaaccc	acagtcacct	tgaggctggtg	ggaatgtaaa											473
atggcgccctc	ttctggatca	tcgtttggca	gtttctcaaa	aggtcaaacg	tagaatcact											533
atttgatcca	acaattctac	tcctaggtat	atccccaaaa	gaattgaaaa	caaggatgca											593
aacatatgcg	tgtacactaa	tgtttataga	aaaaatattc	acaataatca	aaaggcagaa											653
acaacccaag	tgtccaataa	cagaagaatg	aataaacagt	gtgatataaa	cataaaaaaa											713
aaaaaaaaaan	aaa															726

<210> 40
 <211> 1039
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 100..852
 <220>
 <221> sig_peptide
 <222> 100..159
 <223> Von Heijne matrix
 score 6.10
 seq FLILFLFLMECQL/HL

<220>
 <221> polyA_signal
 <222> 998..1003

<220>
 <221> polyA_site
 <222> 1019..1039

<400> 40																
agaacttctt	gattcctcag	ataaatagag	gacagatgct	ggactgtagc	taagtatttc											60
ctttcatcta	cgggataaaa	tactgataat	ttgagagtg	atg gac aag gtt cag												114
				Met Asp Lys Val Gln												
				-20												
agt ggt ttc ctc att ttg ttt ttg ttt tta atg gaa tgc caa ctt cat																162
Ser Gly Phe Leu Ile Leu Phe Leu Phe Leu Met Glu Cys Gln Leu His																
				-15			-10			-5				1		
tta tgc ttg ccg tat gca gat gga ctc cat ccc act gga aac ata aca																210
Leu Cys Leu Pro Tyr Ala Asp Gly Leu His Pro Thr Gly Asn Ile Thr																
				5			10			15						
ggc tta cca ggt agc ttc aac cac tgg ttt tat gtg act cag gga gaa																258
Gly Leu Pro Gly Ser Phe Asn His Trp Phe Tyr Val Thr Gln Gly Glu																
				20			25			30						
ttg aaa agc tgt ttc agg gga gat aaa aag aag gta att aca ttt cac																306
Leu Lys Ser Cys Phe Arg Gly Asp Lys Lys Lys Val Ile Thr Phe His																

```

      35              40              45
cgc aaa aag ttt tct ttt caa ggc agt aaa cgg tca caa cca ccc aga      354
Arg Lys Lys Phe Ser Phe Gln Gly Ser Lys Arg Ser Gln Pro Pro Arg
50              55              60              65
aac atc acc aaa gag ccc aaa gtg ttc ttt cat aaa acc cag ttg cct      402
Asn Ile Thr Lys Glu Pro Lys Val Phe Phe His Lys Thr Gln Leu Pro
      70              75              80
ggg att caa ggg gct gcc tcg aga tcc acg gct gca tcc cct acg aac      450
Gly Ile Gln Gly Ala Ala Ser Arg Ser Thr Ala Ala Ser Pro Thr Asn
      85              90              95
ccc atg aaa ttc ctg agg aat aaa gca ata att cgg cat aga cct gct      498
Pro Met Lys Phe Leu Arg Asn Lys Ala Ile Ile Arg His Arg Pro Ala
      100              105              110
ctt gtt aaa gta att tta att tcg agc gta gcc ttc agc att gcc ctg      546
Leu Val Lys Val Ile Leu Ile Ser Ser Val Ala Phe Ser Ile Ala Leu
      115              120              125
ata tgt ggg atg gca atc tcc tat atg ata tat cga ctg gca cag gct      594
Ile Cys Gly Met Ala Ile Ser Tyr Met Ile Tyr Arg Leu Ala Gln Ala
      130              135              140              145
gag gaa aga caa cag ctc gag tca ctt tat aag aac ctc agg ata ccg      642
Glu Glu Arg Gln Gln Leu Glu Ser Leu Tyr Lys Asn Leu Arg Ile Pro
      150              155              160
tta tta gga gat gaa gaa gag ggc tca gag gac gag ggt gag tcc acg      690
Leu Leu Gly Asp Glu Glu Glu Gly Ser Glu Asp Glu Gly Glu Ser Thr
      165              170              175
cac cta ctt cca aag aac gaa aat gag ctg gaa aag ttc atc cac tca      738
His Leu Leu Pro Lys Asn Glu Asn Glu Leu Glu Lys Phe Ile His Ser
      180              185              190
gtt att ata tca aaa aga agc aaa aat att aag aag aaa ctg aag gaa      786
Val Ile Ile Ser Lys Arg Ser Lys Asn Ile Lys Lys Lys Leu Lys Glu
      195              200              205
gag caa aac tca gta aca gaa aac aaa aca aag aat gcg tca cat aat      834
Glu Gln Asn Ser Val Thr Glu Asn Lys Thr Lys Asn Ala Ser His Asn
      210              215              220              225
gga aaa atg gaa gac ttg tgaacgcaga cgacagaggt gccggctgag      882
Gly Lys Met Glu Asp Leu
      230
gcagaggaga aactatgggg gtgctgggag actgagcctg tgggcgtggc ttgctcccag      942
agaaccttat ggaagaggac atcaaagaaa gaaatgccag acctgtatcc cagaaaataa      1002
agccacatga tatagcaaaa aaaaaaaaaa aaaaaaa      1039

```

<210> 41
 <211> 1355
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 238..1152

<220>
 <221> sig_peptide
 <222> 238..339
 <223> Von Heijne matrix
 score 8.50
 seq SIFLLLSFPDSNG/KA

<220>
 <221> polyA_signal
 <222> 1298..1303

<220>
 <221> polyA_site
 <222> 1324..1355

<400> 41

aatttttcttg	aaatcacatg	gtaccaatca	caagtcttgt	tattttggtt	cattatgaga	60
aagataatct	actaaatatt	aaaatactgg	aaggagcaag	atagctttga	tccagggaga	120
ccttttccat	ttatgtgctt	tagtaatctg	cgccaacaa	gctatcttct	ttatgttctt	180
ctacaactga	tggtgttttg	ttttctcatg	tttgtctctt	aatagacaaa	tgagggc	237
atg agc ttc ctt aga att acc cct tgc acg cat	agt tct gtt tca tct	285				
Met Ser Phe Leu Arg Ile Thr Pro Ser Thr His	Ser Ser Val Ser Ser					
	-30 -25 -20					
gga ctt ttg agg ctt agt atc ttt cta cta ctt	agc ttt cct gac tca	333				
Gly Leu Leu Arg Leu Ser Ile Phe Leu Leu Ser	Phe Pro Asp Ser					
	-15 -10 -5					
aac gga aaa gcc att tgg aca gct cac ctg aat	ata aca ttt cag gtt	381				
Asn Gly Lys Ala Ile Trp Thr Ala His Leu Asn	Ile Thr Phe Gln Val					
	1 5 10					
gga aat gag atc aca tgc gaa tta gga gag agt	gga gtg ttc ggg aat	429				
Gly Asn Glu Ile Thr Ser Glu Leu Gly Glu Ser	Gly Val Phe Gly Asn					
	15 20 25 30					
cat tct cct ctg gaa agg gtg tct ggt gtg gca	ctt cct gaa gaa	477				
His Ser Pro Leu Glu Arg Val Ser Gly Val Ala	Leu Pro Glu Glu					
	35 40 45					
tgg aat cag aat gcc tgt cat cct ttg acc aat	ttc agc agg ccc aaa	525				
Trp Asn Gln Asn Ala Cys His Pro Leu Thr Asn	Phe Ser Arg Pro Lys					
	50 55 60					
cag gca gac tca tgg ctg gcc ctc atc gaa cgt	gga ggc tgt act ttt	573				
Gln Ala Asp Ser Trp Leu Ala Leu Ile Glu Arg	Gly Gly Cys Thr Phe					
	65 70 75					
aca cat aaa atc aac gtg gca gca gag aag gga	gca aat ggg gtg atc	621				
Thr His Lys Ile Asn Val Ala Ala Glu Lys Gly	Ala Asn Gly Val Ile					
	80 85 90					
atc tac aac tat caa ggt acg ggc agt aaa gta	ttt ccc atg tct cac	669				
Ile Tyr Asn Tyr Gln Gly Thr Gly Ser Lys Val	Phe Pro Met Ser His					
	95 100 105 110					
cag ggg acg gaa aat ata gtc gcg gtg atg ata	agc aac ctg aaa ggc	717				
Gln Gly Thr Glu Asn Ile Val Ala Val Met Ile	Ser Asn Leu Lys Gly					
	115 120 125					
atg gaa att ttg cac tgc att cag aaa gga gtc	tat gtg aca gtc atc	765				
Met Glu Ile Leu His Ser Ile Gln Lys Gly Val	Tyr Val Thr Val Ile					
	130 135 140					
att gaa gtg ggg aga atg cac atg cag tgg gtg	agc cat tac atc atg	813				
Ile Glu Val Gly Arg Met His Met Gln Trp Val	Ser His Tyr Ile Met					
	145 150 155					
tat cta ttt acc ttc ctg gct gcc aca att gcc	tac ttt tac tta gat	861				
Tyr Leu Phe Thr Phe Leu Ala Ala Thr Ile Ala	Tyr Phe Tyr Leu Asp					
	160 165 170					
tgc gtc tgg aga ctt aca cct aga gtg ccc aat	tct ttc acc agg agg	909				
Cys Val Trp Arg Leu Thr Pro Arg Val Pro Asn	Ser Phe Thr Arg Arg					
	175 180 185 190					
cga agt caa ata aag aca gat gtg aag aaa gct	att gac cag ctt caa	957				
Arg Ser Gln Ile Lys Thr Asp Val Lys Lys Ala	Ile Asp Gln Leu Gln					
	195 200 205					
ctg cga gtt ctc aaa gaa ggg gat gag gaa tta	gac cta aat gaa gac	1005				
Leu Arg Val Leu Lys Glu Gly Asp Glu Glu Leu	Asp Leu Asn Glu Asp					
	210 215 220					
aac tgt gtt gtt tgc ttt gac aca tac aaa ccc	caa gat gta cgc	1053				
Asn Cys Val Val Cys Phe Asp Thr Tyr Lys Pro	Gln Asp Val Val Arg					
	225 230 235					
att tta act tgc aaa cat ttt ttc cat aag gca	tgc att gac ccc tgg	1101				

Ile	Leu	Thr	Cys	Lys	His	Phe	Phe	His	Lys	Ala	Cys	Ile	Asp	Pro	Trp		
240						245					250						
ctt	tta	gcc	cat	agg	aca	tgt	ccc	atg	tgc	aag	tgt	gac	atc	ctg	aaa	1149	
Leu	Leu	Ala	His	Arg	Thr	Cys	Pro	Met	Cys	Lys	Cys	Asp	Ile	Leu	Lys		
255					260					265				270			
act	taagaaatct	ggagaatttt	ctgaagatgt	aaccagatct	ttccaaatac											1202	
Thr																	
aaagattaga	taaattgtct	tattgtactt	tatgtagaga	gaaaatttca	gcttctctac											1262	
ccaagtatga	acaaggggtga	aatttgtgtt	ttaaaaataa	aactccttat	catgcccagc											1322	
taaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaa													1355	

<210> 42
 <211> 572
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 187..369

<220>
 <221> sig_peptide
 <222> 187..312
 <223> Von Heijne matrix
 score 7.10
 seq LLPCSSVLTCGQA/SQ

<220>
 <221> polyA_signal
 <222> 489..494

<220>
 <221> polyA_site
 <222> 558..572

<220>
 <221> misc_feature
 <222> 94,527,537..538
 <223> n=a, g, c or t

<400>	42																
cttcttcag	cagtggtgg	ataatcta	atataatgt	taatccat	ca tttctct	tttt										60	
tgaacagt	ca atttagt	tta acatttg	cct aacnag	ccat tatgtat	gcc aggta	atgtg										120	
ctagatg	ctg gtggtt	caaaa gaaagga	acg atgtgg	acct gacct	caaag aaatcc	attg										180	
gagaat	atg aca gat	tta gat tta	atg atc aac	ttt act ttt	cct ata											228	
	Met Thr	Asp Leu	Asp Leu	Met Ile	Asn Phe	Thr Phe	Pro	Ile									
	-40			-35			-30										
cag tgg	gtc aac	caa aac	cgc atg	gcg tac	tac tct	ctg aag	cct cta									276	
Gln Trp	Val Asn	Gln Asn	Arg Met	Ala Tyr	Tyr Ser	Leu Lys	Pro Leu										
	-25		-20		-15												
cta ccc	tgc tcc	tcc gtg	ttg aca	tgt ggt	cag gca	agc cag	gac tta									324	
Leu Pro	Cys Ser	Ser Val	Leu Thr	Cys Gly	Gln Ala	Ser Gln	Asp Leu										
	-10		-5		1												
ctc aca	tca gct	aca tca	ggt act	ggg atg	gag aaa	att gaa	gcc									369	
Leu Thr	Ser Ala	Thr Ser	Val Thr	Gly Met	Glu Lys	Ile Glu	Ala										
5		10		15													
tagaaag	atc aagaa	acttt ctccagg	cca taaatag	agg aatcagg	att caaatc	agat										429	
agacccc	agc gcttg	ttctc ttcaac	acca cattacc	ccta cattatt	att caattat	taa										489	
ataaaac	ctt gcattag	tgg catttcc	aaa tgcata	anca aaaaaat	nna aaaaaaa	agta										549	
acactgg	caa aaaaaaaa	aaa														572	

109360-109360

Variable	Mean	SD	Min	Max
Age	38.5	10.5	25	55
Gender	50%	50%	0	100
Marital status	75%	25%	0	100
Education	12.5	2.5	9	16
Income	15.5	3.5	10	25
Occupation	1.5	1.5	0	3
Health status	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	100
Self-esteem	75%	25%	0	100
Life satisfaction	75%	25%	0	100
Stress	75%	25%	0	100
Depression	75%	25%	0	100
Loneliness	75%	25%	0	1

```
<220>
<221> sig_peptide
<222> 121..165
<223> Von Heijne matrix
      score 4.20
      seq FYLLLLASSILCAL/IV
```

```
<220>  
<221> polyA_site  
<222> 521..535
```

```
<220>  
<221> misc_feature  
<222> 486,489  
<223> n=a, g, c or t
```

```
<210> 44
<211> 572
<212> DNA
<213> Homo Sapiens
```

<220>
 <221> CDS
 <222> 34..336

<220>
 <221> sig_peptide
 <222> 34..123
 <223> Von Heijne matrix
 score 7.80
 seq SVTLAQLQLVQQ/GQ

<220>
 <221> polyA_signal
 <222> 536..541

<220>
 <221> polyA_site
 <222> 556..572

<220>
 <221> misc_feature
 <222> 545
 <223> n=a, g, c or t

<400> 44
 gcattacacg ccggtcagga ttcgcgaccc gac atg gag cgt ccc cgc agt ccc 54
 Met Glu Arg Pro Arg Ser Pro
 -30 -25
 caa tgc tcg gcc ccg gcc tct gcc tca gct tcg gtt acc ctg gcg cag 102
 Gln Cys Ser Ala Pro Ala Ser Ala Ser Val Thr Leu Ala Gln
 -20 -15 -10
 ctc ctg cag ctg gtc cag cag ggc cag gaa ctc ccg ggc ctg gag aaa 150
 Leu Leu Gln Leu Val Gln Gln Gly Gln Glu Leu Pro Gly Leu Glu Lys
 -5 1 5
 cgc cac atc gcg gcg atc cac ggc gaa ccc aca gcg tcc cgg ctg ccg 198
 Arg His Ile Ala Ala Ile His Gly Glu Pro Thr Ala Ser Arg Leu Pro
 10 15 20 25
 cgg agg ccc aag ccc tgg gag gcc gcg gct ttg gct gag tcc ctt ccc 246
 Arg Arg Pro Lys Pro Trp Glu Ala Ala Ala Leu Ala Glu Ser Leu Pro
 30 35 40
 cct ccg acc ctc agg ata gga acg gcc ccg gcg gag cct ggc ttg gtt 294
 Pro Pro Thr Leu Arg Ile Gly Thr Ala Pro Ala Glu Pro Gly Leu Val
 45 50 55
 gag gca gcg act gcg cct tct tca tgg cat aca gtg ggc ccc 336
 Glu Ala Ala Thr Ala Pro Ser Ser Trp His Thr Val Gly Pro
 60 65 70
 tgaggttcca ggtcctttgc ggcggcgatc tggagggcgt ggctacagga cccgggatgc 396
 cattcagtta ctcattttt atgctttcgt cctgacctgt ctcaactaga cttgctcctg 456
 caaccacccat ggggggttttg catttacatt tgtggaccat gttacagtta agaaaaatcc 516
 tgtttcagtc cttatatgta ataaaatgnt ttatgatgca aaaaaaaaaa aaaaaa 572

<210> 45
 <211> 804
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 119..409

<220>
 <221> sig_peptide
 <222> 119..388
 <223> Von Heijne matrix
 score 4.30
 seq TCLTACWTALCCC/CL

<220>
 <221> polyA_signal
 <222> 769..774

<220>
 <221> polyA_site
 <222> 789..804

<220>
 <221> misc_feature
 <222> 274
 <223> n=a, g, c or t

<220>
 <221> unsure
 <222> -39
 <223> Xaa = His,Gln

<400> 45
 acttgctctg agacaggtgc ggcaagtcta ctgcgggctg gtccgggctc ctcaggttca 60
 gacccgaccg ttatccagtc ggttcgtgga gaggagaggt gcactttaca ggtcccca 118
 atg aac caa gag aac cct cca cca tat cca ggc cct ggt cca acg gcc 166
 Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
 -90 -85 -80 -75
 cca tac cca cct tat cca cca caa cca atg ggt cca gga cct atg ggg 214
 Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Pro Met Gly
 -70 -65 -60
 gga ccc tac cca cct cct caa ggg tac ccc tac caa gga tac cta cag 262
 Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Leu Gln
 -55 -50 -45
 tac ggc tgg can ggt gga cct cag gag cct cct aaa acc aca gtg tat 310
 Tyr Gly Trp Xaa Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
 -40 -35 -30
 gtg gta gaa gac caa aga aga gat gag cta gga cca tcc acc tgc ctc 358
 Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
 -25 -20 -15
 aca gcc tgc tgg acg gct ctc tgt tgc tgc tgt ctc tgg gac atg ctc 406
 Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp Asp Met Leu
 -10 -5 1 5
 acc tgaccagacc agcccagccg tctgtctctg ccagctctgc tgccacctct 459
 Thr
 gacaggtgtg cctgccccca tctcttctga ttgctgttaa caaatgacta gctttgcaca 519
 gacacctcta ccttcagcac tatgggattc tagattaatg ggggttgcta ctgtttaatt 579
 cagtgacttg atctttttta tgtccaaaat ccatttctta ttgatcttta aagatgtgct 639
 aaatgacttt tttggccaaa ggcttagttg tgaaaaatat aattttttaa ttatacatc 699
 aaggtagtgg ccaaatgtaa cacatcaatc atggaatgat ttctctgcta acagccgcct 759
 gtatgtttca ataaatttgt ccaaagctca aaaaaaaaaa aaaaa 804

<210> 46
 <211> 629
 <212> DNA
 <213> Homo Sapiens

<220>

```

<221> CDS
<222> 232..534

<220>
<221> sig_peptide
<222> 232..306
<223> Von Heijne matrix
      score 3.70
      seq AKTCLVLCSRVLV/VI

<220>
<221> polyA_signal
<222> 595..600

<220>
<221> polyA_site
<222> 615..629

<400> 46
tatcactggtt acgaaccaag gatttacaga tcaactggcaa aaattctgag aactttcaca      60
ccagtatact gtccaagccc attaagtggc atcacacctc tcttttatgt agctcagaca      120
agacagtcta atatcttcaa aatactactg caatatggaa tcttagaaaag agaaaaaaaaac      180
cctatcaaca ttgtcttaac aatagtactc tacccttcga gagtaagagt a atg gtt      237
                                   Met Val
                                   -25
gat cgt gaa ttg gct gac atc cat gaa gat gcc aaa aca tgt ttg gta      285
Asp Arg Glu Leu Ala Asp Ile His Glu Asp Ala Lys Thr Cys Leu Val
                                   -20               -15               -10
cta tgt tcc aga gtg ctt tct gtc att tca gtc aag gaa ata aag aca      333
Leu Cys Ser Arg Val Leu Ser Val Ile Ser Val Lys Glu Ile Lys Thr
                                   -5               1               5
cag ctg agt tta gga aga cat cca att att tca aat tgg ttt gat tac      381
Gln Leu Ser Leu Gly Arg His Pro Ile Ile Ser Asn Trp Phe Asp Tyr
10               15               20               25
att cct tca aca aga tac aaa gat cca tgt gaa cta tta cat ctt tgc      429
Ile Pro Ser Thr Arg Tyr Lys Asp Pro Cys Glu Leu Leu His Leu Cys
                                   30               35               40
aga cta acc atc agg aat caa cta tta acc aac aat atg ctc cca gat      477
Arg Leu Thr Ile Arg Asn Gln Leu Leu Thr Asn Asn Met Leu Pro Asp
                                   45               50               55
gga ata ttt tca ctt cta att cct gct cgt cta caa aac tat ctg aat      525
Gly Ile Phe Ser Leu Leu Ile Pro Ala Arg Leu Gln Asn Tyr Leu Asn
60               65               70
tta gaa atc taacatacgt cagtgtccta agttccttaa caatgcttac      574
Leu Glu Ile
75
caatgtatgg cttagaagtt aataaaaatt cacttcatgc aaaaaaaaaa aaaaa      629

<210> 47
<211> 669
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 140..595

<220>
<221> sig_peptide
<222> 140..442
<223> Von Heijne matrix

```


[illegible]

```
<220>
<221> polyA_site
<222> 655..669
```

```
<210> 48
<211> 973
<212> DNA
<213> Homo Sapiens
```

```
<220>  
<221> CDS  
<222> 32..658
```

```
<220>
<221> sig_peptide
<222> 32..289
<223> Von Heijne matrix
      score 4.00
```

seq KLWKLLFLMKSQG/WI

<220>
<221> polyA_signal
<222> 936..941

<220>
<221> polyA_site
<222> 959..973

<220>
<221> misc_feature
<222> 934
<223> n=a, g, c or t

<400> 48
aggagagagg atggctagt aggttttagat c atg ttg agc cct acc ttt gtt 52
Met Leu Ser Pro Thr Phe Val
-85 -80
ttg tgg gat gtt gga tat ccc tta tac acc tat gga tcc atc tgc att 100
Leu Trp Asp Val Gly Tyr Pro Leu Tyr Thr Tyr Gly Ser Ile Cys Ile
-75 -70 -65
att gca tta att att tgg caa gtg aaa aag agc tgc caa aaa tta agc 148
Ile Ala Leu Ile Ile Trp Gln Val Lys Lys Ser Cys Gln Lys Leu Ser
-60 -55 -50
ttg gta cct aac agg agc tgt tgc cgg tgt cac cga aga gtc caa caa 196
Leu Val Pro Asn Arg Ser Cys Cys Arg Cys His Arg Arg Val Gln Gln
-45 -40 -35
aag tct gga gat aga aca tca aga gct agg aga act tca cag gaa gaa 244
Lys Ser Gly Asp Arg Thr Ser Arg Ala Arg Arg Thr Ser Gln Glu Glu
-30 -25 -20
gcc gag aag ttg tgg aag ctg ctg ttt ctc atg aaa agc cag ggc tgg 292
Ala Glu Lys Leu Trp Lys Leu Leu Phe Leu Met Lys Ser Gln Gly Trp
-15 -10 -5 1
att cct cag gaa gga agt gtg cgg cga atc ctg tgt gca gac ccc tgc 340
Ile Pro Gln Glu Gly Ser Val Arg Arg Ile Leu Cys Ala Asp Pro Cys
5 10 15
tgc caa atc tgc aat gtt atg gct ctg gag att aag caa ttg ctg gca 388
Cys Gln Ile Cys Asn Val Met Ala Leu Glu Ile Lys Gln Leu Leu Ala
20 25 30
gaa gct cca gaa gtt ggc ttg gat aac aag atg aag ctg ttt ctg cac 436
Glu Ala Pro Glu Val Gly Leu Asp Asn Lys Met Lys Leu Phe Leu His
35 40 45
tgg att aac cct gaa atg aaa gat cga agg cat gag gaa tcc att ctc 484
Trp Ile Asn Pro Glu Met Lys Asp Arg Arg His Glu Glu Ser Ile Leu
50 55 60 65
ctt tct aag gct gag aca gtg acc caa gac agg aca aaa aac att gag 532
Leu Ser Lys Ala Glu Thr Val Thr Gln Asp Arg Thr Lys Asn Ile Glu
70 75 80
aag agt cca act gtc acc aaa gat cat gtg tgg gga gct aca aca cag 580
Lys Ser Pro Thr Val Thr Lys Asp His Val Trp Gly Ala Thr Thr Gln
85 90 95
aag aca aca gag gac cct gag gct cag cct cct tct act gag gag gaa 628
Lys Thr Thr Glu Asp Pro Glu Ala Gln Pro Pro Ser Thr Glu Glu Glu
100 105 110
ggc ctg atc ttc tgt gat gcc ccc agt gcc taaataatct gctctagcaa 678
Gly Leu Ile Phe Cys Asp Ala Pro Ser Ala
115 120
cactcccttc agtccagcca atcctgggtc ctgtgccact cctacaaatg ctccaaactc 738
tgtcctcaaa tgacttgtgc cactcaacca ggaaatctat cccaggtcta actcacctca 798
gcagaaggca ctgttttatg caagaatacc catcacaaga aaaaggagtt cataggttcc 858

0993350 "101501

tgaacctctg caatcccctg aaaaaggctt tcattgccat ttccattaac atgcagggtga 918
 agcaggggcat tctccnaaat atactttgta cctttaagct aaaaaaaaaa aaaaaa 973

<210> 49
 <211> 791
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 14..280

<220>
 <221> sig_peptide
 <222> 14..76
 <223> Von Heijne matrix
 score 9.50
 seq ALVVLCAFQLVAA/LE

<220>
 <221> polyA_site
 <222> 776..791

<220>
 <221> misc_feature
 <222> 607
 <223> n=a, g, c or t

<400> 49
 ataggcgcg acc atg ggc tcc tgc tcc ggc cgc tgc gcg ctc gtc gtc 49
 Met Gly Ser Cys Ser Gly Arg Cys Ala Leu Val Val
 -20 -15 -10
 ctc tgc gct ttt cag ctg gtc gcc gcc ctg gag agg cag gtg ttt gac 97
 Leu Cys Ala Phe Gln Leu Val Ala Ala Leu Glu Arg Gln Val Phe Asp
 -5 1 5
 ttc ctg ggc tac cag tgg gcg ccc atc ctg gcc aac ttt gtc cac atc 145
 Phe Leu Gly Tyr Gln Trp Ala Pro Ile Leu Ala Asn Phe Val His Ile
 10 15 20
 atc atc gtc atc ctg gga ctc ttc ggc acc atc cag tac cgg ctg cgc 193
 Ile Ile Val Ile Leu Gly Leu Phe Gly Thr Ile Gln Tyr Arg Leu Arg
 25 30 35
 tat gtc atg tgt aca cgc tgt ggg cag cgg tct ggg tca cct gga acg 241
 Tyr Val Met Cys Thr Arg Cys Gly Gln Pro Ser Gly Ser Pro Gly Thr
 40 45 50 55
 tct tca tca tct gct tct acc tgg aag tgc gtg gcc tct taaaggacag 290
 Ser Ser Ser Ser Ala Ser Thr Trp Lys Ser Val Ala Ser
 60 65
 cgagctactg accttcagcc tctcccggca tcgctcctgg tggcgtgagc gctggccagg 350
 ctgtctgcat gaggaggtgc cagcagtggg cctcgggggc ccccatggcc aggccttggg 410
 gtcagggtgct ggctgtgcca tggagcccag ctatgtggag gccctacaca gtgcctgca 470
 gatcctgata gcgcttctgg gctttgtctg tggctgccag gtggtcagcg tgtttacgga 530
 ggaagaggac agctgcctgc gtaagtgagg aaacagctga tctgtctcct gtggcctcca 590
 gcctcagcga ccgaccnagt gacaatgaca ggagctccca ggccttggga cgcgccccca 650
 ccagcagccc ccagggcggc cggcagcacc tgccctgggt tctaagtact ggacaccagc 710
 cagggcggca gggcagtgcc acggctggct gcagcgtcaa gagagtttgt aatttccttt 770
 ctcttaaaaa aaaaaaaaaa a 791

<210> 50
 <211> 1110
 <212> DNA
 <213> Homo Sapiens

09360101601

score 4.19999980926514
seq MLAVSLTVPLLGA/MM

<220>

<221> polyA_site

<222> 1042..1053

<400> 51

gagcgagtcg	gacgggctgc	gacagcgccg	gccctgcgg	ccgcaggtcg	tcacagacga	60
tgatggccag	gccccggagg	ctaaggacgg	cagctccttt	agcggcagag	ttttccgagt	120
gaccttcttg	atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc	169				
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala						
-10						
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa	217					
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys						
1 5 10 15						
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga	265					
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg						
20 25 30						
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata	313					
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile						
35 40 45						
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc	361					
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val						
50 55 60						
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg	409					
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser						
65 70 75 80						
ggc cct tgc aaa acc cga ggt gat gag cct gtg tgt ggg aga ccc ctg	457					
Gly Pro Cys Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu						
85 90 95						
ggg atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tac	505					
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr						
100 105 110						
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg	553					
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu						
115 120 125						
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat	601					
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn						
130 135 140						
gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc gat tct	649					
Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser						
145 150 155 160						
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc	697					
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly						
165 170 175						
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta	745					
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val						
180 185 190						
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct	793					
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser						
195 200 205						
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata	841					
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile						
210 215 220						
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt	889					
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe						
225 230 235 240						
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct	937					
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser						
245 250 255						

0998360 "10501

```

ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
                260                265                270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att      1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
                275                280                285
ttt aag gta aaaaaaaaaa a      1053
Phe Lys Val
                290

```

```

<210> 52
<211> 675
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> polyA_signal
<222> 638..643

```

```

<220>
<221> polyA_site
<222> 662..675

```

```

<400> 52
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      60
gtagcagtgg ttcagcacac tttggtatgt tgactgtta atg atg tac gtt tct      114
                                Met Met Tyr Val Ser
                                1         5
ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc      162
Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
                10                15                20
tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa      210
Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
                25                30                35
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      258
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
                40                45                50
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat      306
Tyr Val Cys Val Phe Ile
                55
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca      366
tattttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga      426
tattttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg      486
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt      546
cagagaagaa catttaaagg gttaatatatt ttgaaacggt ttcagataat atctatttga      606
ttattgtggc ttctatttga aatgtgtcta aaataaatgc tgtttattta aaatgaaaaa      666
aaaaaaaaa      675

```

```

<210> 53
<211> 1112
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> 111..194
<223> Von Heijne matrix
      score 4.80000019073486
      seq GVLLEPFVHQVGG/HS

```

```

<220>

```



```

ggttttattg tgagctggcc ttggaattaa accaccacca acacactttt ggattatcag 180
aaggtggaag gagggtcaaaa atgtcattcc catgcttgtc tgccaggcaa cctgggtgtcc 240
attctttatg acgcctttcc tgaatcacag gtgcattggg gtgcttcctc ctccccagga 300
ctccccacca actttgtgaa cacaaccac ttagaggagt tatctcagca cattatga 358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct 406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
      -30                -25                -20
ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct 454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
      -15                -10                -5
gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc 502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1          5          10          15
acc ttt gcc cat taaagtcaat tctccacca taaaaaaaaa aaa 547
Thr Phe Ala His
      20

```

```

<210> 55
<211> 1198
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> 26..316
<223> Von Heijne matrix
      score 4
      seq RLPLVVSFIASSS/AN

```

```

<220>
<221> polyA_signal
<222> 1164..1169

```

```

<220>
<221> polyA_site
<222> 1187..1198

```

```

<400> 55
atcctgcgaa agaaggggggt tcatc atg gcg gat gac cta aag cga ttc ttg 52
                        Met Ala Asp Asp Leu Lys Arg Phe Leu
                        -95                -90
tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca 100
Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
      -85                -80                -75
gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca 148
Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
      -70                -65                -60
gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca 196
Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
      -55                -50                -45
gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt 244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
      -40                -35                -30                -25
tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg 292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
      -20                -15                -10
gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc 340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
      -5                1                5
cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg 388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val

```


Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala		
80						85					90						
gta	gca	ggg	gga	gtc	ttt	ttc	atc	ctt	gga	ggc	ctc	ctg	gga	ttc	att	437	
Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile		
95					100					105					110		
cct	gtt	gcc	tgg	aat	ctt	cat	ggg	atc	cta	cgg	gac	ttc	tac	tca	cca	485	
Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro		
				115					120					125			
ctg	gtg	cct	gac	agc	atg	aaa	ttt	gag	att	gga	gag	gct	ctt	tac	ttg	533	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	Leu		
			130					135					140				
ggc	att	att	tct	tcc	ctg	ttc	tcc	ctg	ata	gct	gga	atc	atc	ctc	tgc	581	
Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	Leu	Cys		
		145					150					155					
ttt	tcc	tgc	tca	tcc	cag	aga	aat	cgc	tcc	aac	tac	tac	gat	gcc	tac	629	
Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	Asp	Ala	Tyr		
	160				165					170							
caa	gcc	caa	cct	ctt	gcc	aca	agg	agc	tct	cca	agg	cct	ggg	caa	cct	677	
Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	Pro	Gly	Gln	Pro		
175					180					185				190			
ccc	aaa	gtc	aag	agt	gag	ttc	aat	tcc	tac	agc	ctg	aca	ggg	tat	gtg	725	
Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser	Leu	Thr	Gly	Tyr	Val		
			195					200						205			
tgaagaacca	ggggccagag	ctgggggggtg	gctggggtctg	tgaaaaaacag	tggacagcac	785											
cccgaggggcc	acagggtgagg	gacactacca	ctggatcgtg	tcagaagggtg	ctgctgaggg	845											
tagactgact	ttggccattg	gattgagcaa	aggcagaaat	gggggctagt	gtaacagcat	905											
gcagggttgaa	ttgccaaagga	tgctcgccat	gccagccttt	ctgttttcct	caccttgctg	965											
ctcccctgcc	ctaagtcccc	aaccctcaac	ttgaaacccc	attcccttaa	gccaggactc	1025											
agagggatccc	tttgccctct	ggttttacctg	ggactccatc	cccaaaccga	ctaatacacat	1085											
cccactgact	gaccctctgt	gatcaaagac	cctccctctg	gctgagggttg	gctcttagct	1145											
cattgctggg	gatgggaagg	agaagcagtg	gcttttgtgg	gcattgctct	aacctaacttc	1205											
tcaagcttcc	ctccaaagaa	actgattggc	cctggaacct	ccatcccact	cttgttatga	1265											
ctccacagtg	tccagactaa	tttgtgcatg	aactgaaata	aaaccatcct	acggtatcca	1325											
gggaacagaa	agcaggatgc	aggatgggag	gacaggaagg	cagcctggga	catttaaaaa	1385											
aataaaaaaa	aaaaa					1400											

<210> 57
 <211> 538
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 35..130
 <223> Von Heijne matrix
 score 8
 seq VPMLLLIAGGSFG/LR

<220>
 <221> polyA_signal
 <222> 505..510

<220>
 <221> polyA_site
 <222> 526..538

<400> 57
 gcttgaggtt ctgagccgat ggaggagttc actc atg ttt gca ctc gcg gtg atg 55
 Met Phe Ala Leu Ala Val Met
 -30
 cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg 103

Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu	
-25 -20 -15 -10	
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc	151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile	
-5 1 5	
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa	199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys	
10 15 20	
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc	247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile	
25 30 35	
tgt tgaagggcta ctatctttcc ttggcccttc tcccttgttg ggactcaatc	300
Cys	
40	
tccagactat ctccccagag aatcttgtca aggcttggct ttaagctttg ttgggaaaat	360
caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt gggaagatcc	420
tgacctcttc caaggaagaa atccagaaaag ccttaagact aagacaactt gactctgctg	480
attctttttt cctttttttt tttaaataaa aatactatta actggaaaaa aaaaaaaa	538
<210> 58	
<211> 1167	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> sig_peptide	
<222> 169..267	
<223> Von Heijne matrix	
score 7.80000019073486	
seq LTFLFLHLPPTS/LF	
<220>	
<221> polyA_signal	
<222> 1132..1137	
<220>	
<221> polyA_site	
<222> 1155..1167	
<400> 58	
gtaggaacta ctgtcccaga gctgaggcaa ggggatttct caggtcattt ggagaacaag	60
tgcttttagta gtagtttaaa gtagtaactg ctactgtatt tagtggggtg gaattcagaa	120
gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag	177
Met Ser Gln	
aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct	225
Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser	
-30 -25 -20 -15	
gcc ctt aca ttt ttg ttt ctc cat cta cca cca tcc acc agt cta ttt	273
Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe	
-10 -5 1	
att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg	321
Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu	
5 10 15	
ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc	369
Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser	
20 25 30	
tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa	417
Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys	
35 40 45 50	
aga aaa aca aaa tgc taatgaagcc atcagtcaag gggtcacatgc caataaacia	472
Arg Lys Thr Lys Cys	

55

taaat	ttttcc	agaaga	aatg	aatcca	act	agacaa	ataa	agtaga	gctt	atgaa	atggt	532
tcagta	agga	tgagct	tgtt	gttttt	tgtt	ttgttt	tgtt	ttgttt	tttt	aaaga	cggag	592
tctcgct	ctg	tcactc	aggc	tggagt	gcag	tggtat	gatc	ttggct	cact	gtaac	ctccg	652
cctcccg	gggt	tcaagc	catt	ctcctg	cctc	agtctc	cctga	gtagct	ggga	ttgcag	gtgc	712
gtgccac	cat	gcctgg	ctaa	tttttg	tgtt	tttggt	tagag	acaggg	tttc	accacg	ttgg	772
tcgggct	ggt	ctcggg	ctcc	tgacct	cttg	atccgc	cctgc	cttggc	ctcc	caaagt	gatg	832
ggattac	aga	tgtgag	ccac	cgtgc	ctagc	caaggat	gag	attttta	aaag	tatgtt	ccag	892
ttctgtg	tca	tggttg	gaag	acagag	tagg	aaggat	atgg	aaaagg	gtcat	gggga	agcag	952
aggtgatt	ca	tggctc	tgtg	aatttg	aggt	gaatgg	ttcc	ttattg	tcta	ggccac	ttgt	1012
gaagaat	atg	agtcag	ttat	tgccag	cctt	ggaatt	tact	tctcta	gctt	acaatg	ggacc	1072
ttttga	actg	ggaaac	acct	tgtctg	catt	cacttta	aaaa	tgtcaaa	act	aattttt	tata	1132
ataaatg	gttt	attttc	acat	cgaaaa	aaaaa	aaaaa						1167

<210> 59

<211> 730

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 143..238

<223> Von Heijne matrix

score 8.80000019073486

seq VPMLLLIVGGSFG/LR

<220>

<221> polyA_signal

<222> 697..702

<220>

<221> polyA_site

<222> 721..730

<220>

<221> misc_feature

<222> 1,14,28,52

<223> n=a, g, c or t

<400> 59

nctttg	cctt	tctntc	caca	gggtgc	cnct	cccagg	tcca	actgcag	act	tngaatt	cgt	60
cttggt	gaga	gcgtga	gctg	ctgagatt	tgg	ggagtc	tgcg	ctaggccc	gc	ttggagt	tct	120
gagccg	atgg	aagagt	tcac	tc	atg	ttt	gca	ccc	gcg	gtg	acg	172

Met Phe Ala Pro Ala Val Thr Arg Ala Phe

-30

-25

cgc	aag	aac	aag	act	ctc	ggc	tat	gga	gtc	ccc	atg	ttg	ttg	ctg	att	220
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Arg	Lys	Asn	Lys	Thr	Leu	Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

-20

-15

-10

ggt	gga	ggt	tct	ttt	ggg	ctt	cgt	gag	ttt	tct	caa	atc	cga	tat	gat	268
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val	Gly	Gly	Ser	Phe	Gly	Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

-5

1

5

10

gct	gtg	aag	agt	aaa	atg	gat	cct	gag	ctt	gaa	aaa	aaa	ctg	aaa	gag	316
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala	Val	Lys	Ser	Lys	Met	Asp	Pro	Glu	Leu	Glu	Lys	Lys	Leu	Lys	Glu	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

15

20

25

aat	aaa	ata	tct	tta	gag	tcg	gaa	tat	gag	aaa	atc	aaa	gac	tcc	aag	364
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asn	Lys	Ile	Ser	Leu	Glu	Ser	Glu	Tyr	Glu	Lys	Ile	Lys	Asp	Ser	Lys	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

30

35

40

ttt	gat	gac	tgg	aag	aat	att	cga	gga	ccc	agg	cct	tgg	gaa	gat	cct	412
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Phe	Asp	Asp	Trp	Lys	Asn	Ile	Arg	Gly	Pro	Arg	Pro	Trp	Glu	Asp	Pro	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

45

50

55

gac	ctc	ctc	caa	gga	aga	aat	cca	gaa	agc	ctt	aag	act	aag	aca	act	460
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp	Leu	Leu	Gln	Gly	Arg	Asn	Pro	Glu	Ser	Leu	Lys	Thr	Lys	Thr	Thr	
60						65					70					
tgactctgct	gattctcttt	tccttttttt	ttttaataaa	aaatactatt	aactggactt											520
cctaatatat	acttctatca	agtggaaagg	aaattccagg	cccatggaaa	cttggatatg											580
ggtaatttga	tgacaaaata	tcttcactaa	aggtcatgta	caggttttta	tacttcccag											640
ctattccatc	tgtggatgaa	agtaacaatg	ttggccacgt	atattttaca	cctcgaaata											700
aaaaatgtga	atactgctcc	aaaaaaaaaa														730

<210> 60
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 108..170
 <223> Von Heijne matrix
 score 5.5
 seq SFLPSALVIWTSA/AF

<220>
 <221> polyA_signal
 <222> 1141..1146

<220>
 <221> polyA_site
 <222> 1161..1174

<400> 60																	
cacgttcctg	ttgagtacac	gttcctgttg	atttacaaaa	ggtgcaggta	tgagcaggtc												60
tgaagactaa	cattttgtga	agttgtaaaa	cagaaaacct	gtagaa	atg tgg tgg												116
					Met Trp Trp												
					-20												
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca																	164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr																	
	-15					-10											
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat																	212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His																	
	1					5											
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca																	260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro																	
	15					20											30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc																	308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys																	
						35											45
att gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct																	356
Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro																	
						50											60
gaa gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga																	404
Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly																	
						65											75
ata ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag aaa aca																	452
Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Lys Thr																	
						80											90
acc ctt ttt gct gca cat gta agt gga gct gtg ctt acc ttt ggt atg																	500
Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr Phe Gly Met																	
						95											110
ggc tca tta tat atg ttt gtt cag acc atc ctt tcc tac caa atg cag																	548
Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln																	
						115											125
ccc aaa atc cat ggc aaa caa gtc ttc tgg atc aga ctg ttg ttg gtt																	596

```

Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val
      130      135      140
atc tgg tgt gga gta agt gca ctt agc atg ctg act tgc tca tca gtt      644
Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val
      145      150      155
ttg cac agt ggc aat ttt ggg act gat tta gaa cag aaa ctc cat tgg      692
Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
      160      165      170
aac ccc gag gac aaa ggt tat gcg ctt cac atg atc act act gca gca      740
Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr Thr Ala Ala
      175      180      185      190
gaa tgg tct atg tca ttt tcc ttc ttt ggt ttt ttc ctg act tac att      788
Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile
      195      200      205
cgt gat ttt cag aaa att tcc tta cgg gtg gaa gcc aac tta cat gga      836
Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn Leu His Gly
      210      215      220
tta acc ctc tat gac act gca cct tgc cct att aac aat gaa cga aca      884
Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn Glu Arg Thr
      225      230      235
cgg cta ctt tcc aga gat att aga tgaaaggata aaatatttct gtaatgatta      938
Arg Leu Leu Ser Arg Asp Ile Arg
      240      245
tgattctcag ggattgggga aaggttcaca gaagttgctt attcttctct gaaattttca      998
accacttaat caaggctgac agtaacactg atgaatgctg ataatcagga aacatgaaag      1058
aagccatttg atagattatt cttaaaggata tcatcaagaa gactattaaa aacacctatg      1118
cctatacttt tttatctcag aaaataaagt caaaagacta tgaaaaaaaa aaaaaa      1174

<210> 61
<211> 1158
<212> DNA
<213> Homo sapiens

<220>
<221> polyA_signal
<222> 1133..1138

<220>
<221> polyA_site
<222> 1146..1158

<220>
<221> misc_feature
<222> 652
<223> n=a, g, c or t

<400> 61
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcatctt ggatttgaaa gttgagagca gcatgttttg ccactgaaa ctcacctgts      120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgctgagct      180
aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca      232
                        Met Gly Cys Val Phe Gln Ser Thr
                        1                5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
      10      15      20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
      25      30      35      40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu

```


actttttcttg	acttgccctgt	tttggccatt	agctgcctta	aacgttaaca	gcacatttga	361
atgccttatt	ctacaatgca	gcgtgttttc	ctttgccttt	tttgcacttt	ggtgaattac	421
gtgcctccat	aacctgaact	gtgccgactc	cacaaaacga	ttatgtactc	ttctgagata	481
gaagatgctg	ttcttctgag	agatacgta	ctctctcctt	ggaatctgtg	gatttgaaga	541
tggctcctgc	cttctcacgt	gggaatcagt	gaagtgttta	gaaactgctg	caagacaaac	601
aagactccag	tggggtgggc	agtaggagag	cacgttcaga	gggaagagcc	atctcaacag	661
aatcgcacca	aactatactt	tcaggatgaa	tttcttcttt	ctgccatctt	ttggaataaa	721
tattttcctc	ctttctatgt	aaaaaaaaaa	aaa			754

<210> 63
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 98..181
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PLSDSWALLPASA/GV

<220>
 <221> polyA_signal
 <222> 1035..1040

<220>
 <221> polyA_site
 <222> 1060..1073

<400> 63																					
c	c	g	a	t	t	a	c	a	g	t	t	a	c	a	g	g	a	g	t		60
c	g	t	g	g	g	g	a		g	c	t	c	c	g	c	c		c	g	t	115
Met Trp Arg Leu Leu Ala																					
-25																					
c	g	c		g	c	t	c	t	c	g	g	t	g	c	c	t	t	g	g	a	163
A	r	g	A	S	e	r	A	P	r	o	L	e	u	L	e	u	A	r	g	V	
-20 -15 -10																					
c	t	c	c	c	c	c	g	a	g	t	g	g	c	g	t	a	a	a	c	a	211
L	e	u	L	e	u	P	r	o	A	L	a	S	e	r	A	L	a	G	l	y	
-5 1 5 10																					
t	t	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	259
P	h	e	G	l	u	A	s	p	V	a	l	S	e	r	I	l	e	P	r	o	
15 20 25																					
a	g	g	g	a	c	c	a	c	t	t	g	t	g	c	c	a	a	a	a	a	307
A	r	g	A	L	a	P	r	o	L	e	u	V	a	l	P	r	o	L	ys	V	
30 35 40																					
g	a	c	a	t	a	c	g	g	a	c	c	t	t	c	c	a	a	a	a	a	355
A	s	p	I	l	e	A	r	g	G	l	y	P	r	o	S	e	r	T	h	r	
45 50 55																					
t	t	t	g	a	a	t	t	g	a	a	t	t	g	g	t	g	g	t	g	g	403
P	h	e	A	L	a	I	L	e	u	A	L	a	L	e	u	G	l	y	G	l	
60 65 70																					
g	a	a	a	t	g	a	t	g	c	g	c	t	g	a	c	a	a	c	a	a	451
G	l	u	M	e	t	M	e	t	A	r	g	L	e	u	T	h	r	I	a	s	
75 80 85 90																					
t	t	t	g	c	c	a	t	a	t	g	g	a	g	t	a	a	a	a	a	a	499
P	h	e	A	L	a	I	L	e	u	T	r	p	A	r	g	V	a	l	P	r	
95 100 105																					
a	g	t	g	t	g	g	a	c	a	t	g	g	g	a	g	g	a	a	a	a	547
S	e	r	V	a	l	G	l	y	H	i	s	A	r	g	M	e	t	G	l	y	
110 115 120																					


```

gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt      595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg
      125      130      135
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag      643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys
      140      145      150
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg      691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met
      155      160      165      170
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca      739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr
      175      180      185
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg      787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu
      190      195      200
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac      835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr
      205      210      215
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag      890
Met Pro Lys Arg Val
      220
aaggattctg catttctatt cccctcagcc taccactga agtctttggg tagctcttaa      950
gccataacta aggagcagca tttgagtaga tttctgaaaa acgatgttat ttgttgattt      1010
aaaaagaaaa ctgtattttt attaaataaa atttaaacad cacttcagga aaaaaaaaaa      1070
aaa                                                                1073

<210> 64
<211> 413
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 46..189
<223> Von Heijne matrix
      score 4.09999990463257
      seq VFMLIVSVLALIP/ET

<220>
<221> polyA_signal
<222> 377..382

<220>
<221> polyA_site
<222> 402..413

<400> 64
tgagaagagt tgaggggaaag tgctgctgct ggggtctgcag acgcg atg gat aac gtg      57
                                Met Asp Asn Val
                                -45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
      -40      -35      -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
      -25      -20      -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
      -10      -5      1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys

```

```

5          10          15          20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc 297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
          25          30          35
ggg cct tac cag aaa aag cct gtg cat gaa aaa gaa gtt ttg 342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
          40          45          50
taattttata ttacttttta gtttgatact aagtattaaa catattttctg tattctttcca 402
aaaaaaaaaa a 413

```

```

<210> 65
<211> 609
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> 139..231
<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR

```

```

<220>
<221> polyA_signal
<222> 579..584

```

```

<220>
<221> polyA_site
<222> 598..609

```

```

<400> 65
tgtcggagtt ggaaagggac gcctgggtttc cccccaagcg aaccgggatg ggaagtgact 60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag 120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt 171
          Met Ser Asn Thr His Thr Val Leu Val Ser Leu
          -30          -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac 219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20          -15          -10          -5
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct 267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro
          1          5          10
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc 315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe
          15          20          25
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg 363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser
          30          35          40
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta 411
Ala Asp Arg Cys Asp Leu
          45          50
ttttatcctt gacttggtag aagttttggg atttctgaaa agaccataca gataaccaca 471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct 531
tcccacctcc ttogaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg 591
agctgcaaaaa aaaaaaaaaa 609

```

```

<210> 66
<211> 522
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> polyA_site
<222> 512..522

<220>
<221> misc_feature
<222> 11
<223> n=a, g, c or t

<400> 66
ccaactgcag nttcgaattt accgagcgga gaggagatgc acacggcact cgagtgtgag      60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt      110
          Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys
          1          5          10
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat      158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His
          15          20          25
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa      206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu
          30          35          40          45
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa      254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys
          50          55          60
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta      302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu
          65          70          75
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag      350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu
          80          85          90
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt      398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val
          95          100          105
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca      446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser
          110          115          120          125
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act      494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr
          130          135          140
gtg acc agt gta tcc aca aaaaaaaaaa      522
Val Thr Ser Val Ser Thr
          145

<210> 67
<211> 1322
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..260
<223> Von Heijne matrix
      score 4.59999990463257
      seq VLVYLVTAE RVWS/DD

<220>
<221> polyA_signal
<222> 1283..1288

<220>
<221> polyA_site
<222> 1309..1322

```

```

<400> 67
ccgaaaacct tccccgcttc tggatatgaa attcaagctg cttgctgagt cctattgccg      60
gctgctggga gccaggagag ccctgaggag tagtcactca gtagcagctg acgcgtgggt      120
ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag      170
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
      -45              -40              -35
tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc      218
Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
      -30              -25              -20              -15
cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac      266
Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
      -10              -5              1
cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc      314
His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
      5              10              15
tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg      362
Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
      20              25              30
cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg      410
Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
      35              40              45              50
gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag      458
Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
      55              60              65
aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc      506
Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
      70              75              80
tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc      554
Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
      85              90              95
gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct      602
Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
      100              105              110
cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc      650
Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys
      115              120              125              130
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg      698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val
      135              140              145
gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac      746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr
      150              155              160
ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa      794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln
      165              170              175
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa      842
Ala Met Cys Thr Gly His His Pro His Asp Thr Ser Ser Cys Lys
      180              185              190
caa gac gac ctc ctt tgc ggt gac ctc atc ttt ctg ggc tca gac agt      890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser
      195              200              205              210
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc      938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr
      215              220              225
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct      994
Ile Leu
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag      1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct      1114
gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg tttccttttc      1174
tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg ttcatagaag      1234

```

aacacacatg cgggcacctt catcgtgtgt ggcccactgt cagaacttaa taaaagtcaa 1294
ctcatttgct ggttaaaaaa aaaaaaaa 1322

<210> 68
<211> 1290
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 50..160
<223> Von Heijne matrix
score 4
seq PLSLDCGHSLCRA/CI

<220>
<221> polyA_site
<222> 1280..1290
<400> 68

gaggagagcc tcaggagtta ggaccagaag aagccagggg agcagtgca atg gct tca 58
Met Ala Ser
-35

aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg 106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu
-30 -25 -20

gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc 154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys
-15 -10 -5

cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga 202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly
1 5 10

gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat 250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His
15 20 25 30

cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag 298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu
35 40 45

gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat 346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys Asp His
50 55 60

cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa gtc att 394
His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys Val Ile
65 70 75

tgc tgg ctt tgt gag cgg tct cag gag cac cgt ggt cac cac aca gtc 442
Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr Val
80 85 90

ctc acg gag gaa gta ttc aag gaa tgt cag gag aaa ctc cag gca gtc 490
Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu Gln Ala Val
95 100 105 110

ctc aag agg ctg aag aag gaa gag gag gaa gct gag aag ctg gaa gct 538
Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys Leu Glu Ala
115 120 125

gac atc aga gaa gag aaa act tcc tgg aag tat cag gta caa act gag 586
Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val Gln Thr Glu
130 135 140

aga caa agg ata caa aca gaa ttt gat cag ctt aga agc atc cta aat 634
Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser Ile Leu Asn
145 150 155

aat gag gag cag aga gag ctg caa aga ttg gaa gaa gaa gaa aag aag 682
Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu Glu Lys Lys
160 165 170

```

acg ctg gat aag ttt gca gag gct gag gat gag cta gtt cag cag aag      730
Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val Gln Gln Lys
175                               180                               185                               190
cag ttg gtg aga gag ctc atc tca gat gtg gag tgt cgg agt cag tgg      778
Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg Ser Gln Trp
                               195                               200                               205
tca aca atg gag ctg ctg cag gac atg agt gga atc atg aaa tgg agt      826
Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met Lys Trp Ser
                               210                               215                               220
gag atc tgg agg ctg aaa aag cca aaa atg gtt tcc aag aaa ctg aag      874
Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys Lys Leu Lys
                               225                               230                               235
act gta ttc cat gct cca gat ctg agt agg atg ctg caa atg ttt aga      922
Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln Met Phe Arg
                               240                               245                               250
gaa ctg aca gct gtc cgg tgc tac tgg gtg gat gtc aca ctg aat tca      970
Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr Leu Asn Ser
255                               260                               265                               270
gtc aac cta aat ttg aat ctt gtc ctt tca gaa gat cag aga caa gtg      1018
Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln Arg Gln Val
                               275                               280                               285
ata tct gtg cca att tgg cct ttt cag tgt tat aat tat ggt gtc ttg      1066
Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr Gly Val Leu
                               290                               295                               300
gga tcc caa tat ttc tcc tct ggg aaa cat tac tgg gaa gtg gac gtg      1114
Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu Val Asp Val
                               305                               310                               315
tcc aag aaa act gcc tgg atc ctg ggg gta tac tgt aga aca tat tcc      1162
Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg Thr Tyr Ser
                               320                               325                               330
cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt      1210
Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu
335                               340                               345                               350
tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag      1258
Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln
                               355                               360                               365
aat aaa tgt aag tat ggt gcc aaaaaaaaaa a      1290
Asn Lys Cys Lys Tyr Gly Ala
                               370

```

```

<210> 69
<211> 1364
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> 83..139
<223> Von Heijne matrix
      score 8.60000038146973
      seq LLWLALACSPVHT/TL

```

```

<220>
<221> polyA_site
<222> 1356..1354

```

```

<400> 69
gcctgggagc tgaggcagcc accgtctcag cctggccagc cctctggacc ccgaggttgg      60
accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt      112
                               Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
                               -15                               -10

```

gcc	ctg	gcc	tgc	agc	cct	gtt	cac	act	acc	ctg	tca	aag	tca	gat	gcc	160
Ala	Leu	Ala	Cys	Ser	Pro	Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	
			-5						1				5			
aaa	aaa	gcc	gcc	tca	aag	acg	ctg	ctg	gag	aag	agt	cag	ttt	tca	gat	208
Lys	Lys	Ala	Ala	Ser	Lys	Thr	Leu	Leu	Glu	Lys	Ser	Gln	Phe	Ser	Asp	
		10					15					20				
aag	ccg	gtg	caa	gac	cgg	ggg	ttg	gtg	gtg	acg	gac	ctc	aaa	gct	gag	256
Lys	Pro	Val	Gln	Asp	Arg	Gly	Leu	Val	Val	Thr	Asp	Leu	Lys	Ala	Glu	
	25					30					35					
agt	gtg	gtt	ctt	gag	cat	cgc	agc	tac	tgc	tcg	gca	aag	gcc	cgg	gac	304
Ser	Val	Val	Leu	Glu	His	Arg	Ser	Tyr	Cys	Ser	Ala	Lys	Ala	Arg	Asp	
40					45				50					55		
aga	cac	ttt	gct	ggg	gat	gta	ctg	ggc	tat	gtc	act	cca	tgg	aac	agc	352
Arg	His	Phe	Ala	Gly	Asp	Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	
			60						65					70		
cat	ggc	tac	gat	gtc	acc	aag	gtc	ttt	ggg	agc	aag	ttc	aca	cag	atc	400
His	Gly	Tyr	Asp	Val	Thr	Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	
			75					80					85			
tca	ccc	gtc	tgg	ctg	cag	ttg	aag	aga	cgt	ggc	cgt	gag	atg	ttt	gag	448
Ser	Pro	Val	Trp	Leu	Gln	Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	
		90					95					100				
gtc	acg	ggc	ctc	cac	gac	gtg	gac	caa	ggg	tgg	atg	cga	gct	gtc	agg	496
Val	Thr	Gly	Leu	His	Asp	Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	
	105					110					115					
aag	cat	gcc	aag	ggc	ctg	cac	ata	gtg	cct	cgg	ctc	ctg	ttt	gag	gac	544
Lys	His	Ala	Lys	Gly	Leu	His	Ile	Val	Pro	Arg	Leu	Leu	Phe	Glu	Asp	
120					125					130					135	
tgg	act	tac	gat	gat	ttc	cgg	aac	gtc	tta	gac	agt	gag	gat	gag	ata	592
Trp	Thr	Tyr	Asp	Asp	Phe	Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	
			140					145						150		
gag	gag	ctg	agc	aag	acc	gtg	gtc	cag	gtg	gca	aag	aac	cag	cat	ttc	640
Glu	Glu	Leu	Ser	Lys	Thr	Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	
		155						160					165			
gat	ggc	ttc	gtg	gtg	gag	gtc	tgg	aac	cag	ctg	cta	agc	cag	aag	cgc	688
Asp	Gly	Phe	Val	Val	Glu	Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	
		170				175						180				
gtg	ggc	ctc	atc	cac	atg	ctc	acc	cac	ttg	gcc	gag	gcc	ctg	cac	cag	736
Val	Gly	Leu	Ile	His	Met	Leu	Thr	His	Leu	Ala	Glu	Ala	Leu	His	Gln	
	185					190					195					
gcc	cgg	ctg	ctg	gcc	ctc	ctg	gtc	atc	ccg	cct	gcc	atc	acc	ccc	ggg	784
Ala	Arg	Leu	Leu	Ala	Leu	Leu	Val	Ile	Pro	Pro	Ala	Ile	Thr	Pro	Gly	
200					205						210				215	
acc	gac	cag	ctg	ggc	atg	ttc	acg	cac	aag	gag	ttt	gag	cag	ctg	gcc	832
Thr	Asp	Gln	Leu	Gly	Met	Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	
			220						225					230		
ccc	gtg	ctg	gat	ggg	ttc	agc	ctc	atg	acc	tac	gac	tac	tct	aca	gcg	880
Pro	Val	Leu	Asp	Gly	Phe	Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	
			235					240					245			
cat	cag	cct	ggc	cct	aat	gca	ccc	ctg	tcc	tgg	gtt	cga	gcc	tgc	gtc	928
His	Gln	Pro	Gly	Pro	Asn	Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	
		250					255					260				
cag	gtc	ctg	gac	ccg	aag	tcc	aag	tgg	cga	agc	aaa	atc	ctc	ctg	ggg	976
Gln	Val	Leu	Asp	Pro	Lys	Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	
	265					270					275					
ctc	aac	ttc	tat	ggg	atg	gac	tac	gcg	acc	tcc	aag	gat	gcc	cgt	gag	1024
Leu	Asn	Phe	Tyr	Gly	Met	Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	
280					285					290					295	
cct	gtt	gtc	ggg	gcc	agg	tac	atc	cag	aca	ctg	aag	gac	cac	agg	ccc	1072
Pro	Val	Val	Gly	Ala	Arg	Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	
			300						305					310		
cgg	atg	gtg	tgg	gac	agc	cag	gcc	tca	gag	cac	ttc	ttc	gag	tac	aag	1120

Arg	Met	Val	Trp	Asp	Ser	Gln	Ala	Ser	Glu	His	Phe	Phe	Glu	Tyr	Lys		
			315					320					325				
aag	agc	cgc	agt	ggg	agg	cac	gtc	gtc	ttc	tac	cca	acc	ctg	aag	tcc	1168	
Lys	Ser	Arg	Ser	Gly	Arg	His	Val	Val	Phe	Tyr	Pro	Thr	Leu	Lys	Ser		
		330					335					340					
ctg	cag	gtg	cgg	ctg	gag	ctg	gcc	cgg	gag	ctg	ggc	gtt	ggg	gtc	tct	1216	
Leu	Gln	Val	Arg	Leu	Glu	Leu	Ala	Arg	Glu	Leu	Gly	Val	Gly	Val	Ser		
		345				350					355						
atc	tgg	gag	ctg	ggc	cag	ggc	ctg	gac	tac	ttc	tac	gac	ctg	ctc		1261	
Ile	Trp	Glu	Leu	Gly	Gln	Gly	Leu	Asp	Tyr	Phe	Tyr	Asp	Leu	Leu			
360					365				370								
taggtgggca	ttgcggcctc	cgcgggtggac	gtgttctttt	ctaagccatg	gagtgagtga											1321	
gcaggtgtga	aatacaggcc	tccactccgt	ttgcaaaaaa	aaa												1364	

<210> 70

<211> 1470

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 57..95

<223> Von Heijne matrix

score 3.90000009536743

seq MLLSIGMLMLSAT/QV

<220>

<221> polyA_signal

<222> 1438..1443

<220>

<221> polyA_site

<222> 1458..1470

<400> 70

gctggcaaga	ctgtttgtgt	tgcgggggcc	ggacttcaag	gtgattttac	aacgag	atg											59
						Met											
ctg	ctc	tcc	ata	ggg	atg	ctc	atg	ctg	tca	gcc	aca	caa	gtc	tac	acc		107
Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr	Thr		
		-10					-5					1					
gtc	ttg	act	gtc	cag	ctc	ttt	gca	ttc	tta	aac	cca	ctg	cct	gta	gaa		155
Val	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Pro	Leu	Pro	Val	Glu		
5				10				15						20			
gca	gac	att	tta	gca	tat	aac	ttt	gaa	aat	gca	tct	cag	aca	ttt	gat		203
Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe	Asp		
				25				30				35					
gac	ctc	cct	gca	aga	ttt	ggc	tat	aga	ctt	cca	gct	gaa	ggc	tta	aag		251
Asp	Leu	Pro	Ala	Arg	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys		
			40					45				50					
ggc	ttt	tta	att	aac	tca	aaa	cca	gag	aat	gcc	tgt	gaa	ccc	ata	gtg		299
Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val		
		55				60					65						
cct	cca	cca	gta	aaa	gac	aat	tca	tct	ggc	act	ttc	atc	gtg	tta	att		347
Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile		
		70				75					80						
aga	aga	ctt	gat	tgt	aat	ttt	gat	ata	aag	gtt	tta	aat	gca	cag	aga		395
Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg		
85					90				95					100			
gca	gga	tac	aag	gca	gcc	ata	gtt	cac	aat	gtt	gat	tct	gat	gac	ctc		443
Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp	Leu		
				105					110					115			


```

att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att      491
Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile
                                120                                125                                130
cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa      539
Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu
                                135                                140                                145
ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt      587
Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe Ser
                                150                                155                                160
ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc      635
Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile
165                                170                                175                                180
tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat      683
Cys Leu Ile Leu Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp
                                185                                190                                195
aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa      731
Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys Lys
                                200                                205                                210
ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc      779
Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala
                                215                                220                                225
att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc      827
Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro
                                230                                235                                240
tgt tcc cat gct tat cat tgc aag tgt gta gac cct tgg cta act aaa      875
Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys
245                                250                                255                                260
acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa      923
Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln
                                265                                270                                275
ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg      971
Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val
                                280                                285                                290
aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag      1019
Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln
                                295                                300                                305
tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa      1067
Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu
310                                315                                320
tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat      1115
Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp
325                                330                                335                                340
gca gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct      1163
Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro
                                345                                350                                355
aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag      1209
Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
                                360                                365
aagatgattg gtttatttcc ctttaaaatg attaggtata tactgtaatt tgattttttg      1269
ctcccttaaa agattttctgt agaaataact tatttttttag tactctacag tttaatcaaa      1329
ttactgaaac aggacttttg atctggtatt tatctgccaa gaatatactt cattcactaa      1389
taatagactg gtgctgtaac tcaagcatca attcagctct tcttttgga tgaaagtata      1449
gccaaaacaa aaaaaaaaaa a      1470

```

<210> 71

<211> 982

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 72..197
 <223> Von Heijne matrix
 score 7.19999980926514
 seq ILFSLSFLLVIIT/FP

<220>
 <221> polyA_site
 <222> 970..982

<400> 71
 gctgcctggtt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc 60
 tcaagaatga g atg gat tct agg gtg tct tca cct gag aag caa gat aaa 110
 Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys
 -40 -35 -30
 gag aat ttc gtg ggt gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg 158
 Glu Asn Phe Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp
 -25 -20 -15
 atc ctg ttt tcc ctc tct ttc ctg ttg gtg atc att acc ttc ccc atc 206
 Ile Leu Phe Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile
 -10 -5 1
 tcc ata tgg atg tgc ttg aag atc att agg gag tat gaa cgt gct gtt 254
 Ser Ile Trp Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val
 5 10 15
 gta ttc cgt ctg gga cgc atc caa gct gac aaa gcc aag ggg cca ggt 302
 Val Phe Arg Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly
 20 25 30 35
 ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aag gtt gac ctc 350
 Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu
 40 45 50
 cga aca gtt act tgc aac att cct cca caa gag atc ctc acc aga gac 398
 Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp
 55 60 65
 tcc gta act act cag gta gat gga gtt gtc tat tac aga atc tat agt 446
 Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser
 70 75 80
 gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa gca aca ttt 494
 Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe
 85 90 95
 ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca cag acc ttg 542
 Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu
 100 105 110 115
 tcc cag atc tta gct gga cga gaa gag atc gcc cat agc atc cag act 590
 Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr
 120 125 130
 tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg 638
 Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val
 135 140 145
 gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga tcc atg gca 686
 Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala
 150 155 160
 gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc ctt gca gct 734
 Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala
 165 170 175
 gaa gga gaa atg agt gct tcc aaa tcc ctg aag tca gcc tcc atg gtg 782
 Glu Gly Glu Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val
 180 185 190 195
 ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg cag acc ttg 830
 Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu
 200 205 210
 agc acg gta gcc acc gag aag aat tct acg att gtg ttt cct ctg ccc 878
 Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro

	215	220	225	
atg aat ata cta gag ggc att ggt ggc gtc agc tat gat aac cac aag				926
Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys				
	230	235	240	
aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaaa				982
Lys Leu Pro Asn Lys Ala				
	245			

<210> 72
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 425..430

<220>
 <221> polyA_site
 <222> 443..455

<400> 72	
ggt atg cca ccc aga aac cta ctg gag tta ctt att aac atc aag gct	48
Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala	
1 5 10 15	
gga acc tat ttg cct cag tcc tat ctg att cat gag cac atg gtt att	96
Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile	
20 25 30	
act gat cgc atc gaa aac att gat cac ctg ggt ttc ttt att tat cga	144
Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg	
35 40 45	
ctg tgt cat gac aag gaa act tac aaa ctg caa cgc aga gaa act att	192
Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile	
50 55 60	
aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat	240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His	
65 70 75	
ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca	289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser	
80 85 90	
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg	349
cagtgattat tttttaagat cttctttcat gtaagtagca aacagggtct tactatcttt	409
tcatctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa	455

<210> 73
 <211> 738
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 90..278
 <223> Von Heijne matrix
 score 3.5
 seq GLVCAGLADMARP/AE

<220>
 <221> polyA_signal
 <222> 704..709

<220>

<221> polyA_site

<222> 724..738

<400> 73

```
gggaaaagtg actagctccc cttcgttggtc agccagggac gagaacacag ccacgctccc      60
acccggctgc caacgatccc tcggcggcg atg tcg gcc gcc ggt gcc cga ggc      113
                               Met Ser Ala Ala Gly Ala Arg Gly
                               -60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg      161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55                               -50                               -45                               -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca      209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
                               -35                               -30                               -25
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga      257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
                               -20                               -15                               -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct      305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
                               -5                               1                               5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta      353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10                               15                               20                               25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg      401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
                               30                               35                               40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa      449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
                               45                               50                               55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct      500
Leu Lys Ala Lys Ala His Lys
60
agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaagcta      560
actgtgtgtt tagaaggcac tgtaactggg agctagttct tgattcaata gaaaaatgca      620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta      680
acatttttct accatttgct cgtaataaac cataacttgct cgtaaaaaaa aaaaaaaa      738
```

<210> 74

<211> 649

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 88..147

<223> Von Heijne matrix

score 12.3999996185303

seq ALLLGALLGTAWA/RR

<220>

<221> polyA_signal

<222> 619..624

<220>

<221> polyA_site

<222> 637..649

<400> 74

```
ccaaagtgag agtccagcgg tttccagcgg cttgggccac ggccggcggcc ctgggagcag      60
aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      114
                               Met Lys Gly Trp Gly Trp Leu Ala Leu
```

bioRxiv preprint doi: <https://doi.org/10.1101/093660>; this version posted July 10, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

```

                                -20                                -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10                                -5                                1                                5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa      210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
                                10                                15                                20
att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg      258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
                                25                                30                                35
atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt      306
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
                                40                                45                                50
ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa      359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
                                55                                60
aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct      419
catttggaag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa      479
tactttgttt ctgctgtaga atttgttagc aaacagggag tcctgatcag cacccttctc      539
cacatccaca tgactggttt ttaatgtagc actgtggtat acatgcaaac atccggtcaa      599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa      649

<210> 75
<211> 714
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 33..92
<223> Von Heijne matrix
      score 12.3999996185303
      seq ALLLGALLGTAWA/RR

<220>
<221> polyA_site
<222> 703..714

<400> 75
agcagaggtg gagcgacccc attacgctaa ag atg aaa ggc tgg ggt tgg ctg      53
                                Met Lys Gly Trp Gly Trp Leu
                                -20                                -15
gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc      101
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser
                                -10                                -5                                1
cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa      149
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu
                                5                                10                                15
tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct      197
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser
                                20                                25                                30                                35
ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat      245
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr
                                40                                45                                50
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac      293
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp
                                55                                60                                65
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag      341
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys
                                70                                75                                80
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac      389

```

Asn	Tyr	Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp		
85						90					95						
cta	caa	ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	437	
Leu	Gln	Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe		
100					105					110					115		
gcg	tgt	ggg	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	485	
Ala	Cys	Gly	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe		
				120					125					130			
ttt	tcc	cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	533	
Phe	Ser	Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg		
				135				140						145			
aca	gat	ctt	tgt	gac	cat	gcc	ctg	cac	ata	tcg	cat	gat	gag	cta		578	
Thr	Asp	Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu			
		150				155					160						
tga	acc	actg	gag	cag	ccca	cactg	gcttg	atg	gat	cacc	ccc	agg	aggg	gaaa	atgg	638	
gca	atg	cctt	ttat	atatta	tg	ttttt	tact	gaa	atta	aact	gaaaa	aatat	gaa	acc	aaaa	698	
gtac	aaaaaa	aaaaaa														714	

<210> 76
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..107
 <223> Von Heijne matrix
 score 5
 seq MFAASLLAMCAGA/EV

<220>
 <221> polyA_signal
 <222> 546..551

<220>
 <221> polyA_site
 <222> 584..596

<400> 76																	
cac	agt	tcct	ctc	ctc	ctag	agc	ctg	ccga	cc	atg	ccc	gcg	ggc	gtg	ccc	atg	53
										Met	Pro	Ala	Gly	Val	Pro	Met	
										-25					-20		
tcc	acc	tac	ctg	aaa	atg	ttc	gca	gcc	agt	ctc	ctg	gcc	atg	tgc	gca	101	
Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala	Ser	Leu	Leu	Ala	Met	Cys	Ala		
			-15				-10						-5				
ggg	gca	gaa	gtg	gtg	cac	agg	tac	tac	cga	ccg	gac	ctg	aca	ata	cct	149	
Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr	Arg	Pro	Asp	Leu	Thr	Ile	Pro		
		1			5						10						
gaa	att	cca	cca	aag	cgt	gga	gaa	ctc	aaa	acg	gag	ctt	ttg	gga	ctg	197	
Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu	Lys	Thr	Glu	Leu	Leu	Gly	Leu		
		15			20				25					30			
aaa	gaa	aga	aaa	cac	aaa	cct	caa	gtt	tct	caa	cag	gag	gaa	ctt	aaa	245	
Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val	Ser	Gln	Gln	Glu	Glu	Leu	Lys		
			35			40								45			
ta	act	atg	cc	aaga	att	ctg	tga	ata	aat	at	aagt	ctt	aaa	tat	gtatt	ttc	305
gc	at	caa	act	act	tg	tcctt	aag	cact	ttag	tcta	atg	ct	act	gca	agag	gag	365
gt	gat	gt	ttt	ag	cc	gata	ctg	ttg	aa	att	ta	att	ac	g	g	ttt	425
tg	caa	ag	ca	cat	at	cat	ca	aacc	att	tca	tga	at	tg	g	ag	at	485
aat	ata	ac	gc	gaa	at	aga	at	tt	g	ta	ag	t	ct	act	ata	t	545
aat	ta	ag	aaa	tt	at	tt	aaaa	ct	at	ga	act	g	tt	tc	at	ta	596

<210> 77
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 375..380

<220>
 <221> polyA_site
 <222> 390..403

<400> 77
 tgaagagaat ggctgttgca gtcggcgtca gagcagctcc agtgccgggg attcggacgg 60
 agagcgcgag gactcggcgg ctgagcgcgc ccgacagcag ctagagggcg tgctcaacaa 120
 gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt 169
 Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
 1 5 10 15
 ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag 217
 Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
 20 25 30
 ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg 265
 Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
 35 40 45
 ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag 313
 Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
 50 55 60
 agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc 363
 Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
 65 70
 tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa 403

<210> 78
 <211> 727
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 126..575
 <223> Von Heijne matrix
 score 8.60000038146973
 seq LELLTSCSPPASA/SQ

<220>
 <221> polyA_signal
 <222> 670..675

<220>
 <221> polyA_site
 <222> 721..727

<220>
 <221> misc_feature
 <222> 257,376..377
 <223> n=a, g, c or t

<400> 78
 ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgtttag 60
 gaccgggggt aggggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg 120

```

gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag 170
Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
-150 -145 -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-135 -130 -125 -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag 266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
-115 -110 -105
ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga 314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
-100 -95 -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc 362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
-85 -80 -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc 410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
-70 -65 -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac 458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
-55 -50 -45 -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag 506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
-35 -30 -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca 554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
-20 -15 -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg 602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
-5 1 5
agc cac cgt gcc cgg cag aga aaa act gct taagggtgaa aagagaaatt 652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10 15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga 712
agcaaaaaaa aaaaa 727

<210> 79
<211> 944
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 90..155
<223> Von Heijne matrix
score 5.90000009536743
seq IILGCLALFLLQ/RK

<220>
<221> polyA_signal
<222> 913..918

<220>
<221> polyA_site
<222> 932..944

<400> 79
gaatcagggtt ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt 60
tctgcttctg gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg 113
Met Glu Leu Ile Ser Pro Thr Val
-20 -15

```



```

att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag      161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
                                -10                                -5                                1
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga      209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
                                5                                10                                15
ggt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca      257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala
                                20                                25                                30
aga atc aag gta tgt ggt cgt ggc aga cgg ggt ctc cag agg aga caa      305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln
                                35                                40                                45                                50
tgc ttt ctt ttt taaactttct ttcattgact cttaagtgcgca gggctagaac      357
Cys Phe Leu Phe
acggggaaca tacctgcttg cctcaactaa aggatctagt catttctgaa ttcctctact      417
aacaattaac aacaatatcc tgtgcaaaat tttgcgaaag aaatgaaata caattgcagc      477
gtgcatcgac atttttggaa gtagagatta acttttcgta tttttacttc atcgaagtta      537
agttccaaat gtgtatgtgt taagtaaatt ttttcagtaa ttgggaaaga taaagtgtaa      597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta      657
ttgtacaaat tgcttgacac gttgggtccgt acacaataga caggctctgt atttttagct      717
gacgttggtta tttgatgatg atgtactcca ttttacttac ggcccgaaga gactagtaat      777
cctccttgta gtagatgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag      837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat      897
ggtatttgat tgtctaataa atttgtatga tattaaaaaa aaaaaaaa      944

<210> 80
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..287
<223> Von Heijne matrix
      score 3.90000009536743
      seq LETCGLLVSLVES/IW

<220>
<221> polyA_signal
<222> 561..566

<220>
<221> polyA_site
<222> 587..598

<400> 80
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gaccgggggt agggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg      120
gtcggg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      170
      Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
                                -50                                -45                                -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
                                -35                                -30                                -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      266
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
                                -20                                -15                                -10
ctg gtt tca cta gtg gaa agc att tgg ctg cat ata aca gaa aac cag      314
Leu Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln
                                -5                                1                                5
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      362

```


<221> polyA_signal

<222> 461..466

<220>

<221> polyA_site

<222> 477..490

<400> 82

```
atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag      60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
                Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
                -15                -10                -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
                1                5                10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
                15                20                25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
                30                35                40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
45                50                55                60
tgg gac tgg gct gag gca ggg gct tgc ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
                65                70
gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcataatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaa      490
```

<210> 83

<211> 488

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_signal

<222> 458..463

<220>

<221> polyA_site

<222> 475..488

<400> 83

```
ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
                Met Lys Val Asp Lys Asp
                1                5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
                10                15                20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac      151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
                25                30                35
agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys
40                45                50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
55                60                65                70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
```

[illegible]

```
<210> 84
<211> 771
<212> DNA
<213> Homo sapiens
```

ggagaaagag aaaaaaaaaa aa

771

<210> 85
<211> 959
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 69..359
<223> Von Heijne matrix
score 4
seq RLPLVVSFIASSS/AN

<220>
<221> polyA_signal
<222> 927..932

<220>
<221> polyA_site
<222> 947..959

<400> 85
cggagagaac caggcagccc agaaacccca ggcgtggaga ttgatcctgc gagagaaggg 60
ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca 110
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro
-95 -90 -85
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta 158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val
-80 -75 -70
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga 206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg
-65 -60 -55
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa 254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys
-50 -45 -40
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac 302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr
-35 -30 -25 -20
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc 350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala
-15 -10 -5
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt 398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
1 5 10
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct 440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
15 20 25
taatctgaca gtggttttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc 500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc 560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt 620
ttctggtgta gggcttttct tatttagtga gatctagggg taccacagaa atgggttcagt 680
ctatcacagc tcccatggag ttagtctggg caccagatat ggatgagaga ttctattcag 740
tggatcagaa tcaaactggg acattgatcc acttgagccg ttaagtgtg ccaattgtac 800
aatatgcccc ggcttgccaga ataaagccaa cttttttattg tgaataataa taaggacata 860
tttttcttca gattatgttt tatttctttg cattgagtga ggaacataaa atggcttggt 920
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa 959

<210> 86
<211> 464
<212> DNA

0997330 101501

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 33..98

<223> Von Heijne matrix

score 9.80000019073486

seq LVVFCLALQLVPG/SP

<220>

<221> polyA_signal

<222> 437..442

<220>

<221> polyA_site

<222> 455..464

<400> 86

gccagaactt actcaccat cccactgaca cc atg aag cct gtg ctg cct ctc 53
Met Lys Pro Val Leu Pro Leu

-20

cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt 101

Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser

-15 -10 -5 1

ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata 149

Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile

5

10

15

tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc 197

Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys

20

25

30

gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca 245

Glu Lys Gly Phe Gln Cys Ser Ser Phe Cys Gly Ile Val Cys Ser

35

40

45

tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa 293

Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu

50 55 60 65

gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc 341

Val Ile Met Pro Ala Asn

70

tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc 401

caatatctaa cctgcaaadc gtttttgagt ttggcaataa aggctaactt accaaaaaaaa 461

aaa 464

<210> 87

<211> 799

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 110..235

<223> Von Heijne matrix

score 5.19999980926514

seq LLFDLVCHEFCQS/DD

<220>

<221> polyA_signal

<222> 764..769

<220>

<221> polyA_site

<222> 787..799

<400> 87

```
ccaacccccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtataactga      60
agctgccaata caagtacgtt ctgaaaatcc agaatggctt gatgtttac atg cac att      118
                                   Met His Ile
                                   -40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat      166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His
                                   -35                                   -30                                   -25
tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc      214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val
                                   -20                                   -15                                   -10
tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa      262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu
                                   -5                                   1                                   5
cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat      310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr
10                                   15                                   20                                   25
gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt      358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu
                                   30                                   35                                   40
cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt      406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys
                                   45                                   50                                   55
cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa      454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys
60                                   65                                   70
agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat      502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp
75                                   80                                   85
att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag      550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu
90                                   95                                   100                                   105
acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt      598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys
110                                   115                                   120
tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa      646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu
125                                   130                                   135
gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac      694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp
140                                   145                                   150
ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga      740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155                                   160                                   165
attggaatta cttctgtaca agaaataaac tttatttttc tcactgaaaa aaaaaaaaaa      799
```

<210> 88

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_site

<222> 308..320

<400> 88

```
tcacatccca gagcagccag tgtccgggag gcagaag atg ccc cac tcc aag cct      55
                                   Met Pro His Ser Lys Pro
                                   1                                   5
```

0997860 "10101

```

ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt      103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
      10      15      20
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta      151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
      25      30      35
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc      199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
      40      45      50
ggg gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt      254
Gly Val Phe Asn Leu
55
tgttgtgagg actgagtgtg tggaagtttt tcataaaactt tggatgctag tgtaaaaaaa      314
aaaaaa      320

```

<210> 89
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 129..209
 <223> Von Heijne matrix
 score 4.90000009536743
 seq CLLSYIALGAIHA/KI

<220>
 <221> polyA_site
 <222> 318..331

```

<400> 89
atggaaacca gatggggcaa cgggggtggtt ctagtgaga ctgtagctgc agctcctctc      60
cacctctagc ctgctcattt ccagctcaga aattctacta atggcggtttt ttcttcctga      120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc      170
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
      -25      -20      -15
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt      218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
      -10      -5      1
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg      266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
      5      10      15
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc      316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
20      25
caaaaaaaaa aaaaa      331

```

<210> 90
 <211> 1075
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 78..359
 <223> Von Heijne matrix
 score 4.19999980926514
 seq IILTAVYFALSIS/LH

<220>

score 4.59999990463257
seq LPFSLVSMMLVTQG/LV

<220>
<221> polyA_signal
<222> 602..607

<220>
<221> polyA_site
<222> 621..632

<400> 91
cactgggtca aggagtaagc agaggataaaa caactggaag gagagcaagc acaaagtcac 60
c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt 109
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
-65 -60 -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg 157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
-50 -45 -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa 205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
-35 -30 -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt 253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20 -15 -10 -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga 301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
1 5 10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc 349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
15 20 25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt 397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
30 35 40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg 445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
45 50 55 60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt 493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
65 70 75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact 543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
80 85
ttcgaagttt tttaaacctc tgaatttgta cacatttaaa atttcaagtg tacttttaaaa 603
taaaatactt ctaatgtaaa aaaaaaaaaa 632

<210> 92
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> polyA_signal
<222> 402..407

<220>
<221> polyA_site
<222> 419..430

<400> 92
gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca 53

09978360 "101501

```

Met Lys Val Glu Glu Glu His Thr Asn Ala
1      5      10
ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata 101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile
15      20      25
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt 149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser
30      35      40
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat 197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp
45      50      55
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt 245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe
60      65      70
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa 293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln
75      80      85      90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcagaatgac 340
Gly Arg His Thr Lys His Leu Gly Asn
95
ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg 400
aaataaacta gcaaaaccaa aaaaaaaaaa 430

<210> 93
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 42..113
<223> Von Heijne matrix
score 3.70000004768372
seq ILFNLLIFLCGFT/NY

<220>
<221> polyA_site
<222> 172..185

<400> 93
ctttcagaac tcaactgcaa gagccctgaa caggagccac c atg cag tgc ttc agc 56
Met Gln Cys Phe Ser
-20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt 104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
-15 -10 -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg 152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
1 5 10
cat aaa cct gtt aca atg taaaaaaaaa aaaaaa 185
His Lys Pro Val Thr Met
15

<210> 94
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 108..170

```

<223> Von Heijne matrix
score 5.5
seq SFLPSALVIWTS/AF

<220>
<221> polyA_signal
<222> 550..555

<220>
<221> polyA_site
<222> 574..585

<400> 94
cacgttcctg ttgagtagac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc 60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gtttagaa atg tgg tgg 116
Met Trp Trp
-20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca 164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
-15 -10 -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat 212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
1 5 10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca 260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15 20 25 30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt 308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
35 40 45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaaa 364
Gln Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt 424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg 484
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa 544
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa a 585

<210> 95
<211> 613
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 118..171
<223> Von Heijne matrix
score 5.90000009536743
seq ALALLWSLPASDL/GR

<220>
<221> polyA_signal
<222> 583..588

<220>
<221> polyA_site
<222> 602..613

<400> 95
ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg 60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttgga gcctggg 117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct 165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser

	-15		-10		-5		
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt							213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val							
	1		5		10		
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc							261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr							
	15		20		25		30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt							309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val							
	35		40		45		
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca							351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala							
	50		55		60		
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg							411
tcgaaaataa gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt							471
attgattaag ttactgtaaa agcttgggtt tattttttgta ggacttaatg gctaagaatt							531
agaacatagc aagggggctc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat							591
gcaaacccttt aaaaaaaaaa aa							613

<210> 96

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 128..268

<223> Von Heijne matrix

score 5.5

seq SALLFFARPCVFC/FK

<220>

<221> polyA_signal

<222> 410..415

<220>

<221> polyA_site

<222> 424..427

<400> 96

agcttgagatt tacactgggc aacgtgggtg gaatgtatct ggctcagaac tatgatatac 60

caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag aagaaacccc 120

ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct 169

Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser

-45

-40

-35

act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt 217

Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe

-30

-25

-20

tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt 265

Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe

-15

-10

-5

tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca 313

Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr

1

5

10

15

ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg 361

Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly

20

25

30

agg ttc taagactgga attatgggtgc tagattagta aacatgactt ttaatgaaaa 417

Arg Phe

aaaaacaaaa

427

<210> 97

<211> 905
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 149..457
 <223> Von Heijne matrix
 score 4.90000009536743
 seq FLLAQTTLRNVLG/TQ

<220>
 <221> polyA_site
 <222> 893..912

<400> 97
 gctgcctggt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc 60
 tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg 120
 tgggtgtcaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct 172
 Met Trp Leu Asp Pro Val Phe Pro
 -100
 ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg 220
 Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
 -95 -90 -85 -80
 ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa 268
 Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
 -75 -70 -65
 gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc 316
 Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
 -60 -55 -50
 acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga 364
 Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
 -45 -40 -35
 atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa 412
 Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln
 -30 -25 -20
 gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca 460
 Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
 -15 -10 -5 1
 cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc 508
 Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
 5 10 15
 atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg 556
 Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
 20 25 30
 gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga 604
 Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
 35 40 45
 tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc 652
 Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
 50 55 60 65
 ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc 700
 Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
 70 75 80
 tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg 748
 Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
 85 90 95
 cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt 796
 Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
 100 105 110
 cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat 844

CCCTGCTGTT

Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp
 115 120 125
 aac cac aag aag ctt cca aat aaa gcc tgaggctctc ttgcggtagt 891
 Asn His Lys Lys Leu Pro Asn Lys Ala
 130 135
 caaaaaaaaa aaaa 905

<210> 98
 <211> 560
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11)..(439)

<220>
 <221> polyA_site
 <222> (547)..(560)

<220>
 <221> polyA_signal
 <222> (530)..(535)

<400> 98
 cagaacaatc atg tct gac tcc ctg gtg gtg tgc gag gta gac cca gag 49
 Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu
 1 5 10
 cta aca gaa aag ctg agg aaa ttc cgc ttc cga aaa gag aca gac aat 97
 Leu Thr Glu Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn
 15 20 25
 gca gcc atc ata atg aag gtg gac aaa gac cgg cag atg gtg gtg ctg 145
 Ala Ala Ile Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu
 30 35 40 45
 gag gaa gaa ttt cgg aac att tcc cca gag gag ctc aaa atg gag ttg 193
 Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu
 50 55 60
 ccg gag aga cag ccc agg ttc gtg gtt tac agc tac aag tac gtg cgt 241
 Pro Glu Arg Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg
 65 70 75
 gac gat ggc cga gtg tcc tac cct ttg tgt ttc atc ttc tcc agc cct 289
 Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro
 80 85 90
 gtg ggc tgc aag ccg gaa caa cag atg atg tat gca ggg agt aaa aac 337
 Val Gly Cys Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn
 95 100 105
 agg ctg gtg cag aca gca gag ctc aca aag gtg ttc gaa atc cgc acc 385
 Arg Leu Val Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr
 110 115 120 125
 act gat gac ctc act gag gcc tgg ctc caa gaa aag ttg tct ttc ttt 433
 Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe
 130 135 140
 cgt tga tctctgggct ggggactgaa ttcctgatgt ctgagtcctc aagggtgactg 489
 Arg
 gggacttgga acccctagga cctgaacaac caagacttta aataaatttt aaaatgcaaa 549
 aaaaaaaaa a

<210> 99
 <211> 568
 <212> DNA

"09101" 09E9Z660

<213> Homo sapiens

<220>

<221> CDS

<222> 7..471

<221> sig_peptide

<222> 7..99

<223> Von Heijne matrix

score 6.9

seq LLLVPSALSLLLA/LL

<221> polyA_signal

<222> 537..542

<221> polyA_site

<222> 554..568

<400> 99

```
gggacc atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct      48
      Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro
            -30                -25                -20
ctg tcg aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc      96
Leu Ser Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu
            -15                -10                -5
gcc ctc ctc ctg cct cac tgc cag aag ccc ttt gtg tat gac ctt cac      144
Ala Leu Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His
            1                5                10                15
gca gtc aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata      192
Ala Val Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile
            20                25                30
att tgc ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat      240
Ile Cys Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr
            35                40                45
aat ttt agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc      288
Asn Phe Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser
            50                55                60
ttt ttg ctg ggt acc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc      336
Phe Leu Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu
            65                70                75
att gaa gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg      384
Ile Glu Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu
            80                85                90                95
cct tct gga tta atc ttt tgt tgt gct ttt tgc tct gag act aaa ctc      432
Pro Ser Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu
            100                105                110
ttc tta tca aga caa gct atg gca gag aac ttt tcc atc taataaattt      481
Phe Leu Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
            115                120
aagagtagat tcattctgtat gggttgagagt aggctctgac tatgtatatg tgtataataa      541
acctacatat ccaaaaaaaaa aaaaaaa      568
```

<210> 100

<211> 569

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 168..332

<221> polyA_signal

<222> 557..562

<400> 100

```

agggggcggtg gggccatggt ggtcttgctg gcggggaaga agacctttct cccccctctc      60
tgccgcgcct tcgcctgccg cggctgtcaa ctgcgtccgg agcgcggcgc cgagcgagcagg    120
gatacgggcgc ccagcgggggt cagaaagcaa cattgaatgc agaagaa atg gcg gac      176
                                   Met Ala Asp
                                   1
ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cgc atg tat tat      224
Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg Met Tyr Tyr
      5              10              15
aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg gga      272
Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly
20              25              30              35
aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa aag      320
Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys
              40              45              50
aag agg agc aac taggagtgcca ctctgaccca gccagagtcc aggtttccac      372
Lys Arg Ser Asn
              55
aggaagcaga tggagctcct ttcacagggg ctctgagaaa aactggagcc gatctcaaga      432
agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggtag gtcctggggc      492
actgtggggc gctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtacgtggg      552
gtgaaataaa gccaag
569

```

<210> 101

<211> 895

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 51..251

<221> sig_peptide

<222> 51..110

<223> Von Heijne matrix

score 5.3

seq ALIFGGFISLIGA/AF

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 882..895

<400> 101

```

ccgagagtgc cgggcggtcg gcgggtcagg gcagcccggg gcctgacgcc atg tcc      56
                                   Met Ser
                                   -20
cgg aac ctg cgc acc gcg ctc att ttc ggc ggc ttc atc tcc ctg atc      104
Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile
              -15              -10              -5
ggc gcc gcc ttc tat ccc atc tac ttc cgg ccc cta atg aga ttg gag      152
Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg Leu Glu
      1              5              10
gag tac aag aag gaa caa gct ata aat cgg gct gga att gtt caa gag      200
Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val Gln Glu
15              20              25              30
gat gtg cag cca cca ggg tta aaa gtg tgg tct gat cca ttt ggc agg      248

```


<210> 104
<211> 2036
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 276..1040

<221> sig_peptide
<222> 276..485
<223> Von Heijne matrix
score 3.9
seq SVIGVMLAPFTAG/LS

<221> polyA_site
<222> 2024..2036

<400> 104
gatcctgggt gcagctcatc acaagcgctcg ggggtgcagca aaaccatcca ggctggacag 60
tggttgga gttccaagaa aagaaacgct tcaccgaaga agtcattgaa tacttccaga 120
agaaagttag ccagtgcat ctgaaaatcc tgctgactag cgatgaagcc tggaagagat 180
tcgtgcgtgt ggctggattg ccaggggaag aagcagatgc tctctatgaa gctctgaaga 240
atcttacacc atatgtgggt attgaggaca aagac atg cag caa aaa gaa cag 293
Met Gln Gln Lys Glu Gln
-70 -65
cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag 341
Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys
-60 -55 -50
att cag gag tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa 389
Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn Glu Ile Glu
-45 -40 -35
aag gtc cac aga ggc tgc gtc atc gcc aat gtg gtg tct ggc tcc act 437
Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser Gly Ser Thr
-30 -25 -20
ggc atc ctg tct gtc att ggc gtt atg ttg gca cca ttt aca gca ggg 485
Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe Thr Ala Gly
-15 -10 -5
ctg agc ctg agc att act gca gct ggg gta ggg ctg gga ata gca tct 533
Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly Ile Ala Ser
1 5 10 15
gcc acg gct ggg atc gcc tcc agc atc gtg gag aac aca tac aca agg 581
Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr Tyr Thr Arg
20 25 30
tca gca gaa ctc aca gcc agc agg ctg act gca acc agc act gac caa 629
Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser Thr Asp Gln
35 40 45
ttg gag gca tta agg gac att ctg cat gac atc aca ccc aat gtg ctt 677
Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro Asn Val Leu
50 55 60
tcc ttt gca ctt gat ttt gac gaa gcc aca aaa atg att gcg aat gat 725
Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp
65 70 75 80
gtc cat aca ctc agg aga tct aaa gcc act gtt gga cgc cct ttg att 773
Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg Pro Leu Ile
85 90 95
gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg aga aca cgt 821
Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg
100 105 110
ggg gcc ccc acc cgg ata gtg aga aaa gta gcc cgg aac ctg ggc aag 869

099360 1040

Gly	Ala	Pro	Thr	Arg	Ile	Val	Arg	Lys	Val	Ala	Arg	Asn	Leu	Gly	Lys	
		115					120					125				
gcc	act	tca	ggt	gtc	ctc	ggt	gtg	ctg	gat	gta	gtc	aac	ctt	gtg	caa	917
Ala	Thr	Ser	Gly	Val	Leu	Val	Val	Leu	Asp	Val	Val	Asn	Leu	Val	Gln	
		130					135					140				
gac	tca	ctg	gac	ttg	cac	aag	ggg	gaa	aaa	tcc	gag	tct	gct	gag	ttg	965
Asp	Ser	Leu	Asp	Leu	His	Lys	Gly	Glu	Lys	Ser	Glu	Ser	Ala	Glu	Leu	
145					150					155					160	
ctg	agg	cag	tgg	gct	cag	gag	ctg	gag	gag	aat	ctc	aat	gag	ctc	acc	1013
Leu	Arg	Gln	Trp	Ala	Gln	Glu	Leu	Glu	Glu	Asn	Leu	Asn	Glu	Leu	Thr	
				165						170				175		
cat	atc	cat	cag	agt	cta	aaa	gca	ggc	taggccaat	tggtgcggga						1060
His	Ile	His	Gln	Ser	Leu	Lys	Ala	Gly								
			180						185							
agtcaggggac	cccaaaccgga	gggactggct	gaagccatgg	cagaagaacg	tggtattgtga											1120
agatttcatg	gacattttatt	agttccccc	attaatactt	ttataatttc	ctatgcctgt											1180
ctttaccgca	atctctaaac	acaaattgtg	aagatttcat	ggacacttat	cacttcccca											1240
atcaataccc	ttgtgatttc	ttatgcctgt	ctttacttta	atctccta	cctgtcagct											1300
gaggagggtg	tatgtcacct	caggaccatg	tgataattgc	gttaactgca	caaattgtag											1360
agcatgtgtg	tttgaacaat	atgaaatctg	ggcaccttga	aaaaagaaca	ggataacagc											1420
aatcgttcag	gggataagag	agataacctt	aaactctgac	caacagtgag	ccgggtggag											1480
cagagtcata	tttcttttct	ttcaaaagca	aatgggagaa	atategctga	attctttttc											1540
tcagcaagga	acatccctga	gaaagagaat	gcaccctga	gggtgggtct	ataaatggcc											1600
tccttgggtg	tggccatctt	ctatggtcga	gactgtaggg	atgaaataaa	cccagtcctc											1660
ccatagtgtc	cccaggctta	ttaggaagag	gaaattccc	cctaataaat	tttggtcaga											1720
ccggttgctc	tcaaaacctt	gtctcctgat	aagatgttat	caatgacaat	ggtgcctgaa											1780
acctcattag	caattttaat	ttctccccgg	tcctgtggtc	ctgtgatctc	accctgcctc											1840
cacttgccct	gtgatattct	attaccttgt	gaagtaggtg	atctttgtga	cccacaccct											1900
attcatacac	tcctccccct	tttggaagtc	cctaataaaa	acttgctggg	tttgagctt											1960
gtgagggcatc	acggaacctt	ctgatgtgtg	atgtctcccc	tggaaccta	gctttaaaat											2020
ttcaaaaaaa	aaaaaa															2036

<210> 105
 <211> 1276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 443..619
 <221> sig_peptide
 <222> 443..589
 <223> Von Heijne matrix
 score 7
 seq LICVVCLYIVCRC/GS

<221> polyA_site
 <222> 1267..1276

<400> 105																
gaggcactca	cggcatttca	ttgctacttt	aattttcatt	attatgggat	tgattgctgt											60
cacagctact	gctgcagtag	ctggagttgc	tttgcattcc	acagtacaaa	cagcagacta											120
tgtaaataat	tggtagaaaa	attctactct	gctgtggaat	taccaagata	atatagacca											180
gaaactagct	gatcaaatta	atgatctcca	acaaactgta	atgtggctag	gggatcatat											240
agttagttta	gaatatagaa	tgcggttaca	atgtgattga	aataacctctg	attttttgcat											300
tactctcat	ctgtgtaatg	aaacagagca	tgagtgggaa	aaagttaaga	gatattttaa											360
aggtcatact	agaaatttat	ctttggatat	tgcaaagcta	aaggaacaag	tattttcaagc											420
ccctcagata	catctgacac	ta atg cca	gga act gaa	gtg ctt gaa	gga gct											472
		Met Pro	Gly Thr	Glu Val	Leu Glu	Gly Ala										

```

aca gac gga tta gca gct att aac ctg cta aaa tgg atc aag aca ctt      520
Thr Asp Gly Leu Ala Ala Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu
-35 -30 -25
gga ggc tct gtg att tca atg att gtg ctt tta atc tgt gtt gtt tgt      568
Gly Gly Ser Val Ile Ser Met Ile Val Leu Leu Ile Cys Val Val Cys
-20 -15 -10
ctt tat ata gtc tgt aga tgc gga agc cac ctg tgg aga gaa agc cac      616
Leu Tyr Ile Val Cys Arg Cys Gly Ser His Leu Trp Arg Glu Ser His
-5 1 5
cac tgagagcaag caatgatagc tgtggcggtt ttgcaaaaag aaaagggaga      669
His
10
caagcgccca gctatagtta ccaataaagc atggtactgg tattaataata ggcattgtgtt      729
ctgttccaat ggaacagaat agagaaccca gaaacaaagc caaatattta cagccaactg      789
atctctgaca aagcaaacaa aaacataaag tggggaaaagg acaccctatt ccacaaatag      849
tgcagggata attggcaagc cacatgtaga aaaatgaagc tggatcctcg tctctcactt      909
tatacaaaaa tcaactcaaa atgggtcaaa gtcttaactc taagacctga aaccataaca      969
attctagaaa ataacattgg aaaaactctt ctagacattg gtttaggcaa aaagttcatg      1029
accaagaacc caaaagcaaa tgcaataaaa aggaagataa atagatggga cctaattaag      1089
ctgaaaagct tctgcatagc aaaaggaata atcagcagag caaacagaca acccacaggg      1149
tgggagaaaa tatttgcaag ctatgtatct gacaatggac taatatccag aatctacaag      1209
gaattcaaac aattagcaag aaaaaacact tgtatttgtt ttgctctgta aatcagcaaa      1269
aaaaaaa      1276

<210> 106
<211> 747
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 206..745

<400> 106
accagaagca ggtgatttcc gagctcagca atgctcagct cataatgatg tcaagcacca      60
tggccagttt tatgaatggc ttctgtgtc taatgaccct gacaacccat gttcactcaa      120
gtgccaagcc aaaggaacaa ccctggttgt tgaactagca cctaaggtct tagatggtac      180
gcgttgctat acagaatctt tggat atg tgc atc agt ggt tta tgc caa att      232
Met Cys Ile Ser Gly Leu Cys Gln Ile
1 5
gtt ggc tgc gat cac cag ctg gga agc acc gtc aag gaa gat aac tgt      280
Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys
10 15 20 25
ggg gtc tgc aac gga gat ggg tcc acc tgc cgg ctg gtc cga ggg cag      328
Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln
30 35 40
tat aaa tcc cag ctg tcc gca acc aaa tgc gat gat act gtg gtt gca      376
Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala
45 50 55
att ccc tat gga agt aga cat att cgc ctt gtc tta aaa ggt cct gat      424
Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp
60 65 70
cac tta tat ctg gaa acc aaa acc ctg cag ggg act aaa ggt gaa aac      472
His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn
75 80 85
agt ctg agc tcc aca gga act ttc ctt gtg gac aat tct agt gtg gac      520
Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asn Ser Ser Val Asp
90 95 100 105
ttc cag aaa ttt cca gac aaa gag ata ctg aga atg gct gga cca ctg      568
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu
110 115 120

```

```

aca gca gat ttc att gtc aag att cgt aac tcg ggc tcc gct gac agt      616
Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser
          125          130          135
aca gtc cag ttc atc ttc tat caa ccc atc atc cac cga tgg agg gag      664
Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu
          140          145          150
acg gat ttc ttt cct tgc tca gca acc tgt gga gga ggt tat cag ctg      712
Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu
          155          160          165
aca tcg gct gag tgc tac gat ctg agg agc aac cg                        747
Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn
170          175          180

```

```

<210> 107
<211> 561
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 36..521

<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
      score 7.4
      seq VLLLAALPPVLLP/GA

```

```

<221> polyA_signal
<222> 528..533

```

```

<221> polyA_site
<222> 548..561

```

```

<400> 107
gacgcctctt tcagccccggg atcgccccag caggg atg ggc gac aag atc tgg      53
                               Met Gly Asp Lys Ile Trp
                               -20
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg      101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu
          -15          -10          -5
cct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt      149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
          1          5          10          15
acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg      197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
          20          25          30
aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta      245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
          35          40          45
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt      293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
          50          55          60
gaa caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt      341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly
          65          70          75
gat tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag      389
Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
80          85          90          95
gtg att ttc ttt gaa tta atc ccg gat aat atg gga gaa cag gca caa      437
Val Ile Phe Phe Glu Leu Ile Pro Asp Asn Met Gly Glu Gln Ala Gln

```

```

          100          105          110
gaa caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat      485
Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp
          115          120          125
atg aaa ctg gaa gac atc ctg gtc agt atg gtc ttc taataaaata      531
Met Lys Leu Glu Asp Ile Leu Val Ser Met Val Phe
          130          135
aaaattatta acagccaaaa aaaaaaaaaa      561

<210> 108
<211> 632
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..395

<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
      score 7.4
      seq VLLLLAALPPVLLP/GA

<221> polyA_signal
<222> 599..604

<221> polyA_site
<222> 619..632

<400> 108
gacgcctctt tcagccccggg atcgccccag caggg atg ggc gac aag atc tgg      53
                               Met Gly Asp Lys Ile Trp
                               -20
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg      101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu
          -15          -10          -5
cct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt      149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
          1          5          10          15
acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg      197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
          20          25          30
aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta      245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
          35          40          45
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt      293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
          50          55          60
gaa caa aga aaa tca gat gga gtt cac acg tgt ata aga agt aaa aat      341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Cys Ile Arg Ser Lys Asn
          65          70          75
ggg cca ggc act gcg gtt cac gcc tat aat ccc agc act ttc cga ggc      389
Gly Pro Gly Thr Ala Val His Ala Tyr Asn Pro Ser Thr Phe Arg Gly
          80          85          90          95
caa gtg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc      445
Gln Val
accatttctg agaaggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca      505
caaggacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg      565
gaagacatcc tggtcagtat ggtcttctaa taaaataaaa attattaaca gccaaaaaaa      625
aaaaaaa      632

```

09978360 101501

[illegible]

```
<221> polyA_signal
<222> 328..333
```

[illegible]

```
<220>
<221> CDS
<222> 35..631
```

```
<221> polyA_signal
<222> 901..906
```

<400> 110																
ataattggag ctgcaaagca gatcgtgaca agag atg gac ggt cag aag aaa aat																55
Met Asp Gly Gln Lys Lys Asn																
-40																
tgg aag gac aag gtt gtt gac ctc ctg tac tgg aga gac att aag aag																103
Trp Lys Asp Lys Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys																
-35 -30 -25 -20																
act gga gtg gtg ttt ggt gcc agc cta ttc ctg ctg ctt tca ttg aca																151
Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr																
-15 -10 -5																
gta ttc agc att gtg agc gta aca gcc tac att gcc ttg gcc ctg ctc																199
Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu																
1 5 10																

```

tct gtg acc atc agc ttt agg ata tac aag ggt gtg atc caa gct atc      247
Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile
15      20      25
cag aaa tca gat gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa      295
Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu
30      35      40      45
gtt gct ata tct gag gag ttg gtt cag aag tac agt aat tct gct ctt      343
Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu
50      55      60
ggg cat gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt      391
Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
65      70      75
gat gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt      439
Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
80      85      90
acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg gct      487
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala
95      100      105
ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat cag gca      535
Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala
110      115      120      125
cag ata gat cat tat cta gta ctt gca aat aag aat gtt aaa gat gct      583
Gln Ile Asp His Tyr Leu Val Leu Ala Asn Lys Asn Val Lys Asp Ala
130      135      140
atg gct aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gct gaa      631
Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
145      150      155
tgaaaaacgcc caaaataatt agtaggagtt catctttaaa ggggatattc atttgattat      691
acggggggagg gtcaggggaag aacgaacctt gacgttgtag tgcagtttca cagatcgttg      751
ttagatcttt atttttagcc atgcactgtt gtgaggaaaa attacctgtc ttgactgcca      811
tgtgttcac atcttaagta ttgtaagctg ctatgtatgg atttaaaccg taatcatatc      871
tttttcctat ctatctgagg cactgggtgga ataaaaaacc tgtatatttt actttgttgc      931
agatagtctt gccgcactct ggcaagttgc agagatgggt gagctagaaa aaaaaaaac      991
aaa
<210> 111
<211> 412
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 271..399

<400> 111
gccgctagcg cctcgagcga tgcacctcct ttccaactgg gcaaaccctg cttccagcag      60
acgtccttct atggccgctt caggcacttc ttggatatca tcgacctcg cacactcttt      120
gtcactgaga gacgtctcag agaggctgtg cagctgctgg aggactataa gcatgggacc      180
ctgcgcccg gggtcaccaa tgaacagctc tggagtgcac agaaaatcaa gcaggctatt      240
ctacatccgg acaccaatga gaagatcttc atg cca ttt aga atg tca ggt tat      294
Met Pro Phe Arg Met Ser Gly Tyr
1      5
att cct ttt ggg acg cca att gta agt gtt acc ttc aaa gga ttt cct      342
Ile Pro Phe Gly Thr Pro Ile Val Ser Val Thr Phe Lys Gly Phe Pro
10      15      20
ttt cta aaa aat tat ttt aaa tgt cta act tta tgt tat tgc tca cgg      390
Phe Leu Lys Asn Tyr Lys Cys Leu Thr Leu Cys Tyr Cys Ser Arg
25      30      35      40
gta ttt gac tgaattgttg att
Val Phe Asp      412

```

<210> 112
 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..252

<221> sig_peptide
 <222> 103..213
 <223> Von Heijne matrix
 score 3.9
 seq PGPSLRLFSGSQA/SV

<221> polyA_site
 <222> 588..597

<400> 112
 gaaagggtcag aggaaggagc tgtgggaagc tcgcagcagg tatcggagct taagccagtg 60
 gattttggggg ccctgggctc cctagccggc tgcggtgtga ga atg gag tgg gca 114
 Met Glu Trp Ala
 -35
 gga aag cag cgg gac ttt cag gta agg gca gct ccg ggc tgg gat cat 162
 Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro Gly Trp Asp His
 -30 -25 -20
 ttg gcc tcc ttt cct ggc cct tct ctc cgg ctg ttt tct ggg agt cag 210
 Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe Ser Gly Ser Gln
 -15 -10 -5
 gcg agt gtc tgt agt ctc tgc tcg ggg ttt ggg gct cag gaa 252
 Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala Gln Glu
 1 5 10
 tgatgtcatg ctccaacagt tggattctat tagcttaagg aggagggaaa cagccaattt 312
 tcttgacttt gcaaatctag ctgatctcac tcttgctgaa tctgaggtgt ttagacttca 372
 ctctaaaaag catcatttta cttttattta gcacaaaggc acaggatatt tttacaggaa 432
 gaatctttta tatggaaaaa tctgagttaa catcactccc gtggtgtttg tagttcttac 492
 aggggaaactc cagtgccttt tgagccgctt gttcgtccta gtgaacactg tctgttttgt 552
 ctcttggtgc tgctatgtct gacctgtaat gggagaaaaa aagaa 597

<210> 113
 <211> 748
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..460

<221> polyA_signal
 <222> 713..718

<221> polyA_site
 <222> 735..748

<400> 113
 c aca gtt cct ctc ctc cta gag cct gcc gac cat gcc cgc ggg cgt gcc 49
 Thr Val Pro Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 cat gtc cac cta cct gaa aat gtt cgc agc cag tct cct ggc cat gtg 97
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30

099850.1050
 TGGTCT"099850

```

cgc agg ggc aga agt ggt gca cag gta cta ccg acc gga cct gat gag      145
Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
      35      40      45
aaa cag gtt gag aag agt gaa gtt gat ttc tca aag tca cat agc tta      193
Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
      50      55      60
gtg aga cga ttt gag gat ctg aag ccc aag ctt tct gtt tgc aaa act      241
Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
      65      70      75      80
gga tca caa gtc ttt cgg tgc gag aac tgg aag gtc tgg gca gag tgc      289
Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
      85      90      95
agc aga gga gac cat gat gac tgc cta gac ttg tgc tca gtg ctg tgt      337
Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
      100      105      110
tgg gga gaa ctg cta cgg aca ata cct gaa att cca cca aag cgt gga      385
Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
      115      120      125
gaa ctc aaa acg gag ctt ttg gga ctg aaa gaa aga aaa cac aaa cct      433
Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
      130      135      140
caa gtt tct caa cag gag gaa ctt aaa taactatgcc aagaattctg      480
Gln Val Ser Gln Gln Glu Leu Lys
      145      150
tgaataatat aagtcttaaa tatgtatttc ttaatttatt gcatcaaact acttgtcctt      540
aagcacttag tctaagtcta actgcaagag gaggtgctca gtggatgttt agccgatacg      600
ttgaaattta attacggttt gattgatatt tcttgaaaac cgccaaagca catatcatca      660
aaccatttca tgaatatggt ttggaagatg tttagtcttg aatataatgc gaaatagaat      720
atttgtaagt ctaccaaaaa aaaaaaaaaa      748

```

<210> 114
 <211> 703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..231

<221> polyA_signal
 <222> 769..774

<221> polyA_site
 <222> 690..703

```

<400> 114
ctctggtggc tctgctacgg cggcgcagaa atg agg cag aag cgg aaa gga gat      54
      Met Arg Gln Lys Arg Lys Gly Asp
      1      5
ctc agc cct gct aag ctg atg atg ctg act ata gga gat gtt att aaa      102
Leu Ser Pro Ala Lys Leu Met Met Leu Thr Ile Gly Asp Val Ile Lys
      10      15      20
caa ctg att gaa gcc cac gag cag ggg aaa gac atc gat cta aat aag      150
Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp Leu Asn Lys
      25      30      35      40
gtg aga acc aag aca gct gcc aaa tat ggc ctt tct gcc cag ccc cgc      198
Val Arg Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala Gln Pro Arg
      45      50      55
ctg gtg gat atc att gct gcc gtc cct cct gag tagctgggat tacaggcacc      251
Leu Val Asp Ile Ile Ala Ala Val Pro Pro Glu
      60      65

```

```

cgccgctgcc aatTTTTgtA tttttagtag ggatgggggt ttcaccatat tggtcaggct 311
ggtctcgaac tcttgacctc aggtgatcaa cccaccttgg cctccctaaa tgccgggatt 371
acaggcatga gccaccgctc cgggcctttg attttttaag gtggattttg gttgttataa 431
atggagaaaag gtaagagttc aagttcaacc cgtgtgtgaa agcaaaaaca tggaaaacag 491
gattggcttc ttcaaaggct cctctttagt aactgcctct ttgaaatttc gaggtaatct 551
actttggaga ctctgcctgg agagggtcag ttcctaagtt aaaagcatcg cttaaccttg 611
gctcctgtgg catTTTtaca aggttttaaag gaattgattc ctctgaaagg gcctgaaaat 671
aaaaagtctt taacatacaa aaaaaaaaaa aa 703

```

```

<210> 115
<211> 725
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 305..565

```

```

<221> polyA_signal
<222> 694..699

```

```

<221> polyA_site
<222> 713..725

```

```

<400> 115
ctcacggtgg tgaaggtcac agggttgcag cactcccagt agaccaggag ctccgggagg 60
cagggccggc cccacgtcct ctgcgcacca ccctgagttg gatcctctgt gcgccacccc 120
tgagttggat ccagggctag ctgctgttga cctccccact cccacgctgc cctcctgcct 180
gcagccatga cgccccctgt caccctgatc ctgggtggcc tcatgggctt acctctggcc 240
caggccttgg actgccacgt gtgaggacta caaatccctc caggatatca ttgccatcct 300
gggt atg gat gaa ctt tct gag gaa gac aag ttg acc gtg tcc cgt gca 349
Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala
1 5 10 15
cgg aaa ata cag cgt ttc ttg tct cag cca ttc cag gtt gct gag gtc 397
Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val
20 25 30
ttc aca ggt cat atg ggg aag ctg gta ccc ctg aag gag acc atc aaa 445
Phe Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys
35 40 45
gga ttc cag cag att ttg gca ggt gaa tat gac cat ctc cca gaa cag 493
Gly Phe Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln
50 55 60
gcc ttc tat atg gtg gga ccc att gaa gaa gct gtg gca aaa gct gat 541
Ala Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp
65 70 75
aag ctg gct gaa gag cat tca tcg tgaggggtct ttgtcctctg tactgtctct 595
Lys Leu Ala Glu Glu His Ser Ser
80 85
ctccttgccc ctaacccaaa aagcttcatt tttctgtgta ggctgcacaa gagccttgat 655
tgaagatata ttctttctga acagtattta aggtttccaa taaagtgtac acccctcaaa 715
aaaaaaaaaa 725

```

```

<210> 116
<211> 1705
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 124..873

```

<221> sig_peptide
 <222> 124..378
 <223> Von Heijne matrix
 score 3.6
 seq HLSVVTLAAKVKC/IP

<221> polyA_signal
 <222> 1673..1678

<221> polyA_site
 <222> 1694..1705

<400> 116
 cggaggtgag gagcggcggc cccgcccggg gcgctggagg tcgaagcttc caggtagcgg 60
 cccgcagagc ctgacccagg ctctggacat cctgagccca agtccccac actcagtgca 120
 gtg atg agt gcg gaa gtg aag gtg aca ggg cag aac cag gag caa ttt 168
 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe
 -85 -80 -75
 ctg ctc cta gcc aag tcg gcc aag ggg gca gcg ctg gcc aca ctc atc 216
 Leu Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile
 -70 -65 -60 -55
 cat cag gtg ctg gag gcc cct ggt gtc tac gtg ttt gga gaa ctg ctg 264
 His Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu
 -50 -45 -40
 gac atg ccc aat gtt aga gag ctg naa gcc cgg aat ctt cct cca cta 312
 Asp Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu
 -35 -30 -25
 aca gag gct cag aag aat aag ctt cga cac ctc tca gtt gtc acc ctg 360
 Thr Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu
 -20 -15 -10
 gct gct aaa gta aag tgt atc cca tat gca gtg ttg ctg gag gct ctt 408
 Ala Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu
 -5 1 5 10
 gcc ctg cgt aat gtg cgg cag ctg gaa gac ctt gtg att gag gct gtg 456
 Ala Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val
 15 20 25
 tat gct gac gtg ctt cgt ggc tcc ctg gac cag cgc aac cag cgg ctc 504
 Tyr Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu
 30 35 40
 gag gtt gac tac agc atc ggg cgg gac atc cag cgc cag gac ctc agt 552
 Glu Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser
 45 50 55
 gcc att gcc cga acc ctg cag gaa tgg tgt gtg ggc tgt gag gtc gtg 600
 Ala Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val
 60 65 70
 ctg tca ggc att gag gag cag gtg agc cgt gcc aac caa cac aag gag 648
 Leu Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu
 75 80 85 90
 cag cag ctg ggc ctg aag cag cag att gag agt gag gtt gcc aac ctt 696
 Gln Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu
 95 100 105
 aaa aaa acc att aaa gtt acg acg gca gca gca gcc gca gcc aca tct 744
 Lys Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Ala Thr Ser
 110 115 120
 cag gac cct gag caa cac ctg act gag ctg agg gaa cca gct cct ggc 792
 Gln Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly
 125 130 135
 acc aac cag cgc cag ccc agc aag aaa gcc tca aag ggc aag ggg ctc 840
 Thr Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu
 140 145 150
 cga ggg agc gcc aag att tgg tcc aag tcg aat tgaaagaact gtcgtttcct 893

Arg	Gly	Ser	Ala	Lys	Ile	Trp	Ser	Lys	Ser	Asn	
155				160				165			
ccctgggggat	gtgggggtccc	agctgcctgc	ctgcctctta	ggagtcctca	gagagccttc					953	
tgtgcccctg	gccagctgat	aatcctaggt	tcatgaccct	tcacctcccc	taaccccaaaa					1013	
catagatcac	accttctcta	gggaggagtc	aaatgtaggt	catgtttttg	ttggtacttt					1073	
ctgttttttg	tgacttcatg	tgttccattg	ctccccgctg	ccatgctctc	tcccttgttt					1133	
ccttaagagc	tcagcatctg	tccctgttca	ttacatgtca	ttgagtaggt	gggtagccct					1193	
gatgggggtc	gctctgtctg	gagcataacc	cacaggcggt	ttttctgcca	ccccatccct					1253	
gcatgcctga	tccccagttc	ctatacccta	cccctgacct	attgagcagc	ctctgaagag					1313	
ccatagggcc	cccaccttta	ctcacaccct	gagaattctg	ggagccagtc	tgccatgcca					1373	
ggagtcactg	gacatgttca	tcctagaatc	ctgtcacact	acagtcattt	cttttcctct					1433	
ctctggccct	tgggtcctgg	gaatgctgct	gcttcaaccc	cagagcctaa	gaatggcagc					1493	
cgtttcttaa	catgttgaga	gatgattctt	tcttgccct	ggccatctcg	ggaagcttga					1553	
tggcaatcct	ggaagggttt	aatctccttt	tgtgagtttg	gtggggaagg	gaagggtata					1613	
tagattatat	taaaaaaaaa	aaggatatata	tgcatatatc	tatatataat	atgacgcaga					1673	
aataaatcta	tgagaaatcc	aaaaaaaaaa	aa							1705	

<210> 117
 <211> 1069
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..206

<221> polyA_signal
 <222> 850..855

<221> polyA_site
 <222> 1056..1069

<400> 117											
cccactccgc	tctcagcact	aagctctcac	gattaaggca	cgctgcctc	gattgtccag					60	
cctctgccag	aagaaagctt	agcagccagc	gcctcagtag	agacctaaagg	gcgctgaatg					120	
agtgggaaag	ggaa atg ccg acc aat tgc gct gcg	gcg ggc tgt gcc act								170	
	Met Pro Thr Asn Cys Ala Ala	Ala Gly Cys Ala Thr									
	1	5	10								
acc tac aac aag cac att aac atc agc ttc cac	agg taacctgggc									216	
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg											
	15	20									
aggagtgagg	ggtagcggaa	actggagttc	ctattgtggc	tatcgcttgt	gtggaaggaa					276	
caggaggatt	ctgctaattc	taataacttt	cccagctggg	agcaggggaag	catcgatatgt					336	
cctttgtgtt	tctcaaattc	gcccaattgt	tctctgcttt	cggggaagct	ttactcattt					396	
tctaaaagaa	atccaagtac	tgtttgggtca	ttacccttta	gtaaaaaaaa	gtaacaggag					456	
gatatcgtaa	ttttctactg	ttttattcct	ctgttagacc	gggccttgac	atgaatgacg					516	
ccgtaaggga	gaaagagatc	ttcccaatca	gcaatcaccc	taaaagcctg	ctgtgttccc					576	
gttaaaaatta	ggaaattctc	actagatgaa	ttgacatggg	aggcatttag	atttctaata					636	
gtcacatagt	aattctgcgg	aggaattgag	tcattcttga	tagccatgga	attaagcgat					696	
gttaattaaa	gtgcaaacga	taacctttct	gttcttacta	gaatagagta	ataaaaagaa					756	
cctagggtttt	cttttggttg	ctggaagaaa	aatcaaaatt	ctttagttct	gtcaaaccag					816	
aactcttgaa	agcactttga	acaatgcctg	gaaaataaca	ggtactctgt	aaatgtttac					876	
cttctctgca	agtgcctgcc	acgtgcccg	agaaaagaca	cattaaaaag	ttaagtgcga					936	
ccagtccctga	ttttatatat	tttatatacc	taacaacgta	tatgttagta	tgtagaaatt					996	
atatccttga	cctttttccc	tacctattac	gaactgtact	tttattaaaa	gctgccacta					1056	
aaaaaaaaaa	aaa									1069	

<210> 118
 <211> 1084
 <212> DNA
 <213> Homo sapiens

[illegible]

```
<221> polyA_site
<222> 1071..1084
```

<400> 118																	
cccactccgc	tctcacgact	aagctctcac	gattaaggca	cgctgcctc	gattgtccag												60
cctctgccag	aagaaagctt	agcagccagc	gcctcagtag	aggcctaagg	gcgctgaatg												120
agtgggaaag	ggaa	atg	ccg	acc	aat	tgc	gct	gcg	gcg	ggc	tgt	gcc	act				170
	Met	Pro	Thr	Asn		Cys	Ala	Ala	Ala	Gly	Cys	Ala	Thr				
	1					5					10						
acc	tac	aac	aag	cac	att	aac	atc	agc	ttc	cac	agg	ttt	cct	ttg	gat		218
Thr	Tyr	Asn	Lys	His	Ile	Asn	Ile	Ser	Phe	His	Arg	Phe	Pro	Leu	Asp		
	15					20					25						
cct	aaa	aga	aga	aaa	gaa	tgg	gtt	cgc	ctg	gtt	agg	cgc	aaa	aat	ttt		266
Pro	Lys	Arg	Arg	Lys	Glu	Trp	Val	Arg	Leu	Val	Arg	Arg	Lys	Asn	Phe		
	30				35						40						
gtg	cca	gga	aaa	cac	act	ttt	ctt	tgt	tca	aag	cac	ttt	gaa	gcc	tcc		314
Val	Pro	Gly	Lys	His	Thr	Phe	Leu	Cys	Ser	Lys	His	Phe	Glu	Ala	Ser		
45					50					55				60			
tgt	ttt	gac	cta	aca	gga	caa	act	cga	cga	ctt	aaa	atg	gat	gct	gtt		362
Cys	Phe	Asp	Leu	Thr	Gly	Gln	Thr	Arg	Arg	Leu	Lys	Met	Asp	Ala	Val		
				65				70					75				
cca	acc	att	ttt	gat	ttt	tgt	acc	cat	ata	aag	tct	atg	aaa	ctc	aag		410
Pro	Thr	Ile	Phe	Asp	Phe	Cys	Thr	His	Ile	Lys	Ser	Met	Lys	Leu	Lys		
			80					85				90					
tca	agg	aat	ctt	ttg	aag	aaa	aac	aac	agt	tgt	tct	cca	gct	gga	cca		458
Ser	Arg	Asn	Leu	Leu	Lys	Lys	Asn	Asn	Ser	Cys	Ser	Pro	Ala	Gly	Pro		
		95				100						105					
tct	agt	tta	aaa	tca	aac	att	agt	agt	cag	caa	gta	cta	ctt	gaa	cac		506
Ser	Ser	Leu	Lys	Ser	Asn	Ile	Ser	Ser	Gln	Gln	Val	Leu	Leu	Glu	His		
		110				115					120						
agc	tat	gcc	ttt	agg	aat	cct	atg	gag	gca	aaa	aag	agg	atc	att	aaa		554
Ser	Tyr	Ala	Phe	Arg	Asn	Pro	Met	Glu	Ala	Lys	Lys	Arg	Ile	Ile	Lys		
125				130						135				140			
ctg	gaa	aaa	gaa	ata	gca	agc	tta	aga	aga	aaa	atg	aaa	act	tgc	cta		602
Leu	Glu	Lys	Glu	Ile	Ala	Ser	Leu	Arg	Arg	Lys	Met	Lys	Thr	Cys	Leu		
				145				150					155				
caa	aag	gaa	cgc	aga	gca	act	cga	aga	tgg	atc	aaa	gcc	atg	tgt	ttg		650
Gln	Lys	Glu	Arg	Arg	Ala	Thr	Arg	Arg	Trp	Ile	Lys	Ala	Met	Cys	Leu		
			160					165				170					
gta	aag	aat	tta	gaa	gca	aat	agt	gta	tta	cct	aaa	ggc	aca	tca	gaa		698
Val	Lys	Asn	Leu	Glu	Ala	Asn	Ser	Val	Leu	Pro	Lys	Gly	Thr	Ser	Glu		
		175				180						185					
cac	atg	tta	cca	act	gcc	tta	agc	agt	ctt	cct	ttg	gaa	gat	ttt	aag		746
His	Met	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Leu	Pro	Leu						

aaaaacttca tatggaaatt ttatttgaaa atgagtggaa ggcgccttaca ttagaattac 1028
 ggacttaaaaa attttgctaa taaattgtgt gtttgaaagg tgaaaaaaaa aaaaaa 1084

<210> 119
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..290

<221> sig_peptide
 <222> 33..92
 <223> Von Heijne matrix
 score 5.4
 seq WFFVHSSALGLVLA/PP

<400> 119
 aatggtaggc cttcatgtga gccagttact ac atg aat ctt cat ttc cca cag 53
 Met Asn Leu His Phe Pro Gln
 -20 -15
 tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca cct ttc 101
 Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro Pro Phe
 -10 -5 1
 tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt agg cta 149
 Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys Arg Leu
 5 10 15
 tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc tgt tta 197
 Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr Cys Leu
 20 25 30 35
 tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa aat tgt 245
 Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys Asn Cys
 40 45 50
 aat agt cgg cac gct gga ttt gta ggg cca gca aaa ttg cgg cag 290
 Asn Ser Arg His Ala Gly Phe Val Gly Pro Ala Lys Leu Arg Gln
 55 60 65
 tgaaactagt ttcacttcta aagcccttca tttcccacaa ggtaaagctc tcgaaacccc 350
 atttgatcct tggttcctat ttcgatcctc ctttgggaatc tgaaaatcgg tctccatggt 410
 gtatgcaaa 419

<210> 120
 <211> 682
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 485..616

<221> polyA_site
 <222> 669..682

<400> 120
 ctcctttctc attccttata ttgcgtgttt ttaccttttt ttcataacta agtttttgag 60
 gaagttagtg ttctttttcaa agaaccggtt cgaaatgtac ttttctttgc tactttttgt 120
 tattttattg atcacatctt taatcttttg ttctctatac gtggcctgtt ttgatattatt 180
 ttactattct tgcttttctaa ggtaagtatt ttgttgtgta gtgctttatt tttttcatct 240
 ttctttttga ataataatga catttttagg ttataaattt tcctctggta ctcagtttgc 300
 ctcattaatt ttggcagtaa gcattctcct tttattgctt tctatgtagt ctttaatttt 360
 gcttttaact tcttctttga tctaaggatt acctacttgt taattttcaa atattatctt 420

0003360.101501

```

atctatctat ctatctatct atctatctat ctatctatct acctatgtga gacgaagtct 480
ggct atg tcg ccg agg ctg gag tgc agt ggt gca atc ttg gct cac tgc 529
    Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys
      1           5           10          15
aac ccc cgc ctc cca ggt tca agt tat tct cct gcc tca gct act tgg 577
Asn Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp
      20          25          30
gtg aga gga tcc ctt gag ccg ggg agg ttg agg ctg cag tgagccataa 626
Val Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
      35          40
ccactactct ccagcctgga taacaaaagt gagactctga ccaaaaaaaaa aaaaaa 682

<210> 121
<211> 1191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..995

<221> sig_peptide
<222> 54..227
<223> Von Heijne matrix
      score 4.1
      seq LVHHCPTWQWATG/EE

<221> polyA_signal
<222> 1130..1135

<221> polyA_site
<222> 1181..1191

<400> 121
cacggctgca ctttccatcc cgtcgcgggg ccggccgcta ctccggcccc agg atg 56
                                Met
cag aat gtg att aat act gtg aag gga aag gca ctg gaa gtg gct gag 104
Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala Glu
      -55          -50          -45
tac ctg acc ccg gtc ctc aag gaa tca aag ttt agg gaa aca ggt gta 152
Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly Val
      -40          -35          -30
att acc cca gaa gag ttt gtg gca gct gga gat cac cta gtc cac cac 200
Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His His
      -25          -20          -15          -10
tgt cca aca tgg caa tgg gct aca ggg gaa gaa ttg aaa gtg aag gca 248
Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys Ala
      -5           1           5
tac cta cca aca ggc aaa caa ttt ttg gta acc aaa aat gtg ccg tgc 296
Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro Cys
      10          15          20
tat aag cgg tgc aaa cag atg gaa tat tca gat gaa ttg gaa gct atc 344
Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala Ile
      25          30          35
att gaa gaa gat gat ggt gat ggc gga tgg gta gat aca tat cac aac 392
Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His Asn
      40          45          50          55
aca ggt att aca gga ata acg gaa gcc gtt aaa gag atc aca ctg gaa 440
Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu Glu
      60          65          70
aat aag gac aat ata agg ctt caa gat tgc tca gca cta tgt gaa gag 488

```

Asn	Lys	Asp	Asn	Ile	Arg	Leu	Gln	Asp	Cys	Ser	Ala	Leu	Cys	Glu	Glu		
			75					80					85				
gaa	gaa	gat	gaa	gat	gaa	gga	gaa	gct	gca	gat	atg	gaa	gaa	tat	gaa		536
Glu	Glu	Asp	Glu	Asp	Glu	Gly	Glu	Ala	Ala	Asp	Met	Glu	Glu	Tyr	Glu		
			90				95					100					
gag	agt	gga	ttg	ttg	gaa	aca	gat	gag	gct	acc	cta	gat	aca	agg	aaa		584
Glu	Ser	Gly	Leu	Leu	Glu	Thr	Asp	Glu	Ala	Thr	Leu	Asp	Thr	Arg	Lys		
			105			110					115						
ata	gta	gaa	gct	tgt	aaa	gcc	aaa	act	gat	gct	ggc	ggg	gaa	gat	gct		632
Ile	Val	Glu	Ala	Cys	Lys	Ala	Lys	Thr	Asp	Ala	Gly	Gly	Glu	Asp	Ala		
					125					130					135		
att	ttg	caa	acc	aga	act	tat	gac	ctt	tac	atc	act	tat	gat	aaa	tat		680
Ile	Leu	Gln	Thr	Arg	Thr	Tyr	Asp	Leu	Tyr	Ile	Thr	Tyr	Asp	Lys	Tyr		
				140					145					150			
tac	cag	act	cca	cga	tta	tgg	ttg	ttt	ggc	tat	gat	gag	caa	cgg	cag		728
Tyr	Gln	Thr	Pro	Arg	Leu	Trp	Leu	Phe	Gly	Tyr	Asp	Glu	Gln	Arg	Gln		
			155				160					165					
cct	tta	aca	gtt	gag	cac	atg	tat	gaa	gac	atc	agt	cag	gat	cat	gtg		776
Pro	Leu	Thr	Val	Glu	His	Met	Tyr	Glu	Asp	Ile	Ser	Gln	Asp	His	Val		
			170			175					180						
aag	aaa	aca	gtg	acc	att	gaa	aat	cat	cct	cat	ctg	cca	cca	cct	ccc		824
Lys	Lys	Thr	Val	Thr	Ile	Glu	Asn	His	Pro	His	Leu	Pro	Pro	Pro	Pro		
			185			190					195						
atg	tgt	tca	gtt	cac	cca	tgc	agg	cat	gct	gag	gtg	atg	aag	aaa	atc		872
Met	Cys	Ser	Val	His	Pro	Cys	Arg	His	Ala	Glu	Val	Met	Lys	Lys	Ile		
					205				210						215		
att	gag	act	gtt	gca	gaa	gga	ggg	gga	gaa	ctt	gga	gtt	cat	atg	tat		920
Ile	Glu	Thr	Val	Ala	Glu	Gly	Gly	Gly	Glu	Leu	Gly	Val	His	Met	Tyr		
				220				225						230			
ctt	ctt	att	ttc	ttg	aaa	ttt	gta	caa	gct	gtc	att	cca	aca	ata	gaa		968
Leu	Leu	Ile	Phe	Leu	Lys	Phe	Val	Gln	Ala	Val	Ile	Pro	Thr	Ile	Glu		
			235				240					245					
tat	gac	tac	aca	aga	cac	ttc	aca	atg	taatgaagag	agcataaaat							1015
Tyr	Asp	Tyr	Thr	Arg	His	Phe	Thr	Met									
			250			255											
ctatccta	at	tattggttct															1075
tattcatcaa		tatatacagt															1135
aatatgttcc		actaccagcc															1191
		ttacttgttt															
		aataaaaaatc															
		agtgcaaaaa															
		aaaaaa															

<210> 122
 <211> 1008
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 657..923

 <221> sig_peptide
 <222> 657..896
 <223> Von Heijne matrix
 score 3.5
 seq RGLLSACAPWGDG/ST

 <221> polyA_signal
 <222> 957..962

 <221> polyA_site
 <222> 974..1008

 <400> 122


```

aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      242
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45          50          55          60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa ggt ctt      290
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu
65          70          75
acc tct gaa ccc ctc aca gcc tagggacagg agcggccggc ttacctggtg      341
Thr Ser Glu Pro Leu Thr Ala
80
ggttggggga cgtcggcagc tcgcgtacta cgccagcagg attgaggagc agagaaacag      401
ttgcagttgg ttgtattcag tacctgcatt tccgttggga actccacctg tacttggtat      461
tctgtggaac tttttttatt tgtagaagga gcaagaatat tgaccttact atatagcaca      521
cgaaacaatc tatgctgtat cgtgcctgct caatccttaa agttaac      568

```

```

<210> 124
<211> 538
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 151..426

<221> sig_peptide
<222> 151..258
<223> Von Heijne matrix
      score 5.2
      seq KVALAGLLGFGLG/KV

```

```

<221> polyA_signal
<222> 505..510

```

```

<221> polyA_site
<222> 527..538

```

```

<400> 124
cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac      60
catggcttca gcgtctgctc gtggaaacca agataaagat gcccattttc caccaccaag      120
caagcagctc tgcctttttc tcttgtaagc atg ctt gtc acc cag gga cta gtc      174
                               Met Leu Val Thr Gln Gly Lys Val
                               -35          -30
tac caa ggt tat ttg gca gct aat tct aga ttt gga tca ttg ccc aaa      222
Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys
          -25          -20          -15
gtt gca ctt gct ggt ctc ttg gga ttt ggc ctt gga aag gta tca tac      270
Val Ala Leu Ala Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr
          -10          -5          1
ata gga gta tgc cag agt aaa ttc cat ttt ttt gaa gat cag ctc cgt      318
Ile Gly Val Cys Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg
5          10          15          20
ggg gct ggt ttt ggt cca cag cat aac agg cac tgc ctc ctt acc tgt      366
Gly Ala Gly Phe Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys
          25          30          35
gag gaa tgc aaa ata aag cat gga tta agt gag aag gga gac tct cag      414
Glu Glu Cys Lys Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln
          40          45          50
cct tca gct tcc taaattctgt gtctgtgact ttcgaagttt tttaaacctc      466
Pro Ser Ala Ser
55
tgaatttgta cacatttaaa atttcaagtg tacttttaaaa taaaatactt ctaatggaac      526
aaaaaaaaaa aa      538

```

<210> 125
 <211> 1747
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..1062

<221> sig_peptide
 <222> 10..57
 <223> Von Heijne matrix
 score 4.9
 seq FIYQLQAHFTLCSG/WS

<221> polyA_signal
 <222> 1710..1715

<221> polyA_site
 <222> 1735..1747

<400> 125
 gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt 51
 Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
 -15 -10 -5
 tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
 Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
 1 5 10
 ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
 15 20 25 30
 agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
 35 40 45
 atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
 Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
 50 55 60
 atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Ser Pro
 65 70 75
 gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
 80 85 90
 ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
 Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
 95 100 105 110
 gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
 Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
 115 120 125
 tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
 Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
 130 135 140
 tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
 145 150 155
 aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
 Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
 160 165 170
 ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
 Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val

109.01.09.02.06.0

```

175          180          185          190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc      675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
          195          200          205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg      723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
          210          215          220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac      771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
          225          230          235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg      819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
          240          245          250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca      867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
255          260          265          270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc      915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
          275          280          285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc      963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
          290          295          300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc ccn      1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
          305          310          315
ttt tgt cac ctt gga cat gga aga ctg tgg cta caa cat tcc aca gac      1059
Phe Cys His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp
          320          325          330
aga tgagtcaacc ctcatgacca tagcctatgt catggctgcc atctgcgccc      1112
Arg
335
tcttcatgct gccactctgc ctcatggtgt gtcagtggcg ctgcctccgc tgcctgcgcc      1172
agcagcatga tgactttgct gatgacatct ccctgctgaa gtgaggaggc ccatgggcag      1232
aagataggga ttccccctgga ccacacctcc gtgggttact ttggtcacaa gtaggagaca      1292
cagatggcac ctgtggccag agcacctcag gaccctcccc acccaccaaa tgcctctgcc      1352
ttgatggaga aggaaaaggc tggcaagggtg gggttcaggg actgtacctg taggagacag      1412
aaaagagaag aaagaagcac tctgctggcg ggaatactct tggtcacctc aaatttaagt      1472
cgggaaattc tgctgcttga aacttcagcc ctgaaccttt gtcaccattc ctttaaattc      1532
tccaacccaa agtattcttc ttttcttagt ttcagaagta ctggcatcac acgcagggtta      1592
ccttggcggtg tgtccctgtg gtaccctggc agagaagaga ccaagcttgt ttccctgctg      1652
gccaagtca gtaggaggg atgcacagtt tgctatttgc tttagagaca gggactgtat      1712
aaacaagcct aacattggtg caaaaaaaaa aaaaaa      1747

```

<210> 126
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..491

 <221> sig_peptide
 <222> 78..218
 <223> Von Heijne matrix
 score 5.8
 seq LMCFGALIGLCAC/IC

<221> polyA_signal
 <222> 1652..1657

```

<221> polyA_site
<222> 1673..1686

<400> 126
ggatatagccc accagaaagg acagagtcac ttgatgtggt cacaaaatgt gtgagtttca      60
cactaactga gcagttc atg gag aaa ttt gtt gat ccc gga aac cac aat      110
               Met Glu Lys Phe Val Asp Pro Gly Asn His Asn
               -45               -40
agc ggg att gat ctc ctt agg acc tat ctt tgg cgt tgc cag ttc ctt      158
Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu
               -35               -30               -25
tta cct ttt gtg agt tta ggt ttg atg tgc ttt ggg gct ttg atc gga      206
Leu Pro Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly
               -20               -15               -10               -5
ctt tgt gct tgc att tgc cga agc tta tat ccc acc att gcc acg ggc      254
Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly
               1               5               10
att ctc cat ctc ctt gca ggt ctg tgt aca ctg ggc tca gta agt tgt      302
Ile Leu His Leu Leu Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys
               15               20               25
tat gtt gct gga att gaa cta ctc cac cag aaa cta gag ctc cct gac      350
Tyr Val Ala Gly Ile Glu Leu His Gln Lys Leu Glu Leu Pro Asp
               30               35               40
aat gta tcc ggt gaa ttt gga tgg tcc ttc tgc ctt gct tgt gtc tct      398
Asn Val Ser Gly Glu Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser
               45               50               55               60
gct ccc tta cag ttc atg gct tct gct ctc ttc atc tgg gct gct cac      446
Ala Pro Leu Gln Phe Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His
               65               70               75
acc aac cgg aga gag tac acc tta atg aag gca tat cgt gtg gca      491
Thr Asn Arg Arg Glu Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
               80               85               90
tgagcaagaa actgcctgct ttacaattgc catttttatt tttttaaaat aatactgata      551
ttttccccac ctctcaattg tttttaattt ttatttgtgg atataccatt ttattatgaa      611
aatctatttt atttatacac attcaccact aaatacacac ttaataccac taaaatttat      671
gtggtttact ttaagcgatg ccatctttca aataaaactaa tctaggtcta gacagaaaga      731
aatggataga gacttgacac aaatttatga aagaaaattg ggagtaggaa tgtgaccgaa      791
aacaagttgt gctaattgtct gtttagacttt tcagtaaaac caaagtaact gtatctgttc      851
aactaaaaac tctatattag tttctttggg aaacctctca tcgtcaaaac tttatgttca      911
ctttgctggt gtagatagcc agtcaaccag cagtattagt gctgttttca aagatttaag      971
ctctataaaa ttgggaaatt atctaagatc attttcccta agcattgaca catagcttca      1031
tctgaggtga gatatggcag ctgtttgtat ctgcactgtg tctgtctaca aagagtgaaa      1091
aatacagtgt ttacttgaaa ttttaacttt gtaactgcaa gaattccagt tcggccgggc      1151
gaggattagt attattttta actctccgta agattttcag taccaccaa ttgttttgga      1211
ttttttttct ttctcttca cataccaggg ttattaaaag tgtgctttct ttttacatta      1271
tattacagtt acaaggtaaa attcctcaac tgctatttat ttattccagc ccagtactat      1331
aaagaacggt tcaccataat gacctccag agctgggaaa cctaccacaa gatctaaagt      1391
tctggctgtc cattaacctc caactatggt ctttatttct tgtggttaata tgatgtgctt      1451
ttccttgctt aaatcccttc ctggtgtgta tcaacattat ttaatgtctt ctaattcagt      1511
cattttttat aagtatgtct ataaacattg aactttaaaa aacttattta tttattccac      1571
tactgtagca attgacagat taaaaaaatg taacttcata atttcttacc ataacctcaa      1631
tgtctttttt aaaaaataaa attaaaaatg aaaagagacc caaaaaaaaa aaaaaa      1686

<210> 127
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..371

```


<221> sig_peptide
 <222> 69..287
 <223> Von Heijne matrix
 score 4
 seq AVGFLFWVIVLTS/WI

<221> polyA_signal
 <222> 510..515

<221> polyA_site
 <222> 530..542

<400> 127
 tgttacttag ggtcaaggct tgggtcttgc cccgcaaacc cttgggacga cccggcccca 60
 gcgcagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg 110
 Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
 -70 -65 -60
 tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctc tgg 158
 Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
 -55 -50 -45
 ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc 206
 Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
 -40 -35 -30
 tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg 254
 Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
 -25 -20 -15
 ggc ttc ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc 302
 Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
 -10 -5 1 5
 cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc 350
 Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
 10 15 20
 acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggcctgc 401
 Thr Ile Pro Leu Gly Thr Pro
 25
 ttattctccc aggacaggct ccttaaagca gaggagcctg tcctgggagc cccttctcaa 461
 actcctaaga cttgtttctca tgtcccacgt tctctgctga catcccccaa taaaggaccc 521
 taactttcaa aaaaaaaaaa a 542

<210> 128
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..757

<221> sig_peptide
 <222> 2..205
 <223> Von Heijne matrix
 score 7.3
 seq LRLILSPLPGAQP/QQ

<221> polyA_site
 <222> 1160..1174

<400> 128
 g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag 49
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu

```

-65      -60      -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
-50      -45      -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
-35      -30      -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20      -15      -10      -5
ggg gcc cag cct caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
1      5      10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat      289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
15      20      25
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta      337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
30      35      40
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag      385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45      50      55      60
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc      433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
65      70      75
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc      481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
80      85      90
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac      529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
95      100      105
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag      577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
110      115      120
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg      625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
125      130      135      140
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat tca gac      673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
145      150      155
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggt      721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
160      165      170
gag gcc aaa gat ggc agc aac ctc tgc ttc agc aaa tgattgtgta      767
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
175      180
accctggggc acttgcccc ctctggacct gattcaccca tttggaagtt tgtagcccta      827
gctgatactc aatggactag gcctcctcac ttgtcaatag tggttccagg ctgggcgcag      887
tggctcatgc ctgtgggtccc ggcacttcgg gaggccgagt ggggtggctc acctgaggtc      947
aggagttcga gaccatcctg gccaacatgg tgaaccacca tctccactaa aatgcaaaaa      1007
attagccagg tgtgggtggcg ggcacctgta gtctcagcta ctcgaggagga tgaggcagga      1067
aaatcgcttg aacccaggag gtggaggttg cagttgagct gagatcggtc cattgcactc      1127
cagcctgggc aacgagagca aaactccatc tcaaaaaaaaa aaaaaaa      1174

```

<210> 129
 <211> 1285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 2..1051

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_signal

<222> 1248..1253

<221> polyA_site

<222> 1272..1285

<400> 129

g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag	49
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu	
-65 -60 -55	
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc	97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val	
-50 -45 -40	
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca	145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser	
-35 -30 -25	
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct	193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro	
-20 -15 -10 -5	
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc	241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly	
1 5 10	
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat	289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Pro Arg His	
15 20 25	
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta	337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30 35 40	
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag	385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45 50 55 60	
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc	433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65 70 75	
agg ctg aag atc ccc ccc ttt gag aag gcc cgc tcg gtc ctg gag gcc	481
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala	
80 85 90	
ctg cag cag cac agg ccg agc ccg gag ctg acc ctg agc cag aag ata	529
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile	
95 100 105	
agg acc aag ctg cag aat cca gac ctg ctg gag cta tgt cac tca gtg	577
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val	
110 115 120	
ccc aag gaa gtg gac cag ttg ggg ggc agg ggc tac ggg tca gag agc	625
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser	
125 130 135 140	
ggg gag gag gac ttt gct gcc ttt cga gcc tgg ctg cgc tgc tat ggc	673
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly	
145 150 155	
atg cca ggc atg agc tcc ctg cag gac cgg cat ggc cgt acc atc tgg	721
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp	
160 165 170	
ttc cag ggg gat cct gga ccg ttg gca ccc aaa ggg cgc aag tcc cgc	769

```

Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
      175              180              185
aaa aag aaa tcc aag gcc aca cag ctg agt cct gag gac aga gtg gag      817
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
      190              195              200
gac gct ttg cct cca agc aag gcc cct tcc aag aca cga agg gca aag      865
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
      205              210              215              220
aga gac ctt cct aag agg act gca acc cag cgg cct gag ggg acc agc      913
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
      225              230              235
ctc cag cag gac cca gaa gct ccc aca gtg ccc aag aag ggg agg agg      961
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
      240              245              250
aag ggg cga cag gca gcc tct ggc cac tgc aga ccc cgg aag gtc aag      1009
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
      255              260              265
gct gac atc cca tcc ttg gaa cca gag ggg acc tca gcc tct      1051
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
      270              275              280
tagcaggagg ctctccttgc ttgcaactcac cctttcttat tgtcttgccc tgcattctggg      1111
ggtctgaatt tttgggagca ggcaatatct gaagggtgcaa acaggcccta cggctgttcc      1171
ctgcacaact ctcatgggtt taattgtacc ccatcttcca catctttaaa gctcatgtga      1231
aaaatgctgc atttttaata aactgatata ttggaactcc aaaaaaaaaa aaaa      1285

```

```

<210> 130
<211> 1398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..1171

<221> sig_peptide
<222> 2..205
<223> Von Heijne matrix
      score 7.3
      seq LRLILSPLPGAQP/QQ

<221> polyA_signal
<222> 1368..1373

<221> polyA_site
<222> 1386..1398

```

```

<400> 130
g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag      49
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65              -60              -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50              -45              -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35              -30              -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20              -15              -10              -5
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly

```

				1					5					10					
atg	tcc	ggc	tct	ttt	cag	ctg	gtg	ccc	cgc	gag	gag	ctg	cca	cgc	cat		289		
Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His				
				15					20					25					
gcc	cac	ctg	cgc	ttt	tac	acg	gcc	ccg	cct	ggc	ccc	cgg	ctc	gcc	cta		337		
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu				
				30					35					40					
tgt	ttc	gtg	gac	atc	cgc	cgg	ttc	ggc	cgc	tgg	gac	ctt	ggg	gga	aag		385		
Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys				
				45					50					55					60
tgg	cag	ccg	ggc	cgc	ggg	ccc	tgt	gtc	ttg	cag	gag	tac	cag	cag	ttc		433		
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe				
				65					70					75					
agg	gag	aat	gtg	cta	cga	aac	cta	gcg	gat	aag	gcc	ttt	gac	cgg	ccc		481		
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro				
				80					85					90					
atc	tgc	gag	gcc	ctc	ctg	gac	cag	agg	ttc	ttc	aat	ggc	att	ggc	aac		529		
Ile	Cys	Glu	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn				
				95					100					105					
tat	ctg	cgg	gca	gag	atc	ctg	tac	cgg	ctg	aag	atc	ccc	ccc	ttt	gag		577		
Tyr	Leu	Arg	Ala	Glu	Ile	Leu	Tyr	Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu				
				110					115					120					
aag	gcc	cgc	tcg	gtc	ctg	gag	gcc	ctg	cag	cag	cac	agg	ccg	agc	ccg		625		
Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala	Leu	Gln	Gln	His	Arg	Pro	Ser	Pro				
				125					130					135					140
gag	ctg	acc	ctg	agc	cag	aag	ata	agg	acc	aag	ctg	cag	aat	cca	gac		673		
Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	Arg	Thr	Lys	Leu	Gln	Asn	Pro	Asp				
				145					150					155					
ctg	ctg	gag	cta	tgt	cac	tca	gtg	ccc	aag	gaa	gtg	gtc	cag	ttg	ggg		721		
Leu	Leu	Glu	Leu	Cys	His	Ser	Val	Pro	Lys	Glu	Val	Val	Gln	Leu	Gly				
				160					165					170					
ggc	aga	ggc	tac	ggg	tca	gag	agc	ggg	gag	gag	gac	ttt	gct	gcc	ttt		769		
Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser	Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe				
				175					180					185					
cga	gcc	tgg	ctg	cgc	tgc	tat	ggc	atg	cca	ggc	atg	agc	tcc	ctg	cag		817		
Arg	Ala	Trp	Leu	Arg	Cys	Tyr	Gly	Met	Pro	Gly	Met	Ser	Ser	Leu	Gln				
				190					195					200					
gac	cgg	cat	ggc	cgt	acc	atc	tgg	ttc	cag	ggg	gat	cct	gga	ccg	ttg		865		
Asp	Arg	His	Gly	Arg	Thr	Ile	Trp	Phe	Gln	Gly	Asp	Pro	Gly	Pro	Leu				
				205					210					215					220
gca	ccc	aaa	ggg	cgc	aag	tcc	cgc	aaa	aag	aaa	tcc	aag	gcc	aca	cag		913		
Ala	Pro	Lys	Gly	Arg	Lys	Ser	Arg	Lys	Lys	Lys	Ser	Lys	Ala	Thr	Gln				
				225															

Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu
 85 90 95
 gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg 631
 Val Ile Ser Phe Ala Lys Asp Ser Leu
 100 105
 ttctgggaca gtatcaatac tgatgagcaa cctggcacac aaactatgag cagaccactt 691
 cagcttgaga atgcagtggg tctgaagatg gtcaagtctg tctgccttag attttgatgt 751
 cacctagaca acacttaaac tcatatgaaa caaaaattaa aatacgtatt acaagtaaaa 811
 aaaaaaaaaa 821

 <210> 132
 <211> 916
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 62..916

 <221> sig_peptide
 <222> 62..757
 <223> Von Heijne matrix
 score 4.2
 seq LVTPAALRPLVLG/GN

 <221> polyA_site
 <222> 904..916

 <400> 132
 cctgaatgac ttgaatgttt ccccgccctga gctaacagtc catgtgggtg attcagctct 60
 g atg gga tgt gtt ttc cag agc aca gaa gac aaa cgt ata ttc aag ata 109
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
 -230 -225 -220
 gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 -215 -210 -205
 tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 -200 -195 -190 -185
 gta cac ttg atg ggg gac aac tta tgc aat gat ggc tct ctc ctg ctc 253
 Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
 -180 -175 -170
 caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 -165 -160 -155
 ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 -150 -145 -140
 ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 -135 -130 -125
 cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag 445
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 -120 -115 -110 -105
 gta gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt 493
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
 -100 -95 -90
 cgt tac tac cac aaa ctc agg atg tct gcg gag tac tcc cag agc tgg 541
 Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
 -85 -80 -75
 ggc cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat 589

Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly	Asp	Ile	Phe	Arg	Asn		
		-70					-65					-60					
gac	ggg	tcc	atc	atg	ctt	caa	gga	gtg	agg	gag	tca	gat	gga	gga	aac	637	
Asp	Gly	Ser	Ile	Met	Leu	Gln	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gly	Asn		
		-55					-50				-45						
tac	acc	tgc	agt	atc	cac	cta	ggg	aac	ctg	gtg	ttc	aag	aaa	acc	att	685	
Tyr	Thr	Cys	Ser	Ile	His	Leu	Gly	Asn	Leu	Val	Phe	Lys	Lys	Thr	Ile		
		-40					-35				-30				-25		
gtg	ctg	cat	gtc	agc	ccg	gaa	gag	cct	cga	aca	ctg	gtg	acc	ccg	gca	733	
Val	Leu	His	Val	Ser	Pro	Glu	Glu	Pro	Arg	Thr	Leu	Val	Thr	Pro	Ala		
				-20						-15					-10		
gcc	ctg	agg	cct	ctg	gtc	ttg	ggg	ggg	aat	cag	ttg	gtg	atc	att	gtg	781	
Ala	Leu	Arg	Pro	Leu	Val	Leu	Gly	Gly	Asn	Gln	Leu	Val	Ile	Ile	Val		
			-5					1				5					
gga	att	gtc	tgt	gcc	aca	atc	ctg	ctg	ctc	cct	gtc	ctg	ata	ttg	atc	829	
Gly	Ile	Val	Cys	Ala	Thr	Ile	Leu	Leu	Leu	Pro	Val	Leu	Ile	Leu	Ile		
	10					15					20						
gtg	aag	aag	acc	tgt	gga	aat	aag	agt	tca	gtg	aat	tct	aca	gtc	ttg	877	
Val	Lys	Lys	Thr	Cys	Gly	Asn	Lys	Ser	Ser	Val	Asn	Ser	Thr	Val	Leu		
	25				30					35					40		
gtg	aag	aac	acg	aag	aag	act	aat	cca	aaa	aaa	aaa	aaa				916	
Val	Lys	Asn	Thr	Lys	Lys	Thr	Asn	Pro	Lys	Lys	Lys	Lys					
			45						50								
<210> 133																	
<211> 1153																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> 62..520																	
<221> polyA_signal																	
<222> 1124..1129																	
<221> polyA_site																	
<222> 1141..1153																	
<400> 133																	
cctgaatgac	ttgaatgttt	ccccgcctga	gctaacagtc	catgtgggtg	attcagctct											60	
g	atg	gga	tgt	gtt	ttc	cag	agc	aca	gta	gac	aaa	tgt	ata	ttc	aag	ata	109
	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Val	Asp	Lys	Cys	Ile	Phe	Lys	Ile	
	1			5					10				15				
gac	tgg	act	ctg	tca	cca	gga	gag	cac	gcc	aag	gac	gaa	tat	gtg	cta	157	
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu		
			20				25					30					
tac	tat	tac	tcc	aat	ctc	agt	gtg	cct	att	ggg	cgc	ttc	cag	aac	cgc	205	
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg		
		35				40					45						
gta	cac	ttg	atg	ggg	gac	atc	tta	tgc	aat	gat	ggc	tct	ctc	ctg	ctc	253	
Val	His	Leu	Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu		
	50				55				60								
caa	gat	gtg	caa	gag	gct	gac	cag	gga	acc	tat	atc	tgt	gaa	atc	cgc	301	
Gln	Asp	Val	Gln	Glu													


```

gaatgttgaa tgtctttggc tcagttcatt taaaaaagat atctatttga aagttctcag 1277
agttgtacat atgtttcaca gtacaggatc tgtacataaa agtttctttc ctaaaccatt 1337
caccaagagc caatatctag gcattttctt ggtagcacia attttcttat tgcttagaaa 1397
attgtcctcc ttgttatttc tgtttgtaag acttaagtga gttagggtctt taaggaaagc 1457
aacgctcctc tgaaatgctt gtcttttatg ctgggaggtg accatagggc tctgctttta 1517

```

```

<210> 135
<211> 526
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 22..318

```

```

<221> sig_peptide
<222> 22..93
<223> Von Heijne matrix
      score 4.6
      seq FFIFCSLNTLLLG/GV

```

```

<221> polyA_signal
<222> 497..502

```

```

<221> polyA_site
<222> 516..526

```

```

<400> 135
ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga ttt ctt cta 51
                               Met Lys Ser Ala Lys Leu Gly Phe Leu Leu
                               -20                               -15
aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg ggt ggt gtt 99
Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly Gly Val
                               -10                               -5                               1
aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc tgc aaa 147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
                               5                               10                               15
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc 195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
                               20                               25                               30
tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt 243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
35                               40                               45                               50
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc 291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
                               55                               60                               65
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg 338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
                               70                               75
aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat 398
ctttgtaata tttccataat gctttaagct tccatatgtt tgctattttc ctgaccctag 458
ttttgtcttt cctggaaatt aactgtatga tcattagaat gaaagagtct ttctgtcaaa 518
aaaaaaaaa 526

```

```

<210> 136
<211> 352
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS

```

<222> 8..292

<221> sig_peptide

<222> 8..118

<223> Von Heijne matrix

score 5.6

seq WLLLDALLRLGDT/KK

<221> polyA_signal

<222> 317..322

<221> polyA_site

<222> 339..352

<400> 136

ctgagat	atg	gca	agt	ccc	gct	gta	aac	agg	tgg	aaa	agg	cca	agg	ttg	49	
	Met	Ala	Ser	Pro	Ala	Val	Asn	Arg	Trp	Lys	Arg	Pro	Arg	Leu		
			-35					-30					-25			
aag	ccg	gtg	tgg	cca	cgg	cgc	ttg	gaa	tcc	tgg	ttg	ctg	gat	gct	97	
Lys	Pro	Val	Trp	Pro	Arg	Arg	Leu	Glu	Ser	Trp	Leu	Leu	Leu	Asp	Ala	
		-20					-15					-10				
ctt	ttg	cga	tta	gga	gat	acc	aaa	aaa	aag	cga	cag	cct	gaa	gca	gcc	145
Leu	Leu	Arg	Leu	Gly	Asp	Thr	Lys	Lys	Lys	Arg	Gln	Pro	Glu	Ala	Ala	
		-5				1				5						
aca	aaa	tcc	tgt	gtt	aga	agc	agc	tgt	ggg	ggg	ccc	agt	gga	gat	ggg	193
Thr	Lys	Ser	Cys	Val	Arg	Ser	Ser	Cys	Gly	Gly	Pro	Ser	Gly	Asp	Gly	
10				15					20					25		
cct	ccc	cca	tgc	ctc	cag	cag	cct	gac	cct	cgt	gcc	ctg	tct	cag	gcg	241
Pro	Pro	Pro	Cys	Leu	Gln	Gln	Pro	Asp	Pro	Arg	Ala	Leu	Ser	Gln	Ala	
			30					35					40			
ttc	tct	aga	tcc	ttt	cct	ctg	ttt	ccc	tct	ctc	gct	ggc	aaa	agt	atg	289
Phe	Ser	Arg	Ser	Phe	Pro	Leu	Phe	Pro	Ser	Leu	Ala	Gly	Lys	Ser	Met	
		45					50					55				
atc	taattgaaac	aagactgaag	gatcaataaaa	cagccatctg	ccccttcaaaa											342
Ile																
aaaaaaaaa																352

<210> 137

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 16..378

<221> sig_peptide

<222> 16..84

<223> Von Heijne matrix

score 9.8

seq FLLFFFLFLLTRG/SL

<221> polyA_signal

<222> 502..507

<221> polyA_site

<222> 522..542

<400> 137

cacgacctgt	gggcc	atg	atg	cta	ccc	caa	tgg	ctg	ctg	ctg	ctg	ttc	ctt	51
	Met	Met	Leu	Pro	Gln	Trp	Leu	Leu	Leu	Leu	Phe	Leu		

```

                                -20                                -15
ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
-10                                -5                                1                                5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
10                                15                                20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tgc cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
25                                30                                35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
40                                45                                50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
55                                60                                65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
70                                75                                80                                85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
90                                95
tccttcttgctc tgctctctcc tctctccacct gctctctctcc ctaccagag ctctgtgttc      448
accctgttcc ccagagcctc caccatgagt ggagggaagt ggggagtgat tgaaataaag      508
agcttttttca atgaaaaaaaa aaaaaaaaaa aaaa      542

```

<210> 138
 <211> 233
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..233

```

<400> 138
gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
Met
1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
5                                10                                15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155
Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg Glu
20                                25                                30
gag aga aaa caa ata aat ggg aaa aaa gaa agg aca aaa tat gaa aca      203
Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu Thr
35                                40                                45
cca aga aaa aga gaa gga aaa aaa aaa aaa
Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
50                                55

```

<210> 139
 <211> 660
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..340

<221> sig_peptide
 <222> 83..124
 <223> Von Heijne matrix
 score 7.5
 seq VALNLILVPCCAA/WC

<221> polyA_signal
 <222> 573..578

<221> polyA_site
 <222> 607..660

<400> 139
 gaatttgtaa aacttctgct cgtttacact gcacattgaa tacaggtaac taattggaag 60
 gagaggggag atcactcttt tg atg gtg gcc ctg aac ctc att ctg gtt ccc 112
 Met Val Ala Leu Asn Leu Ile Leu Val Pro
 -10 -5
 tgc tgc gct gct tgg tgt gac cca cgg agg atc cac tcc cag gat gac 160
 Cys Cys Ala Ala Trp Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp
 1 5 10
 gtg ccc cgt agc tct gct gct gat act ggg tct gcg atg cag cgg cgt 208
 Val Pro Arg Ser Ser Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg
 15 20 25
 gag gcc tgg gct ggt tgg aga agg tca caa ccc ttc tct gtt ggt ctg 256
 Glu Ala Trp Ala Gly Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu
 30 35 40
 cct tct gct gaa aga ctc gag aac caa cca ggg aag ctg tcc tgg agg 304
 Pro Ser Ala Glu Arg Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg
 45 50 55 60
 tcc ctg gtc gga gag gga tat aga atc tgt gac ctc tgacaactgt 350
 Ser Leu Val Gly Glu Gly Tyr Arg Ile Cys Asp Leu
 65 70
 gaagccaccc tgggctacag aaaccacagt cttcccagca attattacaa ttcttgaatt 410
 ccttgggggat tttttactgc cctttcaaag cacttaagtg ttagatctaa cgtgttccag 470
 tgtctgtctg aggtgactta aaaaatcaga acaaaacttc tattatccag agtcatggga 530
 gagtacaccc tttccaggaa taatgttttg ggaaacactg aaatgaaatc ttcccagtat 590
 tataaattgt gtatttaaaa aaagaaactt ttctgaatgc ctacctggcg gtgtatacca 650
 ggcatgtgtgc 660

<210> 140
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..541

<221> sig_peptide
 <222> 47..220
 <223> Von Heijne matrix
 score 5.4
 seq QLDSVLWLGLG/LT

<221> polyA_site
 <222> 597..605

<400> 140
 aaagtgggag gagcactagg tcttcccgtc acctccacct ctctcc atg acc cgg 55
 Met Thr Arg
 ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct 103

09978360.101501

```

Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
-55          -50          -45          -40
cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca      151
Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
          -35          -30          -25
cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc      199
Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
          -20          -15          -10
cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc      247
Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
          -5          1          5
act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc ctc acc ttt gac      295
Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
10          15          20          25
ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc      343
Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
          30          35          40
acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag      391
Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
          45          50          55
gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag      439
Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
          60          65          70
gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc      487
Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
          75          80          85
tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct      535
Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
90          95          100          105
tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaataac aatgaccacc      591
Trp Ala
cttcttcaaaa aaaa      605

<210> 141
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..285

<221> sig_peptide
<222> 46..150
<223> Von Heijne matrix
      score 3.6
      seq LEPGLSSSAACNG/KE

<221> polyA_signal
<222> 364..369

<221> polyA_site
<222> 385..396

<400> 141
cctctacagg aatcagactc agcctctttt ggttttcagt gaagt atg cct ttt caa      57
                        Met Pro Phe Gln
                        -35
ttt gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca      105
Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser
-30          -25          -20

```

```

att gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag      153
Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys
-15          -10          -5          1
gag atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc      201
Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys
          5          10          15
ctg aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag      249
Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys
          20          25          30
cca cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt      295
Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
          35          40          45
aagtcttttg tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct      355
ggtaaacaaaa taaaagtggg ggcaccttca aaaaaaaaaa a      396

```

```

<210> 142
<211> 432
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 22..240

<221> sig_peptide
<222> 22..84
<223> Von Heijne matrix
      score 12
      seq VLVLCVLLLQAQG/GY

```

```

<221> polyA_signal
<222> 397..402

```

```

<221> polyA_site
<222> 421..432

```

```

<400> 142
gctcacgctc tggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg      51
                        Met Ala Pro Gln Thr Leu Leu Pro Val Leu
                        -20          -15
gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag      99
Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys
-10          -5          1          5
atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat      147
Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp
          10          15          20
cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag      195
Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys
          25          30          35
ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta      240
Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu
          40          45          50
tgagtgggag agtgggctgg gatgtgcac ctgctccctg aacccttcca tccgagactg      300
tgcccacatc cgaagcacia ggacatcaaa tcatcagcac aagaacatca acaggaatgc      360
caccctcccc agtgtctgaa ctccctgtcc ctgtcaaata aaccagaaca aatgcccata      420
aaaaaaaaaa aa      432

```

```

<210> 143
<211> 420
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 89..382

<221> polyA_site
<222> 408..420

<400> 143
gcttgccctga ccccatgctc gcctctgtag gtagaagaag tatgtcttcc tggacccctc 60
ggctggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag 112
                               Met Leu Gly Ala Glu Thr Glu Glu
                               1           5
aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa 160
Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu
    10           15           20
cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg 208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val
    25           30           35           40
cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc 256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala
           45           50           55
aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct 304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser
           60           65           70
gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc 352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala
           75           80           85
gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc 402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr
    90           95
ccaccaaaaa aaaaaaaaaa 420

<210> 144
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..415

<221> sig_peptide
<222> 80..142
<223> Von Heijne matrix
      score 5.4
      seq TFCLIFGLGAVWG/LG

<221> polyA_signal
<222> 471..476

<221> polyA_site
<222> 488..501

<400> 144
cccgttgat tccaagaacc tcttcgatat ttatttttat ttttaaagag ggagacgatg 60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt 112
                               Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
                               -20           -15
ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc 160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser

```



```

-10          -5          1          5
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc      208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr
          10          15          20
gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc      256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu
          25          30          35
ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa      304
Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu
          40          45          50
cag ttt ttt cag aag ctg aga aat aaa cat gaa ttt act att ttg gtg      352
Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val
          55          60          65          70
acc cta aaa cag acc cac tta aat tca gga gtt att ctc tca att cac      400
Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His
          75          80          85
cac ttg gat cac agg taaatgtggg tgctggaggt tcctgtgttt tcattatatg      455
His Leu Asp His Arg
          90
tggttaaagt aatatattaa agagaagtaa acaaaaaaaaa aaaaaa      501

```

<210> 145
 <211> 454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..361
 <221> sig_peptide
 <222> 152..283
 <223> Von Heijne matrix
 score 4.7
 seq FLLSLSLITYCFW/DP

```

<400> 145
gacatttttac ttttttctgt taacgcttac cctagaaatt agaaatgaca ccacgtattc      60
ttagcgaagt ccagttttca gcattttgtc cttattggac aatagcaagg atattagaac      120
gtgttggttc cgcgtgcttc cgtcttgagt t atg tgc tgc tat tgt cgg ata      172
                               Met Cys Cys Tyr Cys Arg Ile
                               -40
ttt tgt ctt aga tgt acg tac ttt cct gtt cat tgt ggt atg tgt aat      220
Phe Cys Leu Arg Cys Thr Tyr Phe Pro Val His Cys Gly Met Cys Asn
          -35          -30          -25
ttg cgt tac ttt gaa ttt tcc acg ttt tta ctt tct ttg tct ctc atc      268
Leu Arg Tyr Phe Glu Phe Ser Thr Phe Leu Leu Ser Leu Ser Leu Ile
          -20          -15          -10
act tac tgc ttt tgg gac ccc ccc cat cgg ggt tca cat tcc ctc tcc      316
Thr Tyr Cys Phe Trp Asp Pro Pro His Arg Gly Ser His Ser Leu Ser
          -5          1          5          10
cta gag cac act ccc ttg gat ttc ctc gag tgg ggt ctg ctg cgg      361
Leu Glu His Thr Pro Leu Asp Phe Leu Glu Trp Gly Leu Leu Arg
          15          20          25
tgaagctttc ccattttatg tgcagattat ttccagaggg tatatagaat tcaggcagct      421
gtttcgttgt agcacattaa aaatattttc ccc      454

```

<210> 146
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..307

<221> sig_peptide
 <222> 32..70
 <223> Von Heijne matrix
 score 4.2
 seq MLFSLSLLSNLNQ/IG

<221> polyA_signal
 <222> 1240..1245

<221> polyA_site
 <222> 1261..1272

<400> 146
 gtcagggtgc accgcccttt gggtcccgag c atg ctg ttt tct ctc agc ctt 52
 Met Leu Phe Ser Leu Ser Leu
 -10
 ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac 100
 Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His
 -5 1 5 10
 att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa 148
 Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln
 15 20 25
 caa cta cag cag cag cct tcg gct aac aaa aaa gca gga aaa atc cac 196
 Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His
 30 35 40
 aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa 244
 Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys
 45 50 55
 cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca 292
 Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser
 60 65 70
 cca ttt cta gct tgc tgaaacccaa aactaatctc caagaaggag aagcttctct 347
 Pro Phe Leu Ala Cys
 75
 cgcagccgga gcaggtcctt ttctagagat aggagaagag agagatcgct gtctcgggag 407
 agaaatcaca agccgtcccg atccttctct aggtctcgta gtcgatttag gtcaaataaa 467
 aggaaataga agacagtttg caagagaagt ggtgtacagg aaattacttc atttgacagg 527
 agtatgtaca gaaaattcaa gttttgtttg agacttcata agcttggtgc atttttaaga 587
 tgttttagct gttcaaactc gtttgtctct tgaaacagtg acacaaaagt gtaattctct 647
 atgggttgaa atggatcata cgaggcatgt aataccaaga attgttactt tacaatgttc 707
 ccttaagcaa aattgaattt gctttgaact tttagttatg cacagactga taataaacct 767
 ctaaacctgc ccagcggaag tgtgtttttt tttaaattta aatacagaaa caactggcaa 827
 aaattgaact aagatttact tttttttcca tagctgggat ataggctgca gctatagttg 887
 aacaagcagt ctttaaaaac tgctgtgaaa cacaggccat cagggaacac gaaatgctgc 947
 actattaaat tagaggtttt tgaaaaatcc aactctcatc ctgggcagag gttgcctagt 1007
 tggatataga tgtaagtgtt caagaaagtt tacctttgct ttaggtcgta agttccttat 1067
 ttgattgccg tatatggata catggctgtt cgtgacattc tttatgtgca aatttgatgat 1127
 ttcaaaaatg tcctgccagt ttaagggtac attgtagagc cgaactttga gttactgtgc 1187
 aagatttttt ttcattgctgt catttgtaat atgttttgtg agaatccttg ggattaaagt 1247
 tttggttaca gattaataaaa aaaaaa 1272

<210> 147
 <211> 804
 <212> DNA
 <213> Homo sapiens

```

<220>
<221> CDS
<222> 114..734

<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
      score 5.2
      seq LLFDLVCHEFCQS/DD

<221> polyA_signal
<222> 768..773

<221> polyA_site
<222> 793..804

<400> 147
ccaacaccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtatacttga      60
agctgccaaa caagtacggt agttctgaaa atccagaatg gcttgatgtt tac atg      116
                                         Met
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att      164
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile
      -40                                -35                                -30
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac      212
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp
      -25                                -20                                -15                                -10
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt      260
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu
                                         -5                                1                                5
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc      308
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala
      10                                15                                20
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta      356
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val
      25                                30                                35
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa      404
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu
      40                                45                                50                                55
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa      452
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu
      60                                65                                70
act aaa agg act gat tta acc caa gat gat ctc cac ttg aaa atc tta      500
Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu
      75                                80                                85
aag gat att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca      548
Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr
      90                                95                                100
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag      596
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln
      105                                110                                115
aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg      644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val
      120                                125                                130                                135
gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct      692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala
      140                                145                                150
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act      734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
      155                                160                                165
taaaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa      794
aaaaaaaaaa
      804

```

<210> 148
 <211> 802
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..801

<221> polyA_signal
 <222> 780..785

<221> polyA_site
 <222> 791..802

<400> 148
 agtcaccgcc tgcttcgcac tgagcctccc gactcagact ctgagtcacag ctccgaagag 60
 gaagaggaat tcggtgtggt tggaaatcgc tctcgctttg ccaagggaga ctatttacga 120
 tgctgcaaga tctgttatcc gctctgtggt tttgtcatcc ttgctgcctg tgttgtggcc 180
 tgtgttggtt tggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc 231
 Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala
 1 5 10
 ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc 279
 Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe
 15 20 25
 caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa 327
 Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln
 30 35 40
 ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata 375
 Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile
 45 50 55
 aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg 423
 Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val
 60 65 70 75
 aac cac ctc aaa gcc aat gtt aag tca gct gca gac ttg att agc ctg 471
 Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu
 80 85 90
 cct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat 519
 Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn
 95 100 105
 act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg 567
 Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val
 110 115 120
 gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag 615
 Asp Glu His Lys Lys Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln
 125 130 135
 cac ttc ttg aag gag act cct gga agc aac cag atc att ccg tca cct 663
 His Phe Leu Lys Glu Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro
 140 145 150 155
 tca gcc aca tca gaa ctt gac aat aaa acc cac agt gag aat ttg aaa 711
 Ser Ala Thr Ser Glu Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys
 160 165 170
 cag atg ggt gat aga tct gcc act ctg aaa aga cag tct ttg gac caa 759
 Gln Met Gly Asp Arg Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln
 175 180 185
 gtc acc aac aga aca gat aca gta aaa atc caa aaa aaa aaa a 802
 Val Thr Asn Arg Thr Asp Thr Val Lys Ile Gln Lys Lys Lys
 190 195 200

<210> 149

090360 10161

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

<221> polyA_signal
<222> 1452..1457

<400> 149

tcatcatcca	gagcagccag	tgtccggggag	gcagaag	atg ccc cac tcc agc ctg		55
				Met Pro His Ser Ser Leu		
				-35		
cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc cag aag gca gcc						103
His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala						
-30				-25		
ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg ggg cta gga gag						151
Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu						
-15				-10		
cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg						199
Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu						
				5		
cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg						247
Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu						
20				25		
cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg						295
Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr Val Arg						
35				40		
gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg ttg ctg ctg tcc						343
Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu Leu Ser						
50				55		
60						
65						
atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc ccg ccc ttc act						391
Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro Phe Thr						
				70		
tggtgatctt gcc ctc ctg ggc ctc tcg cag gca ctg aac atc ctc ctg						439
Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu						
				85		
ggc ctc aag ggc ctg gcc cca gct gag atc tct gca gtg tgt gaa aaa						487
Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys						
100				105		
110						
ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca tat tac atc gga						535
Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly						
115				120		
tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg att cga act tac						583
Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr						
130				135		
aat cag cat tac aac aac ctg cta cgg ggt gca gtg agc cag cgg ctg						631
Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu						
				150		
tat att ctc ctc cca ttg gactgt qqq qtq cct qat aac ctq aqt atq						679

Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val	Pro	Asp	Asn	Leu	Ser	Met		
			165					170					175				
gct	gac	ccc	aac	att	cgc	ttc	ctg	gat	aaa	ctg	ccc	cag	cag	acc	ggt	727	
Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys	Leu	Pro	Gln	Gln	Thr	Gly		
		180					185					190					
gac	cg	gct	ggc	atc	aag	gat	cg	gtt	tac	agc	aac	agc	atc	tat	gag	775	
Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr	Ser	Asn	Ser	Ile	Tyr	Glu		
		195				200					205						
ctt	ctg	gag	aac	ggg	cag	cg	gc	ggc	acc	tgt	gtc	ctg	gag	tac	gcc	823	
Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr	Cys	Val	Leu	Glu	Tyr	Ala		
210					215					220					225		
acc	ccc	ttg	cag	act	ttg	ttt	gcc	atg	tca	caa	tac	agt	caa	gct	ggc	871	
Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser	Gln	Tyr	Ser	Gln	Ala	Gly		
				230					235					240			
ttt	agc	cg	gag	gat	agg	ctt	gag	cag	gcc	aaa	ctc	ttc	tgc	cg	aca	919	
Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala	Lys	Leu	Phe	Cys	Arg	Thr		
			245					250					255				
ctt	gag	gac	atc	ctg	gca	gat	gcc	cct	gag	tct	cag	aac	aac	tgc	cgc	967	
Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu	Ser	Gln	Asn	Asn	Cys	Arg		
		260					265					270					
ctc	att	gcc	tac	cag	gaa	cct	gca	gat	gac	agc	agc	ttc	tgc	ctg	tcc	1015	
Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp	Ser	Ser	Phe	Ser	Leu	Ser		
		275				280					285						
cag	gag	gtt	ctc	cg	cac	ctg	cg	cag	gag	gaa	aag	gaa	gag	gtt	acc	1063	
Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu	Glu	Lys	Glu	Glu	Val	Thr		
290					295					300					305		
gtg	ggc	agc	ttg	aag	acc	tca	gc	gtg	ccc	agt	acc	tcc	acg	atg	tcc	1111	
Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro	Ser	Thr	Ser	Thr	Met	Ser		
				310					315					320			
caa	gag	cct	gag	ctc	ctc	ctc	agt	gga	atg	gga	aag	ccc	ctc	cct	ctc	1159	
Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met	Gly	Lys	Pro	Leu	Pro	Leu		
			325					330				335					
cg	ac	gat	ttc	tct	tgag	acccag	gg	tcaccag	ccag	agcctc	cag	tggtctc				1214	
Arg	Thr	Asp	Phe	Ser													
		340															
caagcctctg	gactggggggc					tctcttcagt			ggctgaatgt			ccagcagagc			tatttccttc		1274
cacagggggc	cttgcaggga					aggggtccagg			acttgacatc			ttaagatgcg			tcttgtcccc		1334
ttgggccagt	catttcccct					ctctgagcct											

```
<210> 150
<211> 361
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 26..361
```

```
<221> polyA_site
<222> 350..361
```

<400> 150															
tcgagaagct	gcccttagc	caacc	atg	ccg	tct	gag	ggg	cgc	tgc	tgg	gag			52	
			Met	Pro	Ser	Glu	Gly	Arg	Cys	Trp	Glu				
			1				5								
acc	ttg	aag	gcc	cta	cgc	agt	tcc	gac	aaa	ggg	cgc	ctt	tgc	tac	100
Thr	Leu	Lys	Ala	Leu	Arg	Ser	Ser	Asp	Lys	Gly	Arg	Leu	Cys	Tyr	
10					15				20				25		
cgc	gac	tgg	ctg	ctg	cgg	cgc	gag	gat	gtt	tta	gaa	gaa	tgt	atg	148

Arg	Asp	Trp	Leu	Leu	Arg	Arg	Glu	Asp	Val	Leu	Glu	Glu	Cys	Met	Ser		
			30						35					40			
ctt	ccc	aag	cta	tct	tct	tat	tct	gga	tgg	gtg	gta	gag	cac	gtc	cta	196	
Leu	Pro	Lys	Leu	Ser	Ser	Tyr	Ser	Gly	Trp	Val	Val	Glu	His	Val	Leu		
			45					50					55				
ccc	cat	atg	cag	gag	aac	caa	cct	ctg	tct	gag	act	tcg	cca	tcc	tct	244	
Pro	His	Met	Gln	Glu	Asn	Gln	Pro	Leu	Ser	Glu	Thr	Ser	Pro	Ser	Ser		
		60					65				70						
acg	tca	gct	tca	gcc	cta	gat	caa	ccc	tca	ttt	gtt	ccc	aaa	tct	cct	292	
Thr	Ser	Ala	Ser	Ala	Leu	Asp	Gln	Pro	Ser	Phe	Val	Pro	Lys	Ser	Pro		
		75				80					85						
gac	gca	agc	tct	gcc	ttt	tcc	cca	gcc	tcc	cct	gca	aca	cca	aat	gga	340	
Asp	Ala	Ser	Ser	Ala	Phe	Ser	Pro	Ala	Ser	Pro	Ala	Thr	Pro	Asn	Gly		
90					95				100					105			
acc	aag	ggc	aaa	aaa	aaa	aaa										361	
Thr	Lys	Gly	Lys	Lys	Lys	Lys											
					110												

<210> 151
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..131

<221> polyA_site
 <222> 591..605

<400>	151																
ca	tcc	ctt	ccc	cag	gct	tta	tgg	ttc	cag	ttc	ttc	tac	cac	tct	gga	47	
	Ser	Leu	Pro	Gln	Ala	Leu	Trp	Phe	Gln	Phe	Phe	Tyr	His	Ser	Gly		
	1				5				10					15			
agc	tcc	cta	gaa	tct	cct	gga	atg	ctt	aat	gga	cct	ttc	cag	cac	cga	95	
Ser	Ser	Leu	Glu	Ser	Pro	Gly	Met	Leu	Asn	Gly	Pro	Phe	Gln	His	Arg		
				20				25					30				
aat	tca	aga	att	atg	act	cat	cgg	tca	gca	gaa	aag	tgaggatacc				141	
Asn	Ser	Arg	Ile	Met	Thr	His	Arg	Ser	Ala	Glu	Lys						
			35				40										
ttttcctaac	ctacctgctt	ccctgcagt	ttcctcacia	tcttactctt	tatatttttag											201	
catatgtagc	ttctcaggat	gttaattctg	ttctctctgt	gttggtgtct	gagcaccag											261	
aaggtagagc	caggggcact	tataaaccag	gagcattatt	tgacaggcac	ttaagaaaga											321	
cactggctac	gtaatcccag	cactttggga	ggctgaggcg	gatggatcac	atgaggtcag											381	
gagttcgaga	ccagcctggc	cagcatgggtg	aaaccctgtc	tctactaaaa	atacaaaaat											441	
tagctgggtg	tggttgcaca	cgctgtaat	cccagctacc	tgggaggctg	aggcaggaga											501	
atcgcttgaa	cttgggaggc	ggaggttgca	gtgagcctag	atthttgccat	tgactccag											561	
cctgggtgac	aagggcgaaa	ctccatccca	aaaaaaaaaa	aaaa												605	

<210> 152
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..185

<221> sig_peptide
 <222> 33..80
 <223> Von Heijne matrix

score 3.7
seq IALTLIPSMLSRA/AG

<221> polyA_signal
<222> 570..575

<221> polyA_site
<222> 586..591

<400> 152
caatcttctc agcttataac cgtctttccc tt atg cta agg ata gcc ctt aca 53
Met Leu Arg Ile Ala Leu Thr
-15 -10
ctc atc cca tct atg ctg tca agg gct gct ggt tgg tgc tgg tac aag 101
Leu Ile Pro Ser Met Leu Ser Arg Ala Gly Trp Cys Trp Tyr Lys
-5 1 5
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg 149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp
10 15 20
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact 195
Asn Lys Lys Gly Asn Val Leu Gln Leu Pro Asn Phe
25 30 35
aatctcagat tggcagttaa agtcaaaatg ttgccaaata tttattcctt ttgcctaagt 255
ttggctaccc ggttcaattg ctttttattt ttaatgtctt gactcttcag agttcgtacc 315
tcaaaaagaac aatgagaaca tttgctttgc tttctgctga atccctaatac tcaacaatct 375
atacctggac tgtccagttc tcctcctgtg ctatcttctc ttctatccaa gtagaatgta 435
tgccaggagc tccttccttc tagcaatttc tactaaaatg tccaagtaga atgtttcctt 495
ttacaatcaa attactgtat ttattaattt gctagaatcc agtaaatacat tttggtagct 555
ctggctgtgc tatcaataaa aagatgaaag caaaaa 591

<210> 153
<211> 1150
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 184..915

<221> sig_peptide
<222> 184..237
<223> Von Heijne matrix
score 3.5
seq LLGLELSEAEATG/AD

<221> polyA_signal
<222> 1119..1124

<221> polyA_site
<222> 1139..1150

<400> 153
cggatttgac gatggtgttc ggtcttgaat ggaaatgtag tcttaggccca gtcttaggtt 60
tttgaacagg atagtaggta tccggagtcg attgagggcc agagcaggca ctgggggttcg 120
gatcctgggc aaagtttccc acgttgaggg tctcgaggac gcctagatct ctttcccagg 180
gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag 228
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
-15 -10 -5
gcg atc ggt gct gat tcg gcg cga ttt gag gag ctg ctg ctg cag gcc 276
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
1 5 10

0998360.101501

tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa	324
Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln	
15 20 25	
atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg	372
Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly	
30 35 40 45	
aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc	420
Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala	
50 55 60	
gac gtg acc gag gag gag ctg ctt cag atg cta gag gag gac caa gct	468
Asp Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala	
65 70 75	
ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat	516
Gly Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp	
80 85 90	
gca aaa ggc cag gga tgt acc gcc tac gac gta gct gtc aac agc gac	564
Ala Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp	
95 100 105	
ttc tac cgg agg atg cag aac agc gat ttc ttg cgg gag ctc gtg atc	612
Phe Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile	
110 115 120 125	
acc atc gcc agg gag ggc ctt gag gac ata tac aac ttg cag ctg aat	660
Thr Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn	
130 135 140	
ccg gaa tgg cgc atg atg aag aac cgg cca ttc atg ggc tcc atc tcg	708
Pro Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser	
145 150 155	
cag cag aac atc cgc tcg gag cag cgt cct cgg atc cag gag ctg ggg	756
Gln Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly	
160 165 170	
gac ctg tac acg ccc gcc ccc ggg aga gct gag tca ggg cct gaa aag	804
Asp Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys	
175 180 185	
cct cac ctg aac ctg tgg ctg gaa gcc ccc gac ctc ctc ttg gcc gaa	852
Pro His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu	
190 195 200 205	
gtt gac ctc ccc aaa ctg gat gga gcc ctg ggg ctg tcg ctg gag atc	900
Val Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile	
210 215 220	
ggg aga acc gcc tgg tgatgggggg ccccccagcag ctgtatcatc tagacgctta	955
Gly Arg Thr Ala Trp	
225	
tatccccgccg cagatcaact ctcattgagag caaggcagcc ttccaccgga agagaaagca	1015
attaatggtg gccatgccgc ttctgcccgt gccttcttga tcagggtgtc tccttgtgtc	1075
tctgagatgt ggagaagagg ctgctggctt ccctaaaagt tgaaataaaa gatttttgcc	1135
tttaaaaaaa aaaaa	1150

<210> 154

<211> 1513

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..1116

<221> sig_peptide

<222> 58..159

<223> Von Heijne matrix

score 4

seq IAVLYLHLYDVFG/DP

<221> polyA_signal

<222> 1486..1491

<221> polyA_site

<222> 1504..1513

<400> 154

ctgactcctg agttctcaca acgcttgacc aataagattc gggagcttct tcagcaa	57
atg gag aga ggc ctg aaa tca gca gac cct cgg gat ggc acc ggt tac	105
Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr	
-30 -25 -20	
act ggc tgg gca ggt att gct gtg ctt tac tta cat ctt tat gat gta	153
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val	
-15 -10 -5	
ttt ggg gac cct gcc tac cta cag tta gca cat ggc tat gta aag caa	201
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln	
1 5 10	
agt ctg aac tgc tta acc aag cgc tcc atc acc ttc ctt tgt ggg gat	249
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp	
15 20 25 30	
gca ggc ccc ctg gca gtg gcc gct gtg cta tat cat aag atg aac aat	297
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn	
35 40 45	
gag aag cag gca gaa gat tgc atc aca cgg cta att cac cta aat aag	345
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys	
50 55 60	
att gat cct cat gct cca aat gaa atg ctc tat ggg cga ata ggc tac	393
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr	
65 70 75	
atc tat gct ctt ctt ttt gtc aat aag aac ttt gga gtg gaa aag act	441
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr	
80 85 90	
cct caa agc cat att cag cag att tgt gaa aca att tta acc tct gga	489
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly	
95 100 105 110	
gaa aac cta gct agg aag aga aac ttc acg gca aag tct cca ctg atg	537
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met	
115 120 125	
tat gaa tgg tac cag gaa tat tat gta ggg gct gct cat ggc ctg gct	585
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala	
130 135 140	
gga att tat tac tac ctg atg cag ccc agc ctt caa gtg agc caa ggg	633
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly	
145 150 155	
aag tta cat agt ttg gtc aag ccc agt gta gac tac gtc tgc cag ctg	681
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu	
160 165 170	
aaa ttc cct tct ggc aat tac cct cca tgt ata ggt gat aat cga gat	729
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp	
175 180 185 190	
ctg ctt gtc cat tgg tgc cat ggc gcc cct ggg gta atc tac atg ctc	777
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu	
195 200 205	
atc cag gcc tat aag gta ttc aga gag gaa aag tat ctc tgt gat gcc	825
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala	
210 215 220	
tat cag tgt gct gat gtg atc tgg caa tat ggg ttg ctg aag aag gga	873
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly	
225 230 235	
tat ggg ctg tgc cac ggt tct gca ggg aat gcc tat gcc ttc ctg aca	921

```

Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
 240                245                250
ctc tac aac ctc aca cag gac atg aag tac ctg tat agg gcc tgt aag      969
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
 255                260                265                270
ttt gct gaa tgg tgc tta gag tat gga gaa cat gga tgc aga aca cca      1017
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
                275                280                285
gac acc cct ttc tct ctc ttt gaa gga atg gct ggg aca ata tat ttc      1065
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
                290                295                300
ctg gct gac ctg cta gtc ccc aca aaa gcc agg ttc cct gca ttt gaa      1113
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
                305                310                315
ctc tgaaaggata gcatgccacc tgcaactcac tgcatagaccc tttctgtata      1166
Leu
ttcaaaccca agctaagtgc ttccgttgct ttccaaggaa acaaagagtc aaactgtgga      1226
cttgattttg ttagcttttt tcagaattta tctttcattc agttcccttc cattatcatt      1286
tacttttact tagaagtatc caaggaagtc ttttaacttt aatttccatt tcttcctaaa      1346
gggagagtgga gtgatatgta cagtgttttg agattgtata catatattcc agaacttgga      1406
ggaaatctta tttaagttta tgaatataac catctgttac tgttctaaaa atgtttaaaa      1466
gaaactcaat acagataaaag ataaatatgt gactattaaa aaaaaaa      1513

<210> 155
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 327..416

<221> polyA_site
<222> 404..417

<400> 155
tgttttgagg tgttggcatt cttoctgat ttggctgttc ccaatgttta cattatttaa      60
tcttgcaaaa atgggttctgt gcacttggat gtgaaatgct gtccagtttt atttttttta      120
tgttgttatc cttggatgta caaaaaattc agaaaatgat ctctgtagat attctgtttt      180
attttggtca tctttagaag ttatcaggaa tgtgttttaa acaagaagag aacttttcta      240
aggaatgata catagaaaag attttatttt aaaatgagtt gtaaagcttg tgtttctttg      300
ttgctgcaag ctatctgccc aagtta atg caa atg gac aca ttt ttt atg tca      353
                Met Gln Met Asp Thr Phe Phe Met Ser
                1                5
gaa aaa cac aca cac aca cac aca cat ata cac aca cac aca cga aaa      401
Glu Lys His Thr His Thr His Thr His Ile His Thr His Thr Arg Lys
10                15                20                25
aca aaa aaa aaa aaa a a
Thr Lys Lys Lys Lys
                30

<210> 156
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..398

<221> sig_peptide

```

<222> 63..206
 <223> Von Heijne matrix
 score 4.9
 seq PSLAAGLLFGSLA/GL

<400> 156
 ggggccttcg tgagaccggt gcaggcctgg ggtagtctcc tgtctggaca gagaagagaa 60
 aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt 107
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35
 ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa 155
 Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys
 -30 -25 -20
 gca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta 203
 Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
 -15 -10 -5
 gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg 251
 Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
 1 5 10 15
 gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg 299
 Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
 20 25 30
 ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc 347
 Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
 35 40 45
 agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc 395
 Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
 50 55 60
 cat tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca 448
 His
 tcttccacta ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt 508
 tacctaaaaa aaaagacacc aaacttggca gagaggtgga aaatcagtca tgattacaaa 568
 cctacagagg tggcgagtat gtaacacaag agctt 603

<210> 157
 <211> 522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 488..493

<221> polyA_site
 <222> 511..522

<400> 157
 c gag att gcg ggc tat ggc gcc gaa ggt ttt tcg tca gta ctg gga tat 49
 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15
 ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat 97
 Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa 145
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 tcc tcc ggg cac ctt cct nntgaaggag tggctaagggt tggacaatac 193
 Ser Ser Gly His Leu Pro

cattttatgt acntnncatt tcctagtaca ggttgagtat cccttatttg a

956

<210> 159
<211> 1041
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..703

<221> sig_peptide
<222> 20..94
<223> Von Heijne matrix
score 3.9
seq ATVGLLMLGVTLP/NS

<221> polyA_signal
<222> 1000..1005

<221> polyA_site
<222> 1023..1041

<400> 159
caggggtcctg catcctacc atg tcg atg gct gtg gaa acc ttt ggc ttc ttc 52
Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe
-25 -20 -15
atg gca act gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc 100
Met Ala Thr Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser
-10 -5 1
tac tgg cga gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc 148
Tyr Trp Arg Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr
5 10 15
atc ttc gag aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc 196
Ile Phe Glu Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val
20 25 30
tac aac tgc tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att 244
Tyr Asn Cys Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile
35 40 45 50
cag gcc tgc cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc 292
Gln Ala Cys Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu
55 60 65
ggc ctc ttg cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc 340
Gly Leu Leu Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly
70 75 80
ctg gag ctc tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ccc 388
Leu Glu Leu Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro
85 90 95
cac att ctg gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc 436
His Ile Leu Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala
100 105 110
ttc aac atc acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag 484
Phe Asn Ile Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys
115 120 125 130
tac gag ctg ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc 532
Tyr Glu Leu Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile
135 140 145
tcc atc ctg ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct 580
Ser Ile Leu Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser
150 155 160
gac gag gac cca gcc gcc agc gcc cgg cgg ccc tac cag gct cca gtg 628

0998360.101501

Asp	Glu	Asp	Pro	Ala	Ala	Ser	Ala	Arg	Arg	Pro	Tyr	Gln	Ala	Pro	Val	
		165					170					175				
tcc	gtg	atg	ccc	gtc	gcc	acc	tcg	gac	caa	gaa	ggc	gac	agc	agc	ttt	676
Ser	Val	Met	Pro	Val	Ala	Thr	Ser	Asp	Gln	Glu	Gly	Asp	Ser	Ser	Phe	
		180					185					190				
ggc	aaa	tac	ggc	aga	aac	gcc	tac	gtg	tagcagctct	ggcccgtggg						723
Gly	Lys	Tyr	Gly	Arg	Asn	Ala	Tyr	Val								
		195				200										
ccccgctgtc	ttcccactgc	cccaaggaga	ggggacctgg	ccggggccca	ttcccctata											783
gtaacctcag	gggccggcca	cgccccgctc	ccgtagcccc	gccccggcca	cggccccgtg											843
tcttgcactc	tcatggcccc	tccaggccaa	gaactgctct	tgggaagtcg	catatctccc											903
ctctgaggct	ggatccctca	tctttctgacc	ctgggttctg	ggctgtgaag	gggacgggtg											963
ccccgcacgt	ttgtattgtg	tataaatata	ttcattaata	aatgcatatt	gtgaccgtta											1023
aaaaaaaaaa	aaaaaaaa															1041

<210> 160
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..294

<221> sig_peptide
 <222> 103..243
 <223> Von Heijne matrix
 score 5.9
 seq TWLGLLSFQNLHC/FP

<400> 160																
ttcccatggg	ttagaagcat	aacctgtaat	gtaatgcaag	tcccctaact	ccctgggttg											60
taacattaac	ttccttaagt	aataatcaat	gaaagaaatt	ct atg cat ggt ttt												114
				Met His Gly Phe												
				-45												
gaa ata ata	tcc ttg aaa	gag gaa tca	cca tta gga	aag gtg agt	cag											162
Glu Ile Ile	Ser Leu Lys	Glu Glu Ser	Pro Leu Gly	Lys Val Ser	Gln											
	-40		-35		-30											
ggg cct ttg	ttt aat gtg	act agt ggc	tca tca tca	cca gtg acc	tgg											210
Gly Pro Leu	Phe Asn Val	Thr Ser Gly	Ser Ser Ser	Pro Val Thr	Trp											
	-25		-20		-15											
ttg ggc cta	ctc tcc ttc	cag aac ctg	cat tgc ttc	cca gac ctc	ccc											258
Leu Gly Leu	Leu Ser Phe	Gln Asn Leu	His Cys Phe	Pro Asp Leu	Pro											
	-10		-5		1				5							
act gag atg	cct cta aga	gcc aaa gga	gtc aac act	tgagcctagg												304
Thr Glu Met	Pro Leu Arg	Ala Lys Gly	Val Asn Thr													
	10		15													
gtgggctaca	acaaaagatt	ctaatttacc	ttgcttcac	taggtccagg	ccccaagtag											364
cttgctgaag	gaacttaaaa	agtagctgtt	atttattgta	ttgtataagc	taaaaacatt											424
tattttttgt	gaatcgaaac	aattccatgt	agcaatcttt	tttctgttca	cgtgtttgt											484
gatagaacct	taaattccgc	aagcatcagt	tttttgaaaa	aatgggaatt	gaccggatag											544
taacaggcaa	agtt															558

<210> 161
 <211> 730
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..518

<221> sig_peptide
 <222> 81..173
 <223> Von Heijne matrix
 score 3.9
 seq ILFHGVFYAGGFA/IV

<400> 161
 ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt gcctttgatg 60
 attttcaaga gagttgtgct atg atg tgg caa aag tat gca gga agc agg cgg 113
 Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
 -30 -25
 tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc 161
 Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
 -20 -15 -10 -5
 ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg 209
 Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
 1 5 10
 gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag 257
 Ala Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu
 15 20 25
 gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc 305
 Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
 30 35 40
 atc gac agg gaa aac ttc gtg gac att gtt gat gcc aag ttg aag att 353
 Ile Asp Arg Glu Asn Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile
 45 50 55 60
 cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc 401
 Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
 65 70 75
 aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag 449
 Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
 80 85 90
 ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 497
 Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
 95 100 105
 ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 548
 Gly Asp Glu Val Lys Lys Glu
 110 115
 ctagtccatc cttccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg 608
 acagacactc ctgcaaccca gttttccagc caccagtggg atgatggtat gtgccagcac 668
 atggtaattt tgggtgtaatt ctaacttggg cacaacgaat gctatttgctc atttttaaac 728
 tg 730

<210> 162
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..326

<221> polyA_signal
 <222> 1066..1071

<221> polyA_site
 <222> 1087..1098

<400> 162
 ctccctttga atgagagaaa ctaacccgct tccgaagccc ctgaaagaca ctgctccttc 60


```

ctctc atg gag ttg gct ccg aca gcc cgt ctg cca cca ggc cat ggt tcc 110
Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser
1 5 10 15
ttg ccc cat ggt gtc ctg gga ccc aga gca aca gga tct gtc acc cac 158
Leu Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His
20 25 30
ctc tct ctt ctc ccc cag atc aag caa cgt gcc tca gag gct ttg ccc 206
Leu Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro
35 40 45
gaa ttg ctt cgt cct gtc acc ccc atc acc aat ttt gag ggc agc cag 254
Glu Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln
50 55 60
tct cag gac cac agt gga atc ttt ggc ctg gta aca aac ctg gaa gag 302
Ser Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu
65 70 75
ctg gag gtg gac gat tgg gag ttc tgagcctctg caaactgtgc gcattctcca 356
Leu Glu Val Asp Asp Trp Glu Phe
80 85
gccagggatg cagaggccac ccagaggccc ttcctgaggg ccggccacat tcccgccctc 416
ctgggcagat tgggtagaaa ggacattctt ccaggaaagt tgactgctgg ctgattggga 476
aagaaaatcc tggagagata cttcactgct ccaaggcttt tgagacacaa gggaatctca 536
acaaccaggg atcaggaggg tccaaagccg acattcccag tcctgtgagc tcaggtgacc 596
tcctccgcag aagagagatg ctgctctggc cctgggagct gaattccaag cccagggttt 656
ggctccttaa acccgaggac cgccacctct tccagtgct tgcgaccagc ctcattctac 716
ttaactttgc tctcagatgc ctcagatgct ataggtcagt gaaagggcga gtagtaagct 776
gcctgcctcc cttccctcag acctctccct cataattcca gagaagggca tttctgtctt 836
tttaagcaca gactaaggct ggaacagtcc atccttatcc ctcttctggc ttgggccctg 896
acacctaagt ctttcccacg gtttatgtgt gtgcctcatt cctttcccac caagaatcca 956
tcttagcgcc tctgcccagc tgccctggtg ctttctccaa gggccatcag tgtcttgctt 1016
agcttgaggg cttaagtctt tatgctgtgt tagtttcgtt gtcagaacaa attaaaattt 1076
tcagagacgc aaaaaaaaaa aa 1098

<210> 163
<211> 346
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 170..289

<221> sig_peptide
<222> 170..250
<223> Von Heijne matrix
score 3.6
seq LTLILLITPSPSPL/LF

<400> 163
ccatttgagc cccaccacgg aggttatgtg gtcccaaaag gaatgatggc caagcaatta 60
atttttccctc ctagttctta gcttgcttct gcattgattg gctttacaca actggcattt 120
agtctgcatt acacaaatag acactaattt atttggaaca agcagcaaa atg aga act 178
Met Arg Thr
-25
tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act ctg ctt cta 226
Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr Leu Leu Leu
-20 -15 -10
atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt ctg tcc ctc 274
Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly Leu Ser Leu
-5 1 5
aga tca gca atg tct tagccccctc cctctcttcc attccttcct gttggtactc 329
Arg Ser Ala Met Ser

```

```

10
attttcttcta acttttta                                     346

<210> 164
<211> 685
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..497

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 663..685

<400> 164
aagttctgcg ctggctcggcg gagtagcaag tggcc atg ggg agc ctc agc ggt      53
                                     Met Gly Ser Leu Ser Gly
                                     1           5
ctg cgc ctg gca gca gga agc tgt ttt agg tta tgt gaa aga gat gtt      101
Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val
               10           15           20
tcc tca tct cta agg ctt acc aga agc tct gat ttg aag aga ata aat      149
Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn
               25           30           35
gga ttt tgc aca aaa cca cag gaa agt ccc gga gct cca tcc cgc act      197
Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr
               40           45           50
tac aac aga gtg cct tta cac aaa cct acg gat tgg cag aaa aag atc      245
Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile
55           60           65           70
ctc ata tgg tca ggt cgc ttc aaa aag gaa gat gaa atc cca gag act      293
Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr
               75           80           85
gtc tcg ttg gag atg ctt gat gct gca aag aac aag atg cga gtg aag      341
Val Ser Leu Glu Met Leu Asp Ala Ala Lys Asn Lys Met Arg Val Lys
               90           95           100
agc agc tat cta atg att gcc ctg acg gtg gta gga tgc atc ttc atg      389
Ser Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met
               105           110           115
gtt att gag ggc aag aag gct gcc caa aga cac gag act tta aca agc      437
Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser
               120           125           130
ttg aac tta gaa aag aaa gct cgt ctg aaa gag gaa gca gct atg aag      485
Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu Ala Ala Met Lys
135           140           145           150
gcc aaa aca gag tagcagaggt atccgtgttg gctggatttt gaaaatccag      537
Ala Lys Thr Glu
gaattatggt ataacgtgcc tgtattaaaa aggatgtggt atgaggatcc atttcataaa      597
gtatgatttg cccaaacctg taccatttcc gtatttctgc cgtagaagta gaaataaatt      657
ttcttaaaaa aaaaaaaaaa aaaaaaaaaa                                     685

<210> 165
<211> 554
<212> DNA
<213> Homo sapiens

<220>

```

<221> CDS
<222> 18..320

<221> polyA_signal
<222> 539..544

<221> polyA_site
<222> 542..554

<400> 165
aaccgctcgtg gggaagg atg gtg tgc gaa aaa tgt gaa aag aaa ctt ggt 50
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly
1 5 10
act gtt atc act cca gat aca tgg aaa gat ggt gct agg aat acc aca 98
Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
15 20 25
gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa 146
Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
30 35 40
aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga 194
Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
45 50 55
att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc 242
Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly
60 65 70 75
tgt gcc tac aaa aaa ggc atc tgt gcg atg tgt ggn aaa aaa gtt ttg 290
Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu
80 85 90
gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt 340
Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val
95 100
ctggcttttct aaatgattttt actttctgcc ttgaattttc aaggcataga tgtcaactta 400
cagaataaca tgttttaaga taattaagtt taaaccagag aatttgattg ttactcattt 460
tgctctcatg ttctaaacag caacagtgtg actagtcttt tgttgtaaag gggtatttttc 520
cttataagaa ttttaagaac taaaaaaaaa aaaa 554

<210> 166
<211> 1678
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 71..1438

<221> sig_peptide
<222> 71..136
<223> Von Heijne matrix
score 3.5
seq AAPVAAGLGPVIS/RP

<221> polyA_signal
<222> 1644..1649

<221> polyA_site
<222> 1665..1678

<400> 166
ccgacttcca gaggagcgt gtgcacgtgg agaagagcgg ggactcggcg accctgccct 60
cccgaccctc atg ttc gaa gag cct gag tgg gcc gag gcg gcc cca gta 109
Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val

				-20					-15					-10					
gcc	gcg	ggc	ctt	ggg	ccc	gta	atc	tca	cga	cct	ccg	cct	gcg	gcc	tcc				157
Ala	Ala	Gly	Leu	Gly	Pro	Val	Ile	Ser	Arg	Pro	Pro	Pro	Ala	Ala	Ser				
				-5					1				5						
tcg	caa	aac	aag	ggc	tcc	aag	cgc	cgc	cag	ctc	ttg	gcc	aca	tta	cgg				205
Ser	Gln	Asn	Lys	Gly	Ser	Lys	Arg	Arg	Gln	Leu	Leu	Ala	Thr	Leu	Arg				
		10					15					20							
gcc	cta	gag	gca	gca	tct	ctt	tcc	cag	cat	ccc	ccc	agc	cta	tgt	ata				253
Ala	Leu	Glu	Ala	Ala	Ser	Leu	Ser	Gln	His	Pro	Pro	Ser	Leu	Cys	Ile				
	25					30				35									
agt	gac	tct	gag	gag	gag	gag	gag	gaa	agg	aag	aag	aaa	tgc	ccc	aaa				301
Ser	Asp	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Lys	Cys	Pro	Lys				
	40			45					50						55				
aag	gca	tca	ttt	gcc	agt	gcc	tct	gct	gaa	gta	ggg	aag	aaa	ggg	aag				349
Lys	Ala	Ser	Phe	Ala	Ser	Ala	Ser	Ala	Glu	Val	Gly	Lys	Lys	Gly	Lys				
			60					65						70					
aag	aaa	tgt	caa	aaa	cag	ggc	cca	cct	tgc	agt	gac	tct	gag	gaa	gaa				397
Lys	Lys	Cys	Gln	Lys	Gln	Gly	Pro	Pro	Cys	Ser	Asp	Ser	Glu	Glu	Glu				
		75					80						85						
gta	gaa	agg	aag	aag	aaa	tgc	cac	aaa	cag	gct	ctt	gtt	ggc	agt	gac				445
Val	Glu	Arg	Lys	Lys	Lys	Cys	His	Lys	Gln	Ala	Leu	Val	Gly	Ser	Asp				
	90					95					100								
tct	gct	gaa	gat	gag	aaa	aga	aag	agg	aaa	tgc	cag	aaa	cat	gcc	cct				493
Ser	Ala	Glu	Asp	Glu	Lys	Arg	Lys	Arg	Lys	Cys	Gln	Lys	His	Ala	Pro				
	105				110					115									
ata	aat	tca	gcc	cag	cac	ctg	gac	aat	gtt	gac	caa	aca	ggt	ccc	aaa				541
Ile	Asn	Ser	Ala	Gln	His	Leu	Asp	Asn	Val	Asp	Gln	Thr	Gly	Pro	Lys				
	120			125				130						135					
gcc	tgg	aag	ggt	agt	act	aca	aat	gat	cca	cca	aag	caa	agc	cct	ggg				589
Ala	Trp	Lys	Gly	Ser	Thr	Thr	Asn	Asp	Pro	Pro	Lys	Gln	Ser	Pro	Gly				
			140					145					150						
tcc	act	tcc	cct	aaa	ccc	cct	cat	aca	tta	agc	cgc	aag	cag	tgg	cgg				637
Ser	Thr	Ser	Pro	Lys	Pro	Pro	His	Thr	Leu	Ser	Arg	Lys	Gln	Trp	Arg				
		155					160					165							
aac	cgg	caa	aag	aat	aag	aga	aga	tgt	aag	aac	aag	ttt	cag	cca	cct				685
Asn	Arg	Gln	Lys	Asn	Lys	Arg	Arg	Cys	Lys	Asn	Lys	Phe	Gln	Pro	Pro				
	170					175						180							
cag	gtg	cca	gac	cag	gcc	cca	gct	gag	gcc	ccc	aca	gag	aag	aca	gag				733
Gln	Val	Pro	Asp	Gln	Ala	Pro	Ala	Glu	Ala	Pro	Thr	Glu	Lys	Thr	Glu				
	185				190					195									
gtg	tct	cct	gtt	ccc	agg	aca	gac	agc	cat	ggg	gct	cgg	gca	ggg	gct				781
Val	Ser	Pro	Val	Pro	Arg	Thr	Asp	Ser	His	Gly	Ala	Arg	Ala	Gly	Ala				
	200			205					210					215					
ttg	cga	gcc	cgc	atg	gca	cag	cgg	ctg	gat	ggg	gcc	cga	ttt	cgc	tac				829
Leu	Arg	Ala	Arg	Met	Ala	Gln	Arg	Leu	Asp	Gly	Ala	Arg	Phe	Arg	Tyr				
			220				225					230							
ctc	aat	gaa	cag	ttg	tac	tca	ggg	ccc	agc	agt	gct	gca	cag	cgt	ctc				877
Leu	Asn	Glu	Gln	Leu	Tyr	Ser	Gly	Pro	Ser	Ser	Ala	Ala	Gln	Arg	Leu				
		235					240					245							
ttc	cag	gaa	gac	cct	gag	gct	ttt	ctt	ctc	tac	cac	cgc	ggc	ttc	cag				925
Phe	Gln	Glu	Asp	Pro	Glu	Ala	Phe	Leu	Leu	Tyr	His	Arg	Gly	Phe	Gln				
	250					255					260								
agc	caa	gtg	aag	aag	tgg	cca	ctg	cag	cca	gtg	gac	cgc	atc	gcc	agg				973
Ser	Gln	Val	Lys	Lys	Trp	Pro	Leu	Gln	Pro	Val	Asp	Arg	Ile	Ala	Arg				
	265					270				275									
gat	ctt	cgc	cag	cgg	cct	gca	tcc	cta	gtg	gtg	gct	gac	ttc	ggc	tgt				1021
Asp	Leu	Arg	Gln	Arg	Pro	Ala	Ser	Leu	Val	Val	Ala	Asp	Phe	Gly	Cys				
	280				285				290						295				
ggg	gat	tgc	cgc	ttg	gct	tca	agt	atc	cgg	aac	cct	gtg	cat	tgc	ttt				1069
Gly	Asp	Cys	Arg	Leu	Ala	Ser	Ser	Ile	Arg	Asn	Pro	Val	His	Cys	Phe				
			300						305					310					

```

gac ttg gct tct ctg gac cct agg gtc act gtg tgt gac atg gcc cag 1117
Asp Leu Ala Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln
          315                      320                      325
gtt cct ttg gag gat gag tct gtg gat gtg gct gtg ttt tgc ctt tca 1165
Val Pro Leu Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser
          330                      335                      340
ctg atg gga acc aac atc agg gac ttc cta gag gag gca aat aga gta 1213
Leu Met Gly Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val
          345                      350                      355
ctg aag cca ggg ggt ctc ctg aaa gtg gct gag gtc agc agc cgc ttt 1261
Leu Lys Pro Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe
          360                      365                      370                      375
gag gat gtt cga acc ttt ctg cgg gct gtg acc aag cta ggc ttc aag 1309
Glu Asp Val Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys
          380                      385                      390
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc 1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe
          395                      400                      405
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc 1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly
          410                      415                      420
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgg atcttccttg 1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg
          425                      430
agaggggagg cagatctcaa actccaggct cagaactgtg aagactgttt ccggcctggc 1518
tgtgagccaa gacctggttc ctggtggacc ctgaggacaa agtgtgataa aacctctggc 1578
tcagacttgc tctactgaag gcttcttggt tataagatgc ataaagtcac tggggctagc 1638
taaacaataa agagttttatt gtgaggaaaa aaaaaaaaaa 1678

```

<210> 167
 <211> 494
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..318
 <221> sig_peptide
 <222> 25..75
 <223> Von Heijne matrix
 score 7.4
 seq FFLLLQFFLRIDG/VL

<221> polyA_signal
 <222> 452..457

<221> polyA_site
 <222> 482..494

```

<400> 167
aggctgagtg tgaagattag agta atg cct tct agc ttt ttc ctg ctg ttg 51
          Met Pro Ser Ser Phe Phe Leu Leu Leu
          -15                      -10
cag ttt ttc ttg aga att gat ggg gtg ctt atc aga atg aat gac acg 99
Gln Phe Phe Leu Arg Ile Asp Gly Val Leu Ile Arg Met Asn Asp Thr
          -5                      1                      5
aga ctt tac cat gag gct gac aag acc tac atg tta cga gaa tat acg 147
Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr Met Leu Arg Glu Tyr Thr
          10                      15                      20
tca cga gaa agc aaa att tct agt ttg atg cat gtt cca cct tcc ctc 195

```


<210> 169
 <211> 805
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..718

<221> sig_peptide
 <222> 32..100
 <223> Von Heijne matrix
 score 7.4
 seq VLLLAALPPVLLP/GA

<221> polyA_signal
 <222> 770..775

<221> polyA_site
 <222> 793..805

<400> 169
 cctcttttcag cccgggatcg ccccagcagg g atg ggc gac aag atc tgg ctg 52
 Met Gly Asp Lys Ile Trp Leu
 -20
 ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct 100
 Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro
 -15 -10 -5
 ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt acc 148
 Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr
 1 5 10 15
 ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag 196
 Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
 20 25 30
 gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta gat 244
 Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
 35 40 45
 att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa 292
 Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
 50 55 60
 caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt gat 340
 Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
 65 70 75 80
 tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg 388
 Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
 85 90 95
 att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa 436
 Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
 100 105 110
 caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg 484
 Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
 115 120 125
 aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta 532
 Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
 130 135 140
 agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt 580
 Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg
 145 150 155 160
 gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct 628
 Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser
 165 170 175

atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat	676
Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr	
180 185 190	
atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act	718
Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr	
195 200 205	
taaaactcca aactagagta cgtaacattg aaaaatgagg cataaaaaatg caataaactg	778
ttacagtcaa gaccaaaaaa aaaaaaa	805

<210> 170
 <211> 787
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..481

<221> sig_peptide
 <222> 26..88
 <223> Von Heijne matrix
 score 4.4
 seq AVASSFFFCASLFS/AV

<221> polyA_signal
 <222> 755..760

<221> polyA_site
 <222> 775..787

<400> 170	
gacagcctgg ataaaggctc acttg atg gct cag ttg gga gca gtt gtg gct	52
Met Ala Gln Leu Gly Ala Val Val Ala	
-20 -15	
gtg gct tcc agt ttc ttt tgt gca tct ctc ttc tca gct gtg cac aag	100
Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys	
-10 -5 1	
ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg	148
Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu	
5 10 15 20	
act tcg acc agc ggc cct ggt ttc cat ctc atg ctc cct ttc atc aca	196
Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr	
25 30 35	
tca tat aag tct gtg cag acc aca ctc cag aca gat gag gtg aag aat	244
Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn	
40 45 50	
gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att	292
Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile	
55 60 65	
gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag	340
Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys	
70 75 80	
aac tat act gct gac tat gac aag gcc ctc atc ttc aac aag atc cac	388
Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His	
85 90 95 100	
cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac	436
His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr	
105 110 115	
att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca	481
Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser	
120 125 130	


```

taaaagggac cctgagcaag aacatttttc atagcagaca ggaggactca tccacatcgc 541
cagcaatcat aattaagcaa accgcctttt gcaccattta agatttagga aatcatccaa 601
attactttta atgtttctgc agtagaaaat gaatctaaat tcattttata gggttttag 661
tcttttatct gttttggatt cactgtgctt ttaagaaaaa gttggtaaat ttgccgttga 721
tttttctttt taacctcaaa ctaatagaat tttataaaat attaattttc tccaaaaaaa 781
aaaaaa 787

```

```

<210> 171
<211> 569
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 26..562

```

```

<221> sig_peptide
<222> 26..187
<223> Von Heijne matrix
      score 4.1
      seq AVVAAAARTGSEA/RV

```

```

<400> 171
agaaacaggt ctgggctaca aaagt atg gcc gct tct gag gcg gcg gtg gtg 52
                               Met Ala Ala Ser Glu Ala Ala Val Val
                               -50
tct tcg ccg tct ttg aaa aca gac aca tcc cct gtc ctt gaa act gca 100
Ser Ser Pro Ser Leu Lys Thr Asp Thr Ser Pro Val Leu Glu Thr Ala
-45 -40 -35 -30
gga acg gtc gca gca atg gct gcg acc ccg tca gca agg gct gca gcc 148
Gly Thr Val Ala Ala Met Ala Ala Thr Pro Ser Ala Arg Ala Ala Ala
-25 -20 -15
gcg gtg gtt gcg gcc gcg gcc agg acc gga tcc gaa gcc agg gtc tcc 196
Ala Val Val Ala Ala Ala Ala Arg Thr Gly Ser Glu Ala Arg Val Ser
-10 -5 1
aag gcc gct ttg gct acc aag ctg ctg tcc ttg agc gcc gtg ttc gcc 244
Lys Ala Ala Leu Ala Thr Lys Leu Leu Ser Leu Ser Gly Val Phe Ala
5 10 15
gtg cac aag ccc aaa ggg ccc act tca gcc gag ctg ctg aat cgg ttg 292
Val His Lys Pro Lys Gly Pro Thr Ser Ala Glu Leu Leu Asn Arg Leu
20 25 30 35
aag gag aag ctg ctg gca gaa gct gga atg cct tct cca gaa tgg acc 340
Lys Glu Lys Leu Leu Ala Glu Ala Gly Met Pro Ser Pro Glu Trp Thr
40 45 50
aag agg aaa aag cag act ttg aaa att ggg cat gga ggg act cta gac 388
Lys Arg Lys Lys Gln Thr Leu Lys Ile Gly His Gly Gly Thr Leu Asp
55 60 65
agc gca gcc cga gga gtt ctg gtt gtt gga att gga agc gga aca aaa 436
Ser Ala Ala Arg Gly Val Leu Val Val Gly Ile Gly Ser Gly Thr Lys
70 75 80
atg ttg acc agt atg ttg tca ggg tcc aag agg tat act gcc att gga 484
Met Leu Thr Ser Met Leu Ser Gly Ser Lys Arg Tyr Thr Ala Ile Gly
85 90 95
gaa ctg ggg aaa gct act gat aca cta gat tct acg ggg aag gta aca 532
Glu Leu Gly Lys Ala Thr Asp Thr Leu Asp Ser Thr Gly Lys Val Thr
100 105 110 115
gaa gaa aaa cct tac ggt atg aac ctc atc taagtag 569
Glu Glu Lys Pro Tyr Gly Met Asn Leu Ile
120 125

```

```

<210> 172

```

<211> 893
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 4..810

 <221> sig_peptide
 <222> 4..279
 <223> Von Heijne matrix
 score 6.8
 seq AVMLYTWRS CSRA/IP

 <221> polyA_signal
 <222> 858..863

 <221> polyA_site
 <222> 881..893

<400> 172
 gcc atg atc acg cac gtc acc ctg gaa gat gcc ctg tcc aac gtg gac 48
 Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp
 -90 -85 -80
 ctg ctt gaa gag ctt ccc ctc ccc gac cag cag cca tgc atc gag cct 96
 Leu Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro
 -75 -70 -65
 cca cct tcc tcc atc atg tac cag gct aac ttt gac aca aac ttt gag 144
 Pro Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu
 -60 -55 -50
 gac agg aat gca ttt gtc acg ggc att gca agg tac att gag cag gct 192
 Asp Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala
 -45 -40 -35 -30
 aca gtc cac tcc agc atg aat gag atg ctg gag gaa gga cat gag tat 240
 Thr Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr
 -25 -20 -15
 gcg gtc atg ctg tac acc tgg cgc agc tgt tcc cgg gcc att ccc cag 288
 Ala Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln
 -10 -5 1
 gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca 336
 Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr
 5 10 15
 gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat 384
 Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr
 20 25 30 35
 ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg 432
 Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu
 40 45 50
 tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg 480
 Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu
 55 60 65
 acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag 528
 Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys
 70 75 80
 aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca 576
 Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala
 85 90 95
 gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tcg 624
 Ala Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser
 100 105 110 115
 cag aac ctt tcc atg ttc ctg gcc aac cac aac agg atc acc cag tgt 672

Gln Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys	
120 125 130	
ctc cac cag caa ctt gaa gtg atc cca ggc tat gag gag ctg ctg gct	720
Leu His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala	
135 140 145	
gac att gtc aac atc tgt gtg gat tac tac gag aac aag atg tac ctg	768
Asp Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu	
150 155 160	
act ccc agt gag aaa cat atg ctc ctc aag gta aaa ctc ccc	810
Thr Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro	
165 170 175	
tgaggccgca cccatggagc ctgggcttac cctctcacct tcttcttatt aaaaatccgt	870
tttaaaaaaac aaaaaaaaaa aaa	893
<210> 173	
<211> 1475	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 55..459	
<221> sig_peptide	
<222> 55..120	
<223> Von Heijne matrix	
score 7.2	
seq GLWLALVDGLVRS/SP	
<221> polyA_signal	
<222> 1444..1449	
<221> polyA_site	
<222> 1462..1475	
<400> 173	
catgtccgca gctacgtgtg ggacccgctg ctgatcctgt cgcagatcgt cctc atg	57
	Met
cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg gcg ctg gtg gac	105
Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp	
-20 -15 -10	
ggg cta gtg cga agc agc ccc tcg ctg gac cag atg ttc gac gcc gag	153
Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala Glu	
-5 1 5 10	
atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc atg atg tcc ttc	201
Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe	
15 20 25	
atc ttc aac gcc ctc acc tgt gcc ctg ggc ttg ctg tac ttc atc cgg	249
Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg	
30 35 40	
cga gga aag cag tgt ctg gat ttc act gtc act gtc cat ttc ttt cac	297
Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His	
45 50 55	
ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc tcg gcg ctg acc	345
Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr	
60 65 70 75	
tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg gct gtc atc ggg	393
Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly	
80 85 90	
gag tac ctg tgc atg cgg acg gag ctc aag gag ata ccc ctc aac tca	441
Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn Ser	

```

          95          100          105
gcc cct aaa tcc aat gtc tagaatcagg ccctttggac atccccgctga      489
Ala Pro Lys Ser Asn Val

      110
cacttggggc ccttaacacc ttgggctgct cagaccctcc agatgaggtc cagcccagat      549
ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag tgagggcctg      609
tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg tctgttgaag      669
ccttggtatc tgagagggtca ggaaggggac ctctttgagg gtaataacat aattggaacc      729
atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga gaaaaaaaaat      789
caaggatata tgattggagc aaaccacttc tttagtcac tgtcttacct ccctgggaca      849
gctgttacct ttgcagtgtt gccgaatcac agcagttacc tttgcaatgt tgccgaatca      909
cagcagttct gttggagaaa cgcttggttt ccggatccag agccacagaa agaaatgtag      969
gtgtgaagta ttaggctgct gtcagggaga ggatggcaga tggaggcatc aagcacaagg     1029
aaaatgcaca acctgtgccc tgttatacac acgttcatgt gcgccaaga acctatgact     1089
ttcttccagt tccttctacc aggtcccat cctgtgcca gctctcaaca tagcaggcca     1149
taggacccag agaagaatcc cagtgttgct caaagtctga ccatcataaa gacactgcct     1209
gtcttctagg aatgaccagg caccagctc ccactggact ccaatttttt ttcttgcctt     1269
atttagaatt ctttggcggg aagggtatga tgggttccca gagacaagaa gccaacctt     1329
ctggcctggg ctgtgctgat agtgctgagg gagataggaa tttgctgcta agatttttct     1389
ttggggtgga gtttctctct tgaggggctt gcagctatcc ttctgtgta tacaataaca     1449
gtattttcca tgaaaaaaaa aaaaaa                                1475

<210> 174
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..248

<221> sig_peptide
<222> 48..161
<223> Von Heijne matrix
      score 6.3
      seq LVFALVTAVCCCLA/DG

<221> polyA_signal
<222> 283..288

<221> polyA_site
<222> 308..321

<400> 174
gctgagaaga gttgaggga agtgctgctg ctgggtctgc agacgcg atg aat aac      56
                                         Met Asn Asn
gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc      104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly
-35          -30          -25          -20
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc      152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys
          -15          -10          -5
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc      200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro
          1          5          10
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
      15          20          25
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      308
aaaaaaaaaa aaa                                321

```

<210> 175
 <211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..399

<221> sig_peptide
 <222> 25..186
 <223> Von Heijne matrix
 score 3.5
 seq SILAQVLDQSARA/RL

<400> 175
 ctgctccagc gctgacgccg agcc atg gcg gac gag gag ctt gag gcg ctg 51
 Met Ala Asp Glu Glu Leu Glu Ala Leu
 -50
 agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt 99
 Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly
 -45 -40 -35 -30
 gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac 147
 Asp Ala Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn
 -25 -20 -15
 agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt 195
 Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser
 -10 -5 1
 aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac 243
 Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr
 5 10 15
 ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa 291
 Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu
 20 25 30 35
 caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag 339
 Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys
 40 45 50
 aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa 387
 Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu
 55 60 65
 gat gac gat tat tgaactacaa gtgctcacag actagaactt aacggaacaa 439
 Asp Asp Asp Tyr
 70
 gtctaggaca g 450

<210> 176
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..1137

<221> sig_peptide
 <222> 10..72
 <223> Von Heijne matrix
 score 6.5
 seq LLTLLLPPPPPLYT/RH

<221> polyA_signal

<222> 1144..1149

<221> polyA_site

<222> 1162..1173

<400> 176

gagctgctt atg gga cac cgc ttc ctg cgc ggc ctc tta acg ctg ctg ctg	51
Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu	
-20 -15 -10	
ccg ccg cca ccc ctg tat acc cgg cac cgc atg ctc ggt cca gag tcc	99
Pro Pro Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser	
-5 1 5	
gtc ccg ccc cca aaa cga tcc cgc agc aaa ctc atg gca ccg ccc cga	147
Val Pro Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg	
10 15 20 25	
atc ggg acg cac aat ggc acc ttc cac tgc gac gag gca ctg gca tgc	195
Ile Gly Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys	
30 35 40	
gca ctg ctt cgc ctc ctg ccg gag tac cgg gat gca gag att gtg cgg	243
Ala Leu Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg	
45 50 55	
acc cgg gat ccc gaa aaa ctc gct tcc tgt gac atc gtg gtg gac gtg	291
Thr Arg Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val	
60 65 70	
ggg ggc gag tac gac cct cgg aga cac cga tat gac cat cac cag agg	339
Gly Gly Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg	
75 80 85	
tct ttc aca gag acc atg agc tcc ctg tcc cct ggg agg ccg tgg cag	387
Ser Phe Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln	
90 95 100 105	
acc aag ctg agc agt gcg gga ctc atc tat ctg cac ttc ggg cac aag	435
Thr Lys Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys	
110 115 120	
ctg ctg gcc cag ttg ctg ggc act agt gaa gag gac agc atg gtg ggc	483
Leu Leu Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly	
125 130 135	
acc ctc tat gac aag atg tat gag aac ttt gtg gag gag gtg gat gct	531
Thr Leu Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala	
140 145 150	
gtg gac aat ggg atc tcc cag tgg gca gag ggg gag cct cga tat gca	579
Val Asp Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala	
155 160 165	
ctg acc act acc ctg agt gca cga gtt gct cga ctt aat cct acc tgg	627
Leu Thr Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp	
170 175 180 185	
aac cac ccc gac caa gac act gag gca ggg ttc aag cgt gca atg gat	675
Asn His Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp	
190 195 200	
ctg gtt caa gag gag ttt ctg cag aga tta gat ttc tac caa cac agc	723
Leu Val Gln Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser	
205 210 215	
tgg ctg cca gcc cgg gcc ttg gtg gaa gag gcc ctt gcc cag cga ttc	771
Trp Leu Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe	
220 225 230	
cag gtg gac cca agt gga gag att gtg gaa ctg gcg aaa ggt gca tgt	819
Gln Val Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys	
235 240 245	
ccc tgg aag gag cat ctc tac cac ctg gaa tct ggg ctg tcc cct cca	867
Pro Trp Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro	
250 255 260 265	
gtg gcc atc ttc ttt gtt atc tac act gac cag gct gga cag tgg cga	915


```

Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
80      85      90      95
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att      494
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
      100      105      110
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac      542
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
      115      120      125
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc      590
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
      130      135      140
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc      638
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
      145      150      155
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc      686
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
160      165      170      175
agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg      734
Arg Pro Ser Arg Gln Leu
      180
tagcccccacat cagaccctgc cccaagcacc atatggaaat aaagttcttt c      785

<210> 178
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..505

<221> sig_peptide
<222> 44..223
<223> Von Heijne matrix
      score 4
      seq LVRRTLLVAALRA/WM

<400> 178
agcaaccaga gggagatgat cacctgaacc actgctccaa acc atg ggc agt aaa      55
                                     Met Gly Ser Lys
                                     -60
tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag agg cgg      103
Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln Arg Arg
-55      -50      -45
cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg aag gca      151
Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val Lys Ala
-40      -35      -30      -25
gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc agg acc      199
Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg Arg Thr
      -20      -15      -10
ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg tgg agg      247
Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp Trp Arg
      -5      1      5
acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg ttg agg      295
Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu Leu Arg
10      15      20
gtc tac gtc atc cag gag cag gcg acg gtc aag ctc cag tcc tgc atc      343
Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu Gln Ser Cys Ile
25      30      35      40
cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat gct ctc      391
Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn Ala Leu

```


	45	50	55	
tgc ttg ttc cag gtc cca gag agc agc ctt gcc ttc cag act gat ggc				439
Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe Gln Thr Asp Gly				
	60	65	70	
ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag ttc cac				487
Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu Phe His				
	75	80	85	
att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg				535
Ile Glu Ile Leu Ser Ile				
	90			
cactacccta ataatgtct gacc				559

<210> 179
 <211> 770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..393

<221> sig_peptide
 <222> 25..150
 <223> Von Heijne matrix
 score 4.6
 seq LDPAVSLSAPAFSA

<221> polyA_signal
 <222> 734..739

<221> polyA_site
 <222> 757..770

<400> 179	
cgcagaaagg agagacacac atac atg aaa gga gga gct ttc tcc aat ctt	51
Met Lys Gly Gly Ala Phe Ser Asn Leu	
-40 -35	
aat gat tcc cag ctc tca gcc tcg ttt ctg caa ccc agc ctg caa gca	99
Asn Asp Ser Gln Leu Ser Ala Ser Phe Leu Gln Pro Ser Leu Gln Ala	
-30 -25 -20	
aac tgt cct gct ttg gac cct gct gtg tca ctc tcc gca cca gcc ttt	147
Asn Cys Pro Ala Leu Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe	
-15 -10 -5	
gcc tct gct ctt cgc tct atg aag tcc tcc cag gct gca cgg aag gac	195
Ala Ser Ala Leu Arg Ser Met Lys Ser Ser Gln Ala Ala Arg Lys Asp	
1 5 10 15	
gac ttt ctc agg tct ctt agt gat gga gac tca ggg aca tca gaa cac	243
Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His	
20 25 30	
atc tca gcg gtg gtg act agc cct cgg att tcc tgc cat ggt gct gcc	291
Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala	
35 40 45	
att ccc acc gcc cgt gcc ctc tgc cta ggc tgt tcc tgc tgc acc gaa	339
Ile Pro Thr Ala Arg Ala Leu Cys Leu Gly Cys Ser Cys Cys Thr Glu	
50 55 60	
cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc	387
Arg Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Glu Ala Pro Ala	
65 70 75	
agc acc tgagctctct gctgattgct gttcctccca gtctgtggaa gctttgccca	443
Ser Thr	
80	

0998360.10.501

tatgctttcc	ttaaaaggg	tctgggcagg	gcaggcgccc	ccattttctca	gggatcccct	503
ccaggacaac	gccttttcct	tgtgtcttca	gctctcctta	ccagatatct	atatatttgt	563
atatattcag	tttcaccaac	aatgcatcaa	gtactttttt	ttttaagtaa	agaaccgcag	623
tcacgaact	ggagcccat	tgattccctc	cccctcgcct	ccccaaatct	ggcacctgcc	683
caaggtatcc	tcagaacat	ttgggggtgc	ctttggcatt	ggataataga	aataaaattt	743
tacctctttc	tacaaaaaaa	aaaaaac				770

<210> 180
 <211> 1213
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..1095

<221> sig_peptide
 <222> 58..114
 <223> Von Heijne matrix
 score 5.4
 seq LSHLLPSLRQVIQ/EP

<221> polyA_site
 <222> 1202..1213

<400> 180	
cctggctttg cctttgccct gctgtgtgat cttagctccc tgcccaggcc cacagcc	57
atg gcc atg gcc cag aaa ctc agc cac ctc ctg ccg agt ctg cgg cag	105
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln	
-15 -10 -5	
gtc atc cag gag cct cag cta tct ctg cag cca gag cct gtc ttc acg	153
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr	
1 5 10	
gtg gat cga gct gag gtg ccg ccg ctc ttc tgg aag ccg tac atc tat	201
Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr	
15 20 25	
gcg ggc tac cgg ccg ctg cat cag acc tgg cgc ttc tat ttc cgc acg	249
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr	
30 35 40 45	
ctg ttc cag cag cac aac gag gcc gtg aat gtc tgg acc cac ctg ctg	297
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu	
50 55 60	
gcg gcc ctg gta ctg ctg ctg ccg ctg gcc ctc ttt gtg gag acc gtg	345
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val	
65 70 75	
gac ttc tgg gga gac cca cac gcc ctg ccc ctc ttc atc att gtc ctt	393
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu	
80 85 90	
gcc tct ttc acc tac ctc tcc ctc agt gcc ttg gct cac ctc ctg cag	441
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln	
95 100 105	
gcc aag tct gag ttc tgg cat tac agc ttc ttc ttc ctg gac tat gtg	489
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val	
110 115 120 125	
ggg gtg gcc gtg tac cag ttt ggc agt gcc ttg gca cac ttc tac tat	537
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr	
130 135 140	
gct atc gag ccc gcc tgg cat gcc cag gtg cag gct gtt ttt ctg ccc	585
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro	
145 150 155	
atg gct gcc ttt ctc gcc tgg ctt tcc tgc att ggc tcc tgc tat aac	633

```

Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
      160              165              170
aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg      681
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
      175              180              185
ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt      729
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
      190              195              200              205
atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac      777
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
      210              215              220
cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct      825
His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
      225              230              235
acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg      873
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
      240              245              250
cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct      921
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
      255              260              265
cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat      969
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
      270              275              280              285
gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg      1017
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
      290              295              300
ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg      1065
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
      305              310              315
gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg      1115
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
      320              325
tagggaggga ggtatagttg ggggacaggg gtctgggttt ggctccaagt gggaacaagg      1175
cctggtaaaag ttgtttgtgt ctggccaaaa aaaaaaaa      1213

<210> 181
<211> 1318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..660

<221> sig_peptide
<222> 31..90
<223> Von Heijne matrix
      score 5.4
      seq AFVIACVLSLIST/IY

<221> polyA_signal
<222> 1288..1293

<221> polyA_site
<222> 1307..1318

<400> 181
ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca      54
      Met Asp Asn Arg Phe Ala Thr Ala
      -20              -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102

```


<223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

<221> polyA_signal
 <222> 816..821

<221> polyA_site
 <222> 840..853

<400> 182
 ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca 54
 Met Asp Asn Arg Phe Ala Thr Ala
 -20 -15
 ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca 102
 Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
 -10 -5 1
 gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa 150
 Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
 5 10 15 20
 gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt 198
 Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
 25 30 35
 gat gaa gca gat gaa aag act tat aat gat gca cct ttt cga tac aat 246
 Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Pro Phe Arg Tyr Asn
 40 45 50
 ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg 294
 Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
 55 60 65
 cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca 342
 His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
 70 75 80
 aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt 390
 Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
 85 90 95 100
 gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt 438
 Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
 105 110 115
 tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc 486
 Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
 120 125 130
 ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat 534
 Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
 135 140 145
 ccc acc att gcc acg ggc att ctc cat ctc ctt gca gat acc atg ctg 582
 Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Asp Thr Met Leu
 150 155 160
 tgaagtccag gccacatgga ggtgtcctgt gtagatgctc cagctgaaat cccaagctaa 642
 gctcccaact gacagccaac atcatttcca gccatgtgtg ggagccatcc tggatgtcca 702
 gccttaacaa gccttcagag gacttcagcc acagctatta tcttactaca tccttgtag 762
 actctaataa agaaccaact agctgagccc aatcaaccta tggaactgat agaaataaaa 822
 tgaattgttg ttttgcgaaa aaaaaaaaaa a 853

<210> 183
 <211> 826
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..695

09978360.101501

<221> sig_peptide
 <222> 15..80
 <223> Von Heijne matrix
 score 8.5
 seq AALLLGGLMMVVTG/DE

<221> polyA_signal
 <222> 795..800

<221> polyA_site
 <222> 814..826

<400> 183
 aaccagaggt gcc atg ggt tgg aca atg agg ctg gtc aca gca gca ctg 50
 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
 -20 -15
 tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc 98
 Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
 -10 -5 1 5
 ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag 146
 Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
 10 15 20
 ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt 194
 Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
 25 30 35
 gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag 242
 Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
 40 45 50
 ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg 290
 Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
 55 60 65 70
 gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga 338
 Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
 75 80 85
 ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag 386
 Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
 90 95 100
 aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc 434
 Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
 105 110 115
 cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt 482
 Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
 120 125 130
 cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga 530
 Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
 135 140 145 150
 ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa 578
 Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
 155 160 165
 cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca 626
 Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
 170 175 180
 acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac 674
 Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
 185 190 195
 cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt 725
 Gln Ala Glu Ile Ala Ala Cys
 200 205
 ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccct 785
 tctttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a 826

<210> 184
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..295

<221> sig_peptide
 <222> 74..196
 <223> Von Heijne matrix
 score 5.4
 seq RLLYIGFLGYCSG/LI

<221> polyA_signal
 <222> 545..550

<221> polyA_site
 <222> 561..571

<400> 184
 cgggtagtggt tcgtcgtggt tttccttgta gttcgtgggtc tgagaccagg cctcaagtgg 60
 aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt 109
 Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe
 -40 -35 -30
 ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg 157
 Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro
 -25 -20 -15
 cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat 205
 Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp
 -10 -5 1
 aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag 253
 Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
 5 10 15
 ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg 295
 Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
 20 25 30
 taaaacgtga agactacctg tatgctgtga gggaccgtga aatgtttgga tatatgaaat 355
 tacatccaga ggattttcct gaagaagata agaaaacata tggtgaaatt tttgaaaaat 415
 tccatccaat acgttgaagt cttcaaaatg cttgctccag tttcactgat acctgctggt 475
 cctgaatttg atggaacatg tttcttatga cagttgaagc ttatgctaatt ctgtatgttg 535
 acaccttgta attaaaatac gtaccaaaaa aaaaaa 571

<210> 185
 <211> 659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 440..658

<221> polyA_signal
 <222> 601..606

<400> 185
 cgccttacga gctgggaggt ggtgcctctc acccagctaa ttgctctcta gcccttggcc 60
 ttcacagggtg ttgggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa 120
 gactttgtgc ctatgggttg ggacagagtg aggtcgttgc cttgacgacg acagcatgcg 180

gcccgtggtc ctcctaagtg tgagcttgcg gcggaccgag gccacactgc ctccctgcct 240
gcttcgcccga ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tggaattgct 300
agtttgctag gcagcatctt ttggacctgc gaaccatatt catttcacct caaatctggt 360
tccaagttga aaaccttttg gtcttttctat gcgaacggat tgaagaaacg caaaaagttt 420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga 472

Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
1 5 10
gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga 520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
15 20 25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg 568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
30 35 40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg 616
Val Lys Lys Ile Ala Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg
45 50 55
cat gaa aac ttg gtg aat ctc ttg gaa gtg tgt aaa aaa aaa a 659
His Glu Asn Leu Val Asn Leu Leu Glu Val Cys Lys Lys Lys
60 65 70

<210> 186
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..283

<221> sig_peptide
<222> 38..85
<223> Von Heijne matrix
score 4.1
seq LLPATSLAGPVLS/TL

<221> polyA_signal
<222> 257..262

<400> 186
cacctgaatc ccaggaaccc tcaatgaggt cttcaag atg aag aga ctg ctg cca 55
Met Lys Arg Leu Leu Pro
-15

gct acc agc ctg gct ggc cct gtc ctg tcc acc ctc att gcc cca act 103
Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile Ala Pro Thr
-10 -5 1 5

ccc atg ttg ttt tgt gaa gat aaa agc tgg gat ctt ttt ctt ttt ttt 151
Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Leu Phe Leu Phe Phe
10 15 20

aag tct cac aag aca tgg ggc atc tcc aca aat tta agt tcc tgt cca 199
Lys Ser His Lys Thr Trp Gly Ile Ser Thr Asn Leu Ser Ser Cys Pro
25 30 35

ttt gga aat ttg ttt cta tgt gta cag ttt gtc aga gaa aaa caa agt 247
Phe Gly Asn Leu Phe Leu Cys Val Gln Phe Val Arg Glu Lys Gln Ser
40 45 50

ttt tgt atg aat aca gaa tgt gat tta cgc aag aat tgacaaaaaa 293
Phe Cys Met Asn Thr Glu Cys Asp Leu Arg Lys Asn
55 60 65

aaaaaaaa 301

<210> 187
<211> 477

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 121..477

<221> sig_peptide
<222> 121..288
<223> Von Heijne matrix
score 3.5
seq SSCADSFVSSSSS/QP

<400> 187
cctcggagca ggcggagtaa agggacttga gcgagccagt tgccggatta ttctatttcc 60
cctccctctc tccgccccg tatctctttt cacccttctc ccaccctcgc tcgcgtagcc 120
atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg 168
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
tcc ttc gga gcc gag ccg tcc gcg ccc ggc ggc ggc ggc agc cca gga 216
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat 264
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
tcc ttt gtt tct tcc tct tcc tct cag cct gta tct cta ttt tcg acc 312
Ser Phe Val Ser Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa 360
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc 408
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggg agc cag cct 456
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
att tta gcc aaa aaa aaa aaa 477
Ile Leu Ala Lys Lys Lys Lys
60

<210> 188
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..163

<221> polyA_signal
<222> 292..297

<221> polyA_site
<222> 310..323

<400> 188
a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca 49
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag 97

092360-01604

Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
aac ccc cgc tgc act gtg gat gct ccc aca gca gca ggc cgg ggc cgt 145
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
ggg cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg 193
Gly Arg Gly Arg Pro His
50
ctggctgctg ggtgcactta cctccttgg cttggttact tcattttaca aggaaggggt 253
agtaattggc ccactctctt cttactggag gctatttaaa taaaatgtaa gacttcaaaa 313
aaaaaaaaa 323

<210> 189
<211> 1392
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..675

<221> sig_peptide
<222> 46..87
<223> Von Heijne matrix
score 5.3
seq LTLGLSFILAGL/IV

<221> polyA_signal
<222> 1364..1369

<221> polyA_site
<222> 1383..1392

<400> 189
ctccgagttg ccaccagga aaaagagggc tcctctggga gatgt atg ctt act ctc 57
Met Leu Thr Leu
tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc 105
Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
-10 -5 1 5
att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg 153
Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
10 15 20
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag 201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
25 30 35
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac 249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
40 45 50
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac 297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
55 60 65 70
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg 345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
75 80 85
gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att 393
Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
90 95 100
gtt atg cct cca aaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt 441
Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
105 110 115
ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct 489

09978360.10501

Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val	Arg	Glu	Asp	Leu	Val	Ala		
120						125					130						
gtg	gag	gaa	att	cgt	gat	ggt	agt	aac	ctt	ggc	atc	ttt	att	tac	caa	537	
Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn	Leu	Gly	Ile	Phe	Ile	Tyr	Gln		
135					140					145					150		
ctt	tgc	aat	aac	aga	aag	tcc	ttc	cgc	ctt	cgt	cgc	aga	gac	ctc	ttg	585	
Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu		
				155					160					165			
ctg	ggg	ttc	aac	aaa	cgt	gcc	att	gat	aaa	tgc	tgg	aag	att	aga	cac	633	
Leu	Gly	Phe	Asn	Lys	Arg	Ala	Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His		
			170					175					180				
ttc	ccc	aac	gaa	ttt	att	ggt	gag	acc	aag	atc	tgt	caa	gag			675	
Phe	Pro	Asn	Glu	Phe	Ile	Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu				
		185				190					195						
taagaggcaa	cagatagagt	gtccttggtg	ataagaagtc	agagatttac	aatatgactt	735											
taacattaag	gtttatggga	tactcaagat	atttactcat	gcatttactc	tattgcttat	795											
gcttttaaaaa	aaggaaaaaa	aaaaaactac	taaccactgc	aagctcttgt	caaatttttag	855											
tttaattggc	attgcttggt	ttttgaaact	gaaattacat	gagtttcatt	ttttctttgc	915											
atztatagg	tttagatttc	tgaaagcagc	atgaatatat	cacctaacat	cctgacaata	975											
aattccatcc	gttggtttttt	ttggtttggtt	gttttttctt	ttcctttaag	taagctcttt	1035											
attcatctta	tggtggagca	attttaaaat	ttgaaatatt	ttaaattggt	tttgaacttt	1095											
ttgtgtaaaa	tatatcagat	ctcaacattg	ttggtttctt	ttgtttttca	ttttgtacaa	1155											
ctttcttgaa	tttagaaatt	acatctttgc	agttctgtta	ggtgctctgt	aattaacctg	1215											
acttatatgt	gaacaatttt	catgagacag	tcatttttaa	ctaatagcagt	gattctttct	1275											
cactactatc	tgtattgtgg	aatgcacaaa	attgtgtagg	tgctgaatgc	tgtaaggagt	1335											
ttaggttgta	tgaattctac	aaccctataa	taaattttac	tctatacaaa	aaaaaaa	1392											

<210> 190
 <211> 999
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..385

<221> polyA_signal
 <222> 974..979

<221> polyA_site
 <222> 987..999

<400> 190																	
cctgaatgac	ttgaatgttt	ccccgcctga	gctaacagtc	catgtgggtg	attcagctct	60											
g	atg	gga	tgt	gtt	ttc	cag	agc	aca	gaa	gac	aaa	tgt	ata	ttc	aag	ata	109
Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile		
1			5					10					15				
gac	tgg	act	ctg	tca	cca	gga	gag	cac	gcc	aag	gac	gaa	tat	gtg	cta	157	
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu		
			20					25				30					
tac	tat	tac	tcc	aat	ctc	agt	gtg	cct	att	ggg	cgc	ttc	cag	aac	cgc	205	
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg		
			35					40				45					
gta	cac	ttg	atg	ggg	gac	atc	tta	tgc	aat	gat	ggc	tct	ctc	ctg	ctc	253	
Val	His	Leu	Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu		
			50					55				60					
caa	gat	gtg	caa	gag	gct	gac	cag	gga	acc	tat	atc	tgt	gaa	atc	cgc	301	
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg		
					70					75				80			
ctc	aaa	ggg	gag	agc	cag	gtg	ttc	aag	aag	gcg	gtg	gta	ctg	cat	gtg	349	
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val		

	85	90	95	
ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg				395
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr				
	100	105		
ccaaggggca agagctttca tgtgcaagag gcaaggaaac tgattatctt gagtaaattgc				455
cagccttttg gctaagtact taccacagag tgaatcttca aaaaatgac ataattatctt				515
cagtcaataa aaatagagtt attttattaa ataaaatatt gataattatt gtattattac				575
tttaaacaca cttccccctc acaaaagccc tgtgaaggat gttttgttca catatatgtc				635
caaatatgtt ttggacacat atttattaaa tggaataaat agtacttgaa ccctggcacc				695
tctgacaaca aagtccatgt tctttttact atgccctaata acctttcatc agttatccac				755
attgatgcta catctgtatt ttataggtac cctatgttag gtgttctggg ggatagaaaa				815
gaaataagca ggccaggctc agtggctcat gcctgtaatc cttagcatttt gggaggctga				875
ggcagcagaa ctgcctgagc cccagggttc aagactgcag tgagctatga tggcaccact				935
gcattctagc ctgggtgaca gagcaagact ctgtctaaaa taaaaaaaga gaaaaaaaaa				995
aaaa				999

<210> 191
 <211> 725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 422..550
 <221> sig_peptide
 <222> 422..475
 <223> Von Heijne matrix
 score 4.5
 seq LRWLMPVIPALWG/AE

<221> polyA_site
 <222> 714..725

<400> 191	
tctgagggg tgggagagaa aattaggggg agaaaggaca gagagagcaa ctaccatcca	60
tagccagata ggtgagtaaa tatatttgca gtaacctatt tgctattcct tgctgcaact	120
gtgtttaatg ttccctccag aatcagagag agtattgcca tccaagaaat cgtttttaga	180
tatgacattt gagctatcat cttgagacca atacctaaaa caatttcagt ttaagaaatg	240
tctaggatat gtgaaaacac agttttaaac cagcaaaaca gaatttattg ccctcagcga	300
ataccacaaa tgtacatata ccttgtattt ctgaaagcaa agcaagcatg ccaagtagtt	360
tttatttacc tgtacctata atacagcaag gtgaaacagg atatattttt gaagttaaaa	420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt	469
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu	
-15 -10 -5	
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc	517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr	
1 5 10	
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaatata aaaattagct	570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr	
15 20 25	
gggtgtggtg gcgggcgcct gtagtcccag ctacttggga gactgaggca ggagaattgc	630
ttgaacacgg aaggcggaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg	690
gcaacagagt gagactccct ctcaaaaaaa aaaaa	725

<210> 192
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>

```

<221> CDS
<222> 124..231

<221> polyA_site
<222> 387..400

<400> 192
ctcgccctctc ctggcttctg gtatgcacca gcaattcctg gcgttccttg gtccttagaa      60
gcatactacc tatcacatgg tcattcttcac cctgtgtgtc ttcacactac cctttctctg      120
tgc atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga      168
    Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
      1             5             10             15
tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag      216
Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
      20             25             30
acc ttt ttc caa ata tagtcactct ctgagggtact gatgggttagg atctcaacat      271
Thr Phe Phe Gln Ile
      35
accttttttg ggaggacaca attgaaccga taacagggtg ttgcaagga agagttaaaa      331
tttgaaagaa aggtggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa      391
aaaaaaaaa      400

<210> 193
<211> 1053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..1051

<221> sig_peptide
<222> 131..169
<223> Von Heijne matrix
      score 4.2
      seq MLAVSLTVPLLGA/MM

<221> polyA_signal
<222> 1019..1024

<400> 193
gagcgaggcg gacgggctgc gacagcgccg gccctgctg cgcaggtcg tcacagacga      60
tgatggccag gccccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt      120
gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc      169
    Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
      -10             -5
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa      217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
      1             5             10             15
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga      265
Glu Pro Pro Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
      20             25             30
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata      313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
      35             40             45
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc      361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
      50             55             60
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg      409
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser
      65             70             75             80

```

```

ggc cct tgc aaa acc cga gat gat gag cct gtg tgt ggg aga ccc ctg      457
Gly Pro Cys Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu
      85      90      95
ggg atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tgc      505
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys
      100      105      110
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg      553
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu
      115      120      125
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat      601
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn
      130      135      140
gat ctt aca gtc tct cag gat ggg agg aag att tat ttc acc gat tct      649
Asp Leu Thr Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser
      145      150      155      160
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc      697
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly
      165      170      175
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta      745
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val
      180      185      190
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct      793
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser
      195      200      205
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata      841
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile
      210      215      220
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt      889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe
      225      230      235      240
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct      937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser
      245      250      255
ggg ggg tac tgg gtg ggc atg tgc acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
      260      265      270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att      1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
      275      280      285
ttt aag gca aaa aaa aaa aa
Phe Lys Ala Lys Lys Lys
      290

```

<210> 194
 <211> 1128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..403

<221> sig_peptide
 <222> 86..181
 <223> Von Heijne matrix
 score 8.8
 seq VPMLLLIVGGSFG/LR

<221> polyA_signal
 <222> 1097..1102

<221> polyA_site

<222> 1117..1128

<400> 194

```

cgtcttggtg agagcgtgag ctgctgagat ttgggagtct gcgctaggcc cgcttggagt      60
tctgagccga tggaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct      112
                               Met Phe Ala Pro Ala Val Met Arg Ala
                               -30                               -25
ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg      160
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu
                               -20                               -15                               -10
att gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat      208
Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr
                               -5                               1                               5
gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa      256
Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys
10                               15                               20                               25
gag aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc      304
Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser
                               30                               35                               40
aag ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat      352
Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp
                               45                               50                               55
cct gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca      400
Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr
                               60                               65                               70
act tgactctgct gattcttttt tccnnntttt ttttttttta aataaaaata      453
Thr
ctattaactg gacttcctaa tatatacttc tatcaagtgg aaaggaaatt ccaggcccat      513
ggaaacttgg atatgggtaa tttgatgaca aataatcttc actaaaggtc atgtacaggt      573
ttttatactt cccagctatt ccatctgttg atgaaagtaa caatgttggc cacgtatatt      633
ttacacctcg aaataaaaaa tgtgaatact gctccaaaaa aaaaaaccag taccgtgtag      693
tctctctcgt ggcttggatt tactctgggc aacgtggttg gaatgtatct ggctcagaac      753
tatgatatac caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaaag      813
aagaaacccc ctagtgcatt agaactgcctc cagcactgcc ttcaggatat accgattcta      873
ctgctcttga gggcctcggt tactatctga accaaaagct tttgttttcg tctccagcct      933
cagcacttct cttcttttgc agaccctgtg ttttttgctt taaagcaagc aaaatggggc      993
cccaatttga gaactaccgc acgttttcaa catactcacc tcttcccata atccctttcc      1053
aactgcatgg gaggttctaa gactggaatt atggtgctag attagtaaac atgactttta      1113
acgaaaaaaaa aaaaaa                                     1128

```

<210> 195

<211> 254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..162

<221> sig_peptide

<222> 37..93

<223> Von Heijne matrix

score 9.5

seq LMCLSLCTAFALS/KP

<221> polyA_signal

<222> 224..229

<221> polyA_site

<222> 243..254

ttggttggat	gaggaacttt	tcttatcttg	ggaaagcctt	aatggctttt	ttttttctta	571
tttactcact	cattaaaata	cttttcatta	ctctaacaca	tggtataaag	aaatagttgg	631
aaaagtgcac	cgaaagactt	ttaaaaatat	ttggtaacta	gtaaaaggac	taccatcgaa	691
aatcaactca	aaaaattgtc	cttttatggg	ttagctgtat	tataatacat	atctatcatt	751
tgccctgtg	tcttagagga	tataatttga	ccagctctac	atttaatctg	tgtaattatg	811
agactgtttt	acaacaatct	tgatgcagag	ttggtaggtt	aagaaatttg	tattacagaa	871
gttaaaaaaa	aaaaaa					886

<210> 197
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..579

<221> sig_peptide
 <222> 46..156
 <223> Von Heijne matrix
 score 3.5
 seq LVFNFLILILT/IW

<400> 197																
cccttatcca	ggttnttatc	tanggaatcc	cnnaagact	gggga	atg	gag	aga	cag			57					
									Met	Glu	Arg	Gln				
												-35				
tca	agg	ggt	atg	tca	gaa	aag	gat	gag	tat	cag	ttt	caa	cat	can	nna	105
Ser	Arg	Val	Met	Ser	Glu	Lys	Asp	Glu	Tyr	Gln	Phe	Gln	His	Xaa	Xaa	
			-30													
gcg	gng	gan	ctg	ctt	gtc	ttc	aat	ttt	ttg	ctc	atc	ctt	acc	att	ttg	153
Ala	Xaa	Xaa	Leu	Leu	Val	Phe	Asn	Phe	Leu	Leu	Ile	Leu	Thr	Ile	Leu	
			-15				-10									
aca	atc	tggtta	ttt	aaa	aat	cat	cga	ttc	cgc	ttc	ttg	cat	gaa	act		201
Thr	Ile	Trp	Leu	Phe	Lys	Asn	His	Arg	Phe	Arg	Phe	Leu	His	Glu	Thr	
	1			5					10					15		
gga	gga	gca	atg	gtg	tat	ggc	ctt	ata	atg	gga	cta	att	tca	cga	tat	249
Gly	Gly	Ala	Met	Val	Tyr	Gly	Leu	Ile	Met	Gly	Leu	Ile	Ser	Arg	Tyr	
			20						25					30		
gct	aca	gca	cca	act	gat	att	gaa	agt	gga	act	gtc	tgt	gac	tgt	gta	297
Ala	Thr	Ala	Pro	Thr	Asp	Ile	Glu	Ser	Gly	Thr	Val	Cys	Asp	Cys	Val	
			35						40					45		
aaa	cta	act	ttc	agt	cca	cca	act	ctg	ctg	ggt	aat	gtc	act	gac	caa	345
Lys	Leu	Thr	Phe	Ser	Pro	Pro	Thr	Leu	Leu	Val	Asn	Val	Thr	Asp	Gln	
			50				55							60		
ggt	tat	gaa	tat	aaa	tac	aaa	aga	gaa	ata	agt	cag	cac	aac	atc	aat	393
Val	Tyr	Glu	Tyr	Lys	Tyr	Lys	Arg	Glu	Ile	Ser	Gln	His	Asn	Ile	Asn	
	65					70					75					
cct	cat	caa	gga	aat	gct	ata	ctt	gaa	aag	atg	aca	ttt	gat	cca	gaa	441
Pro	His	Gln	Gly	Asn	Ala	Ile	Leu	Glu	Lys	Met	Thr	Phe	Asp	Pro	Glu	
	80				85					90					95	
atc	ttc	ttc	aat	ggt	tta	ctg	cca	cca	att	ata	ttt	cat	gca	gga	tat	489
Ile	Phe	Phe	Asn	Val	Leu	Leu	Pro	Pro	Ile	Ile	Phe	His	Ala	Gly	Tyr	
			100						105					110		
agt	cta	aag	aag	aga	cac	ttt	ttt	caa	aac	tta	gga	tct	att	tta	acg	537
Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly	Ser	Ile	Leu	Thr	
			115					120						125		
tat	gcc	ttc	ttg	gga	act	gcc	atc	tcc	tgc	atc	gtc	ata	ggg			579
Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val	Ile	Gly			
			130				135							140		
taagt	gacat	tcg	gag	ctca	agtt	gcaggt	ggct	gtgggg	tct	gtgatct	gtgt	gaggg				639

[illegible]

```
<220>  
<221> CDS  
<222> 92..469
```

```
<221> polyA_signal
<222> 454..459
```

[illegible]

<210> 199
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..675

<221> sig_peptide
 <222> 154..498
 <223> Von Heijne matrix
 score 4.8
 seq PLRLNLNLLILIEG/GV

<221> polyA_signal
 <222> 819..824

<221> polyA_site
 <222> 838..849

<400> 199
 cccctatctc cagacctcat tcgcaatgaa gtagaatgtc tgaaagcaga tttcaaccac 60
 agaatcaagg aggttctctt caactccctc ttcagtgcct actatgttgc atttctcccc 120
 ctgtgttttg tgaagagtac ccagtactat gac atg cgc tgg tca tgt gag cac 174
 Met Arg Trp Ser Cys Glu His
 -115 -110
 ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctc acc acg caa ctg 222
 Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu
 -105 -100 -95
 ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg 270
 Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu
 -90 -85 -80
 ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag 318
 Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln
 -75 -70 -65
 cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg 366
 His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg
 -60 -55 -50 -45
 cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg 414
 His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val
 -40 -35 -30
 cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca 462
 Pro Ser Asp Val Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro
 -25 -20 -15
 tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc 510
 Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe
 -10 -5 1
 tat cag ctc tat tcc ttg ctg cgg tgc gag aag tgg aac cac aca ctt^ 558
 Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu
 5 10 15 20
 tcc atg gct ctc atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt 606
 Ser Met Ala Leu Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu
 25 30 35
 ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac 654
 Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn
 40 45 50
 agt tat gaa ctc aag gca aac taagctgcct ctcaacaatg agggagaact 705
 Ser Tyr Glu Leu Lys Ala Asn

55
cagataaaaa tattttcata cgttctatatt ttttcttggtg atttttataa atattttaaga 765
tggtttatat tttgtatact attatgtttt gaaagtcggg aagagtaagg gatattaaat 825
gtatccgtaa acaaaaaaaaa aaaa 849

<210> 200
<211> 896
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..173

<221> sig_peptide
<222> 18..77
<223> Von Heijne matrix
score 6.5
seq GLCVLQLTTAVTS/AF

<221> polyA_signal
<222> 864..869

<221> polyA_site
<222> 882..893

<400> 200
aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc 50
Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
-20 -15 -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg 98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
-5 1 5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc 146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
10 15 20
cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcctgattca 193
His His Phe Ile His Pro Cys Leu Asp
25 30
aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgcttcag 253
agagggcagc acttatacct ggtgggtcttt ctgatgggtca gttttattcc cctcctgaat 313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaacca cttttagaac 373
tatgagtact acttttgtaa aatgtgaaaa accctcacag aaagtcacg aggcaaaaag 433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atgggtgacgt ccactgctgg 493
ctttattgaa cagctaataa agatttatatt attgtaatac ctcacagacg ttgtaccata 553
tccatgcaca tttagttgcc tgctgtggc tggtaaggta atgtcatgat tcacccctctc 613
ttcagtgaga ctgagcctga tgtgttaaca aataggtgaa gaaagtcctg tgctgtattc 673
ctaatacaaaa gacttaatat attgaagtaa cactttttta gtaagcaaga tacctttttta 733
tttcaattca cagaatggaa tttttttgtt tcatgtctca gatttatatt gtatttcttt 793
tttaacactc tacatttccc ttgtttttta actcatgcac atgtgctctt tgtacagttt 853
taaaaagtgt aataaaatct gacatgtcaa aaaaaaaaaa mcY 896

<210> 201
<211> 851
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..595

<221> sig_peptide
 <222> 17..85
 <223> Von Heijne matrix
 score 3.70000004768372
 seq FLPPPLXRAFACRG/CQ

<221> polyA_signal
 <222> 820..825

<221> polyA_site
 <222> 840..851

<400> 201
 aaggggggcgt gggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc 52
 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
 -20 -15
 ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg 100
 Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
 -10 -5 1 5
 gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga 148
 Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
 10 15 20
 ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat 196
 Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
 25 30 35
 aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa 244
 Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
 40 45 50
 tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa 292
 Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
 55 60 65
 tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa 340
 Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
 70 75 80 85
 aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg 388
 Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu
 90 95 100
 aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg 436
 Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala
 105 110 115
 gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat 484
 Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr
 120 125 130
 tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg 532
 Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met
 135 140 145
 gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa 580
 Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln
 150 155 160 165
 aag aag agg agc aac taggagtgcca ctctgaccca gccagagtcc aggtttccac 635
 Lys Lys Arg Ser Asn
 170
 aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga 695
 agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggttag gtcctggggc 755
 actgtggggc gctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtacgtggt 815
 gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa 851

<210> 202
 <211> 495
 <212> DNA
 <213> Homo sapiens

```

<220>
<221> CDS
<222> 89..334

<221> sig_peptide
<222> 89..130
<223> Von Heijne matrix
      score 3.59999990463257
      seq AFTLXSLQLQAALL/CV

<221> polyA_signal
<222> 462..467

<221> polyA_site
<222> 484..495

<400> 202
agtaggaasg cgccgscgt ggaggcgcca cgtcccttgc sgcggcggga gagamatcgc      60
ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg      112
                               Met Ala Phe Thr Leu Xaa Ser Leu
                               -10
ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag      160
Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
      -5                      1                      5                      10
gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt      208
Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
                        15                      20                      25
gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att      256
Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
                        30                      35                      40
cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca      304
Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
                        45                      50                      55
att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaat      354
Ile Ala Ile Val Leu Leu Leu Leu Phe Gly
      60                      65
ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt      414
atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaat aaaaccaggg      474
tttctattta aaaaaaaaaa a      495

<210> 203
<211> 884
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..614

<221> sig_peptide
<222> 21..83
<223> Von Heijne matrix
      score 10
      seq LWALAMVTRPASA/AP

<221> polyA_signal
<222> 849..854

<221> polyA_site
<222> 873..884

```

```

<400> 203
aataccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc      53
                      Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
                      -20                      -15

ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      101
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
-10                      -5                      1                      5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg      149
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
                      10                      15                      20
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg      197
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg
                      25                      30                      35
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa      245
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
                      40                      45                      50
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt      293
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
55                      60                      65                      70
cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg      341
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu
                      75                      80                      85
cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car      389
Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
                      90                      95                      100
aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc      437
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa
                      105                      110                      115
gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc      485
Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro
120                      125                      130
cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak      533
Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa
135                      140                      145                      150
cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc      581
Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile
                      155                      160                      165
cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac      634
Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala
                      170                      175
tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggcccct gtgcagggag      694
gagctgcctg ttcactggga tcagccaggg cgccggggccc cacttctgag cacagagcar      754
agacagacgc aggcggggac aaaggcagag gatgtagccc cattggggag ggggtggagga      814
aggacatgta ccctttcatr mctacacacc cctcattaaa gcavagtcgt ggcattctcaa      874
aaaaaaaaaa                                         884

```

<210> 204
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..573

<221> sig_peptide
 <222> 94..258
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IGILCSLLGTVLL/WV

<221> polyA_signal
 <222> 862..867

<221> polyA_site
 <222> 886..897

<400> 204

```

aagggcggt gcctagcacc cggaagagcc gtcaacttag cgagcgcaac aggctgccgc      60
tgaggagctg gagctgggtg ggactggggc gca atg gac aag ctg aag aag gtg      114
                               Met Asp Lys Leu Lys Lys Val
                               -55                               -50

ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
                               -45                               -35

gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
                               -30                               -20

tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
                               -15                               -10                               -5

tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1                               5                               10                               15

ggt aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
                               20                               25                               30

aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
                               35                               40                               45

atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
                               50                               55                               60

cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                               70                               75                               80

ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
                               85                               90                               95

aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat      593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
                               100                               105

gaagcttttg aaggcactat ggacagaagc tgggtggacag ttttgtwact atcttcgaaa      653
cctctgtctt acagacatgt gcctttttatc ttgcagcaat gtgttgcttg tgattcgaac      713
at ttgagggg tactttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag      773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcattgtacc tgtttcctct      833
ctggatgttg tccactgaa ttcccatgaa tacaaccta ttcagcaaca gcaaaaaaaaa      893
aaaa
                               897

```

<210> 205
 <211> 518
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..397

<221> sig_peptide
 <222> 74..127
 <223> Von Heijne matrix

score 7.69999980926514
seq LLLLPVLGLLVSS/KT

<221> polyA_signal
<222> 472..477

<221> polyA_site
<222> 507..518

<400> 205
aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gccaccgag 60
aggcgctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg 109
Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
-15 -10
ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
-5 1 5 10
aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
15 20 25
agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
30 35 40
gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
45 50 55
gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
60 65 70
tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc 397
Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
75 80 85 90
tgaggtcgcg cgcagcgct gcacagcgcg ggccgaggcg gctccaggtc cggaggggtt 457
gcgggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa 517
a 518

<210> 206
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..242

<221> sig_peptide
<222> 51..116
<223> Von Heijne matrix
score 6.5
seq SCLCPALFPGTSS/FI

<221> polyA_signal
<222> 319..324

<221> polyA_site
<222> 339..350

<400> 206
acgtcattcc aaaaccacac ccttgcaaag ctttgtactc cgcacccag atg atc 56
Met Ile
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104

09978350_104501

Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro	
-20 -15 -10 -5	
ggt act tcc tcc ttt att gta gca ctc agc tcc cca gcc gat ctg tac	152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr	
1 5 10	
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa	200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys	
15 20 25	
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta	242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val	
30 35 40	
tgatttttgct gaatttttaaa taaaatgaaa accataaatt acatratgct tttattgach	302
cttgacmact ggcctaaata aaaaractct gactccaaaa aaaaaaaa	350

<210> 207
 <211> 996
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 111..191

 <221> sig_peptide
 <222> 111..155
 <223> Von Heijne matrix
 score 5.80000019073486
 seq FLXLMTLTTHVHS/SA

<221> polyA_signal
 <222> 965..970

<221> polyA_site
 <222> 986..996

<400> 207	
atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct	60
cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy	116
Met Gly	
-15	
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag	164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys	
-10 -5 1	
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat	211
Pro Asn Glu Gln Pro Trp Leu Leu Asn	
5 10	
ggtacgcggt gctatacaga atctttggat atgtgcatca gtggtttatg ccaaattggt	271
ggctgcgatc accagctggg aagcaccgtc aaggaarata actgtggggg ctgcaacrga	331
natgggtcca cctgccggct ggtccgaggg cartataaat ccakctctc cgcaaccaa	391
tcrgatgata ctgtggttgc aattccctat ggaagtakac atattcgctc tgtcttaaaa	451
ggtcctgata acttatatct ggaarccawa accctccagg ggactaawgg tgaaaacagt	511
ctcasctcca caggaacttt ccttgtggac aattctagt tggacttcca gaawtttcca	571
gacwdagaga tactgagaat ggctggacca ctcacagcag atttcattgt caawattcgt	631
aactcgggct ccgctgacag tacagtccag kkcattctct atcaacccat catccaccga	691
tggaggggara cggattttct tccttgctca gcaacctgtg gaggagggtta tcagctgaca	751
tcggctgagt gctacgatct gaggagcaac cgtgtggttg ctgaccaata ctgtcactat	811
taccagaga acatcaaacc caaacccaag cttcaggagt gcaacttggg tccttgtcca	871
gccaggtcag tcaaatttgc tagttcattt gtcataaaca taactcaagt tccaaatagg	931
ttattttaa taaaatgaaa cgttttaatt aaaaataaaa tgaaattaaa catcaaaaaa	991
aaaaa	996

0978360 101501

<210> 208
 <211> 860
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..602

<221> sig_peptide
 <222> 45..107
 <223> Von Heijne matrix
 score 8.5
 seq LLTIVGLILPTRG/QT

<221> polyA_signal
 <222> 828..833

<221> polyA_site
 <222> 850..860

<400> 208
 acctctctcc acgaggctgc cggttagga cccccagctc cgac atg tcg ccc tct 56
 Met Ser Pro Ser
 -20
 ggt cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga 104
 Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
 -15 -10 -5
 gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act 152
 Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
 1 5 10 15
 atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca 200
 Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
 20 25 30
 gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca 248
 Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
 35 40 45
 cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct 296
 Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
 50 55 60
 cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc 344
 Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro
 65 70 75
 act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac 392
 Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa
 80 85 90 95
 gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg 440
 Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg
 100 105 110
 atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt 488
 Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys
 115 120 125
 tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg 536
 Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Ser Pro Val
 130 135 140
 gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag 584
 Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu
 145 150 155
 tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag 632
 Ser Ile Arg Asn Arg Ser
 160 165

```

ccccctgccca gctcaccgtg cccagcctcc tgcattccct cgaagagcct ggccagagag 692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtcctc tacctcccc 752
aaccctgccc gccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc 812
tctgctaaga caaaaagtaa agcactgtgg tctttgcaaa aaaaaaaa 860

```

```

<210> 209
<211> 593
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 24..560

```

```

<221> sig_peptide
<222> 24..101
<223> Von Heijne matrix
      score 10.3999996185303
      seq LLLLLLCGPSQDQC/RP

```

```

<221> polyA_signal
<222> 563..568

```

```

<221> polyA_site
<222> 583..593

```

```

<400> 209
aanccagctg csgccggcca gcc atg gag act gga gcg ctg cgg cgc ccg caa 53
              Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
              -25                               -20
ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc 101
Leu Leu Pro Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
      -15                               -10                               -5
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc 149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
1      5      10      15
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga 197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly
      20      25      30
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag 245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
      35      40      45
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac 293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
      50      55      60
aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc 341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65      70      75      80
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac 389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
      85      90      95
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg 437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
      100      105      110
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan 485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
      115      120      125
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa 533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
      130      135      140
acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct 580

```

Thr His Phe Cys Leu Ser Ile Xaa Leu
 145 150
 gtaaaaaaaaaaaa

593

<210> 210
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..558

<221> sig_peptide
 <222> 109..273
 <223> Von Heijne matrix
 score 3.70000004768372
 seq VAFMLTLPILVCK/VQ

<221> polyA_site
 <222> 1104..1114

<400> 210
 attagctstc caaggtctcc cccagcactg aggagctcgc ctgctgccct cttgcgcgcg 60
 ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca 117
 Met Ala Thr
 -55
 aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga 165
 Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
 -50 -45 -40
 ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc 213
 Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
 -35 -30 -25
 aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc 261
 Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
 -20 -15 -10 -5
 ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act 309
 Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
 1 5 10
 cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc 357
 Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
 15 20 25
 gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc 405
 Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe
 30 35 40
 ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat 453
 Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
 45 50 55 60
 gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct 501
 Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
 65 70 75
 gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt 549
 Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
 80 85 90
 tat cgc tat tgaatatatt gtcctgacca tgaataggac caacgtcaat 598
 Tyr Arg Tyr
 95
 gtcttttctg agctttccgc tcctcgtcgc aatgaaaact ttgtcctcct gctcacctac 658
 ktcctcttct tgatggcgct gaccttcctc wtgtcctcct tcaccttctg tggtkccttc 718
 acgggctgga avagacatgg ggccacatc tacctcasga tgctcskctc cattgccatc 778
 tgggtggcct ggatcacct gctcatgctt cctgactttg accgcrngtg ggatgacacc 838

099360.10501

```

atcmtcarct cgccttggs trcsaatggc tgggtgttcc tgttggtta tgtagtccc 898
gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgctttc 958
tgtaaacctc aactcgtgaa gaagagctat ggtgtggrga acagagccta skctcaagag 1018
gaaatcactc aaggttttga agagacaggg gacacgctct atgcccccta ttccacacat 1078
tttcagctgc agaascagcc tccccaaaaa aaaaaa 1114

```

```

<210> 211
<211> 1182
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 128..835

```

```

<221> sig_peptide
<222> 128..220
<223> Von Heijne matrix
      score 4.69999980926514
      seq LAVDSWWLDPGHA/AV

```

```

<221> polyA_signal
<222> 1145..1150

```

```

<221> polyA_site
<222> 1170..1181

```

```

<400> 211
aagaactgcg tctcgcgacc caggcgcgagg ttcccggagg acagccaaca agcgatgctg 60
ccgccgccgt ttcctgattg gttgtgggtg gctacctctt cgttctgatt ggccgctagt 120
gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag gag 169
      Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
      -30 -25 -20
gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac 217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
      -15 -10 -5
gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt 265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
      1 5 10 15
gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg 313
Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro
      20 25 30
gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag 361
Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln
      35 40 45
gcg tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct 409
Ala Ser Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro
      50 55 60
gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc 457
Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala
      65 70 75
ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag 505
Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu
      80 85 90 95
ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc 553
Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly
      100 105 110
cgt agc atc ggg gga wca ccg ccc amc ctg ggt gcc ttg gac ctg ctg 601
Arg Ser Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu
      115 120 125
ggc cca gcc act ggc tgt cta ctg gac aat ggg ctt gag ggc ctg ttt 649

```

Gly	Pro	Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asn	Gly	Leu	Glu	Gly	Leu	Phe	
		130					135					140				
gag	gat	att	gac	acc	tct	atg	tat	gac	aat	gaa	ctt	tgg	gca	cca	gcc	697
Glu	Asp	Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala	
		145					150					155				
tct	gag	ggc	ctc	aaa	cca	ggc	cct	gag	gat	ggg	ccg	ggc	aag	gag	gaa	745
Ser	Glu	Gly	Leu	Lys	Pro	Gly	Pro	Glu	Asp	Gly	Pro	Gly	Lys	Glu	Glu	
		160				165				170					175	
gct	ccg	gag	ctg	gac	gag	gcc	gaa	ttg	gac	tac	ctc	atg	gat	gtg	ctg	793
Ala	Pro	Glu	Leu	Asp	Glu	Ala	Glu	Leu	Asp	Tyr	Leu	Met	Asp	Val	Leu	
				180					185					190		
gtg	ggc	aca	cag	gca	ctg	gag	cga	ccg	ccg	ggg	cca	ggg	cgc			835
Val	Gly	Thr	Gln	Ala	Leu	Glu	Arg	Pro	Pro	Gly	Pro	Gly	Arg			
			195					200				205				
tgagccctcg	tgctggaatg	gttgtctggt	atctgaactg	agcctgctgg	ctggaccaac											895
tgtcctcgaa	aagacacagc	tggcttcctt	agtagacaga	acagggcttg	ggccactttg											955
gagagacaga	atctagtcct	gggcaacttc	acatccgtcc	tcctgtctca	gggctggcag											1015
ggggagcctg	gaattacccc	ctagtgatgg	aatgacaggg	tctggtgggg	actgaattcc											1075
ctggccctgg	ggatcatagct	tgggctgttc	cttctctgat	acgggaagag	acccaatcag											1135
atctttcaaa	ttaaagccag	tcctgggaaa	tctcaaaaaa	aaaaaac												1182

<210> 212
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..505

<221> sig_peptide
 <222> 59..358
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LASSFLFTMGGLG/FI

<221> polyA_signal
 <222> 1042..1047

<221> polyA_site
 <222> 1062..1073

<400> 212																
actgttttngg	ggagggcgcgt	ggggcttgag	gccgagaacg	gcccttgctg	ccaccaac	58										
atg	gag	act	ttg	tac	cgt	gtc	ccg	ttc	tta	gtg	ctc	gaa	tgt	ccc	aac	106
Met	Glu	Thr	Leu	Tyr	Arg	Val	Pro	Phe	Leu	Val	Leu	Glu	Cys	Pro	Asn	
-100					-95					-90					-85	
ctg	aag	ctg	aag	aag	ccg	ccc	tgg	ttg	cac	atg	ccg	tcg	gcc	atg	act	154
Leu	Lys	Leu	Lys	Lys	Pro	Pro	Trp	Leu	His	Met	Pro	Ser	Ala	Met	Thr	
				-80					-75					-70		
gtg	tat	gct	ctg	gtg	gtg	gtg	tct	tac	ttc	ctc	atc	acc	gga	gga	ata	202
Val	Tyr	Ala	Leu	Val	Val	Val	Ser	Tyr	Phe	Leu	Ile	Thr	Gly	Gly	Ile	
			-65				-60						-55			
att	tat	gat	gtt	att	gtt	gaa	cct	cca	agt	gtc	ggg	tct	atg	act	gat	250
Ile	Tyr	Asp	Val	Ile	Val	Glu	Pro	Pro	Ser	Val	Gly	Ser	Met	Thr	Asp	
		-50				-45					-40					
gaa	cat	ggg	cat	cag	agg	cca	gta	gct	ttc	ttg	gcc	tac	aga	gta	aat	298
Glu	His	Gly	His	Gln	Arg	Pro	Val	Ala	Phe	Leu	Ala	Tyr	Arg	Val	Asn	
		-35				-30					-25					
gga	caa	tat	att	atg	gaa	gga	ctt	gca	tcc	agc	ttc	cta	ttt	aca	atg	346
Gly	Gln	Tyr	Ile	Met	Glu	Gly	Leu	Ala	Ser	Ser	Phe	Leu	Phe	Thr	Met	

```

-20          -15          -10          -5
gga ggt tta ggt ttc ata atc ctg gac gga tgc aat gca cca aat atc      394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
              1              5              10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc      442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
              15              20              25
cta twr agt ttt ttc ayg gct aga gta ttc atg aga atg aaa ctg ccg      490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
              30              35              40
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtgatg actggatttg      545
Gly Tyr Leu Met Gly
45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa      605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga      665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttcctgctgg      725
cctattgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata      785
ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat      845
tttttgagaa tgacatttct gattttcaga aattaacata aaatccagaa gcaagattcc      905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag      965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcctga acaataagat     1025
gtatgaacgg agcagaaaata aatacttttt ctaattaaaa aaaaaaaaaa     1073

<210> 213
<211> 818
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..207

<221> sig_peptide
<222> 1..147
<223> Von Heijne matrix
      score 7.59999990463257
      seq HLPFLLLLSCVGX/XP

<221> polyA_signal
<222> 784..789

<221> polyA_site
<222> 807..818

<400> 213
atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat      48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
              -45              -40              -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg      96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
              -30              -25              -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg      144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
              -15              -10              -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat      192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
              1              5              10              15
ttt ttt att cct gac tgagtcacca caccctctc ccctgatcaa agggaatatk      247
Phe Phe Ile Pro Asp
              20
artttttaat ttggatcgac tgaggtgccg ggagaaactg cagkcccagg tatccmvaca      307

```



```

gccaccagga tgggtccctcg cccacacccc accgcctctk cccacaccttt tccaacgtgt 367
tgcattgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga 427
rgtttggar gaaaaatcaac ctgggaracc acccgggccg cggcgccctca gtggacaggt 487
gggargaaaa gaaaacttct taccttggar garggacatc ccgcttcctt atccttagct 547
tttttgttgc tcctccccac tgcccccttt aatttatttg gttgtttgcg gaaggagggg 607
ggaagggggg aagctgggcc gggaactgtc cgaggtgctg agctggggcg ggaccggaat 667
cctcccggtg ggggtaccagg gactgagttg ggcctggggc cgtgtccaag gtgccaatga 727
tgcgggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccga aagaactata 787
aagcgctgga agcgctgca aaaaaaaaaa a 818

```

```

<210> 214
<211> 971
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 12..734

```

```

<221> sig_peptide
<222> 12..101
<223> Von Heijne matrix
      score 4.80000019073486
      seq ILFCVGAVGACTL/SV

```

```

<221> polyA_signal
<222> 914..919

```

```

<221> polyA_site
<222> 961..971

```

```

<400> 214
aatacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg 50
          Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
          -30          -25          -20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act 98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
          -15          -10          -5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag 146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu
          1          5          10          15
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag 194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
          20          25          30
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac 242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn
          35          40          45
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg 290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
          50          55          60
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act 338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
          65          70          75
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg 386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
          80          85          90          95
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta 434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Thr Thr Leu Val Val
          100          105          110
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct 482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala

```

115	120	125	
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc			530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe			
130	135	140	
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata			578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile			
145	150	155	
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa			626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu			
160	165	170	175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa			674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln			
180	185	190	
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac			722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn			
195	200	205	
tat gaa agg cca tagaaacggt ttaattttca atgaagtcac tgaaaatcca			774
Tyr Glu Arg Pro			
210			
actccaggag ctatggcagt gttaatgaac atatatcatc aggtcttaaa aaaaaataaa			834
ggtaaaactga aaagacaact ggctacaaag aaggatgcc aatgtaagg aaactataac			894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa			954
tttgccaaaa aaaaaaw			971

<210> 215
 <211> 640
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 378..518

<221> sig_peptide
 <222> 378..467
 <223> Von Heijne matrix
 score 5.5
 seq SLMTCTTLINASA/IS

<221> polyA_signal
 <222> 607..612

<221> polyA_site
 <222> 628..640

<400> 215

agcctgggta akgcccaaga tggctgtctt cgccttagta ctcgtgtgaa gttggcgggg	60	
acggttcctg tcatcttctt gggcttattt ggtgtgctgt tgaagggggg agactagaga	120	
aatggcaggg aacctcttat ccggggcagg taggcgctg tgggactggg tgcctctggc	180	
gtgcagaagc ttctctcttg gtgtgcctag attgatcggg ataaggctca ctctcccgcc	240	
cccaaaagtg gttgatcggt ggaacgagaa aaggggccatg ttcggagtgt atgacaacat	300	
cgggatcctg ggaaactttg aaaagcacc caaagaactg atcagggggc ccatatggct	360	
tcgagggttg aaaggga atg aat tgc aac gtt gta tcc gaa aga gga aaa	410	
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys		
-30	-25	-20
tgg ttg gaa gta gaa tgt tgc ctg atg acc tgc aca acc tta ata aac	458	
Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn		
-15	-10	-5
gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat	506	
Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp		
1	5	10

```

aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag      558
Arg Arg Glu Ser
    15
ggaaactgta cttttccctg tgaggaaacg gctttgtatt ttctctgtaa taaaatgggg      618
cttcttttga aaaaaaaaaa aa                                           640

<210> 216
<211> 745
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..304

<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
      score 4.59999990463257
      seq PLQWSLLVAVVAG/SV

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..743

<400> 216
acttccgcct gcgcctgcgc agcvcagctc cshgagccct gccaaccatg gtgaacttgg      60
gtctgtcccg ggtggacgac gccgtggctg ccaagcaccg ggcaccggc atg gcc ttt      118
                                     Met Ala Phe
ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg      166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
-25                               -20                               -15                               -10
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg      214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
                               -5                               1                               5
acg aga gtg gag tgc gag aaa tgc aac aac ctc tgg ctc ttc ctg gag      262
Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
    10                               15                               20
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc      304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser
    25                               30                               35
taggagagct ccagcagggg cacagargat tgggggcagg argartcttg aacacakcct      364
tcatgcccc tgaccccagg ccgaccctcc ccacacccta gggtagccca gtcgtatcct      424
ctgtccgcat gtgtggccag gcctgacaaa cmcctgcaga tggctgctgc cccaacctgg      484
gacctgccca ggaggttggg gcagaaaagg ctctccctgg ggtggtgttt ctctctagg      544
gtattgggat gcatgttctg cactgccagc agagaggggt tgtctggggg ccaccaccta      604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc ccctgcatct      664
ccaacaagtc caaggtgaca gctggtgcta ggggcgtggg gttaataaat ggcttatcct      724
tctctccaaa aaaaaaaaaa c                                           745

<210> 217
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..419

```

<221> sig_peptide
 <222> 201..272
 <223> Von Heijne matrix
 score 6.40000009536743
 seq LSYLPLWLGPWP/CS

<221> polyA_signal
 <222> 601..606

<221> polyA_site
 <222> 627..637

<400> 217
 acaaaatata attgcctcts cctctctcca ttttctctct tgggagcaat ggtcacagtc 60
 cctggtacct gaaaaggtag ctaggtctag gcccttcttc cttttccctt cctctccctt 120
 accccagaac tttggctccc tttcccttct ctctctggta gctccaggag gcctgtgatc 180
 cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc 233
 Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
 -20 -15
 ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc 281
 Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
 -10 -5 1
 tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg 329
 Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
 5 10 15
 ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar 377
 Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
 20 25 30 35
 aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg 419
 Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
 40 45
 targaaggtc tggcctgggg tcrngtgaag gagggcccag gtcagttctg ggggtcccagt 479
 gacctgcttt gccattctcc tgggtgccgt gctgctccct gtttctggag ctggatgttc 539
 cccacctggc agttgagctg cctgagccaa tgtgtctgtc tttggtaact gagtgaacca 599
 taataaaggg gaacatttgg ccctgtgaaa aaaaaaaa 637

<210> 218
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 123..302

<221> sig_peptide
 <222> 123..176
 <223> Von Heijne matrix
 score 4.30000019073486
 seq WTCLKSFPSPSTSS/HA

<221> polyA_signal
 <222> 1279..1284

<221> polyA_site
 <222> 1301..1312

<400> 218
 aagagcatcc tgcgccccgg cgcgggggccc tgcggtagcc tcaggcccct cccctggacc 60
 cgccgcagag ccagtgacaga atacagaaac tgcagccatg accacgcacg tcaccctgga 120
 ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167

```

      Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
      -15          -10          -5
acc agc agc cat gca tcg agc ctc cac ctt cct cca tca tgt acc agg      215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
      1          5          10
cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca      263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
      15          20          25
ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat      312
Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
      30          35          40
gctggaggaa ggacatgakt atgcgggtcat gctgtacacc tggcgcagct gttccccgggc      372
cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt      432
araggtgctg gagccggagg tcaccaagct catgaagttc atgtattttc arcgcaaggc      492
catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt      552
tgtctctgag gcctacctcc tgacccttgg caagtccatc aacatgtttg ctgtcctgga      612
tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc      672
acagttcctg cggaagatgg cagatcccca gtctatccag gagtcgcaga acctttccat      732
gttcctggcc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc      792
aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa      852
gatgtacctg actcccagtg agaaacatat gtcctcraag gtaaaaactcc cctgaggccg      912
cacccatgga gcctgggctt accctctcac cttcttctta ttaaaaaatcc gttttaaaaa      972
acaatgtttt ttttttctta aacattgata cagatcttac ggcacataat ggtttgtaac      1032
ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat      1092
ttctacaatg ttatgtgtaa tgactgcca gtattctgtt gtattggaac attgtcatgt      1152
aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt      1212
tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa      1272
aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc                        1315

<210> 219
<211> 1035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..673

<221> sig_peptide
<222> 98..376
<223> Von Heijne matrix
      score 5.59999990463257
      seq VLLLRQLFAQAEK/WY

<221> polyA_site
<222> 1025..1035

<400> 219
aattttctcgt ggtccaacta cctcggcgca tcccaggctt ggcggggcac cgctggcct      60
ctcccgttcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta      115
                                Met Ala Glu Leu Gly Leu
                                -90
aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt      163
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
      -85          -80          -75
tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac      211
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
      -70          -65          -60
ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc      259
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
      -55          -50          -45          -40

```

```

tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa      307
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
      -35                      -30                      -25
tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag      355
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Arg Gln
      -20                      -15                      -10
ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc      403
Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
      -5                      1                      5
tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa      451
Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu
      10                      15                      20                      25
aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca      499
Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr
      30                      35                      40
aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta      547
Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Gly Thr Ala Lys Leu Leu
      45                      50                      55
aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg      595
Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu
      60                      65                      70
tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca      643
Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser
      75                      80                      85
ggt cct ctg agg ata att agt cca ttg cag tagttttact tgatggtacc      693
Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
      90                      95
ccatggggcca gaagagggcca tacttaacct tctagagagc ctgaagtagc tcctgatcac      753
accttttcaa ggtaaagtga agagcatgaa attttgagaca gcgtttattg atggacattt      813
aaagttttgtg atctgcggta acaaggagaa gggtttttaa gtttataaaa attatttatc      873
aattagccgg gtgtggtggt acgtgcctat agtcagagct actcgggagg ctgaggcagg      933
agaattgctt gaaccgggga ggtggagggt gcagtgaact gagatcacgc cactgcactc      993
tagcctgggc gacagagcga gactccatct caaaaaaaaa aa      1035

<210> 220
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..463

<221> sig_peptide
<222> 17..232
<223> Von Heijne matrix
      score 3.79999995231628
      seq LMGLALAVYKCQS/MG

<221> polyA_signal
<222> 657..662

<221> polyA_site
<222> 684..696

<400> 220
actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act      52
      Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
      -70                      -65
atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc      100
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro

```

```

-60          -55          -50          -45
att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt      148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
          -40          -35          -30
tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg      196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
          -25          -20          -15
atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta      244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
          -10          -5          1
cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga      292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5          10          15          20
atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg      340
Met Glu Ser Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
          25          30          35
cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca      388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
          40          45          50
gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac      436
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
          55          60          65
caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca      483
Gln Lys Thr Leu Phe Ser Met Val Gly
70          75
atgtgcatat tacgacaaac acaaaaaaac tataaccataa cccagggctg aaaataatgt      543
aaaaaacttt atttttgttt ccagtacaga gcaaaacaac aacaaaaaaa cataactatg      603
taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat      663
taaattggttg araacaatgc aaaaaaaaaa aaa      696

<210> 221
<211> 868
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 263..481

<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
      score 11.1999998092651
      seq ILVVLMLGLPLAQA/LD

<221> polyA_site
<222> 858..868

<400> 221
aagacacgcc tacgattaga ctcaggcagg cacctaccgg cgagcggccg crvgtgactc      60
ccaggcgccg cggtacctca cggtggtgaa ggtcacaggg ttgcagcact ccagtagac      120
caggagctcc gggaggcagg gccggcccca cgtcctctgc gcaccacct gagttggatc      180
ctctgtgcgc cacccttgag ttggatccag ggctagctgc tgttgacctc cccactccca      240
cgctgccctc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg      292
          Met Thr Pro Leu Leu Thr Leu Ile Leu Val
          -20          -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt      340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10          -5          1          5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg      388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met

```

```

      10      15      20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg      436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met
      25      30      35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta      481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val
      40      45      50
tgatggctac tccaagcacg cgtccaccac ctctgtgtgc cagtacgacc tctgcaacgg      541
caccggcctt gccaccccg ccacctggc cctggccccc atcctcctgg ccacctctg      601
gggtctcttc taaagcccc gaggcagacc cactcaagaa caaagctctc gagacacact      661
gctayaccct ckcacccakc tcacctgcc tcacctcca cactccctgc gacctcctca      721
gccatgcccc gggtcaggac tgtgggcaag aagacacccg acctcccca accaccacac      781
gacctcactt cgaggccttg acctttcgat gctgtgtggg atcccaaaag tgtccggctt      841
tgatgggctg atcagcaaaa aaaaaaa      868

<210> 222
<211> 775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..299

<221> sig_peptide
<222> 42..101
<223> Von Heijne matrix
      score 5.40000009536743
      seq W F V H S S A L G L V L A / P P

<221> polyA_site
<222> 762..775

<400> 222
aacgatacaa atggtaggcc ttcattgtgag ccagtdacta c atg aat ctt cat ttc      56
                                   Met Asn Leu His Phe
                                   -20
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca      104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro
-15      -10      -5      1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt      152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys
      5      10      15
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc      200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr
      20      25      30
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa      248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys
      35      40      45
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg      296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg
      50      55      60      65
cag tgaaactwkk ttccwtttcta aagcccttca tttcccacaa ggttaagctc      349
Gln
tcgaaaccccc atttgatcct tggttcctat ttcgatcctc ctttggaatc tgaaaatcgg      409
tctccatgtt gtatgcaaat taaaaktgtc cttgtttgtt actcttccaa cacagggtat      469
cagggaraaa gaggccttat ctgttctctc atccccctg ttttgacaga ctgctaagaa      529
ttcctcagga ctcccttttg ttggggattt tactttccca aaagtctgat ctgatttctt      589
tcaggggtag acaagcttgt cctagtgtc tgcttcaggt cttatcagaa gaaaccagg      649
aatagaaaag gtagatgcct tgacttttgt ccctgttgtg gggactaaag tgttttttgc      709
cagaattgtc aaaagctccg gttcaaactc tgtagagttt catggaaaaa caaaacaaaa      769

```


aaaaaa

775

<210> 223

<211> 1075

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 198..431

<221> sig_peptide

<222> 198..260

<223> Von Heijne matrix

score 6.90000009536743

seq LLACGSLLPGLWQ/HL

<221> polyA_site

<222> 1064..1074

<400> 223

atatatttct gaggcagtac ccatctcact tgtaaactta aaagacaccg cagagatttg 60
agggactcag aagtcaaata gagtaggta aaaacctctt atttttcaaa ttaattgttt 120
taagaaacaa gcataacctgt gtaagtgaat tatcttaatt tgtgttgaat caagtttagga 180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc 230

Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
-20 -15

tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac 278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His

-10 -5 1 5
tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca 326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
10 15 20

gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt 374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
25 30 35

tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac 422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
40 45 50

tct atc acc tagccattgt akccatacca agccgggctt cctacttccc 471
Ser Ile Thr
55

tctgctcccc ttggttttct cctgtraart aaatctcact gacccttgat gcasctccaa 531
gcatatataa tatatatata ataaaaccat abtctaaaaa attcaaacca ggawaaataa 591
asccaraaat ttgtatggga aaaatctgca caaatatttatt tggccagcat gggtatcatg 651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca 711
actacttacc tctcaatacc aaaaargaag caggaggcaa aatctctcaw taatttcata 771
aaaacaattc ttakctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc 831
saggtgggcg gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc 891
catctctact aaaattacaa aaaatttrgt gggcgagggt gcgggcacct gtggtcccag 951
ctactcggga ggctgaggca agagaatggt gtgaacccca gggggcgag cctgcagtga 1011
gctgagatcg caccactgca ctccagcctg ggcgacagt agactccgtc tcaaaaaaaa 1071
aaah 1075

<210> 224

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

09978360 10501

<222> 279..473

<221> sig_peptide

<222> 279..362

<223> Von Heijne matrix

score 4.40000009536743

seq SCFLVALIIWCYL/RE

<221> polyA_signal

<222> 944..949

<221> polyA_site

<222> 970..981

<400> 224

```
agaatcgtgt cttgtgtgcc ccggcgcccg ggtgagctcc tcaaggtctc ggagggccga      60
gggcagacac cggcgggcgg gcggasgctt actgctctct ctcttcagg gccgtccggg      120
cgctgaggct cataggctgg gcttcccgaa gccttcaccc gttgcccggg tcccgggatc      180
gggcccaccc tgccgcccag gaagaggacg accctgaccg cccattgag ttttctcca      240
gcaaagccaa ccctcaccgc tggtcggtgg gccatacc atg gga aag gga cat cag      296
                                   Met Gly Lys Gly His Gln
                                   -25
cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
      -20                -15                -10
atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
      -5                1                5                10
aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440
Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu
      15                20                25
cct gag act cca gct gcc tac aga gcg aga act tgacggggtg cccgctgggg      493
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
      30                35
ctggcaggaa gggagccgac asccgccctt cggatttgat ktcacgtttg cccgtgactg      553
tcctggctat gcktgcgctc tcagcactra argacttggc tgggtggatgg ggcacttggc      613
tatgctgatt cgcgtgaagg cggavcaaaa tctcagcaaa tcggaaactg ctctctscct      673
ggctcttgat ktccaaggat tccatcggca aaacttctca ratccttggg gaaggtttca      733
gttgcaactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag      793
cacttctggg gacacttgct atccagtgtt agtttgcagg taatttgctt tctgagatag      853
aatactctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc      913
acatgtgagt ttacacaac aacaaatgaa aataaatttt aattttataa tatgggaaaa      973
aaaaaaaaa                                     981
```

<210> 225

<211> 1031

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..644

<221> sig_peptide

<222> 12..92

<223> Von Heijne matrix

score 4

seq LTFFSGVYGTCIG/AT

<221> polyA_signal

<222> 1002..1007

<221> polyA_site

<222> 1020..1031

<400> 225

```
acaccaagga g atg ctc ctt ctt agt att aca act gct tat aca ggt ctg      50
          Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu
          -25          -20          -15
gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca      98
Glu Leu Thr Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr
          -10          -5          1
aat aaa ttt gga gca gaa gag ara agc ctt att gga ctt tct ggc att      146
Asn Lys Phe Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile
          5          10          15
ttc atc ggc att gga gaa att tta ggt gga agc ctc ttc ggc ctg ctg      194
Phe Ile Gly Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu
          20          25          30
agc aag aac aat cgt ttt ggt aga aat cca gtt gtg ctg ttg ggc atc      242
Ser Lys Asn Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile
          35          40          45          50
ctg gtg cac ttc ata gct ttt tat cta ata ttt ctc aac atg cct gga      290
Leu Val His Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly
          55          60          65
gat gcc ccg att gct cct gtt aaa gga act gac agc agt gct tac atc      338
Asp Ala Pro Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile
          70          75          80
aaa tcc agc aaa raa ttt gcc att ctc tgc akt ttt ctg tkg ggc ctt      386
Lys Ser Ser Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu
          85          90          95
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg      434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu
          100          105          110
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag      482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln
          115          120          125          130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt      530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu
          135          140          145
cac tgg caa ctc ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att      578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile
          150          155          160
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc ggc      626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly
          165          170          175
tct gac tac cga agt atc tgatctggtg tccgtgaggg gacacgtatg      674
Ser Asp Tyr Arg Ser Ile
          180
acctcagaaa cacagctgga cacagagctt ggtggaagaa gtcgcctttg atcttcacta      734
tatattgggt gatgttcagt atggaaaatc aagggattaa gactgttaaa tcagccagag      794
tkggtgttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctggt      854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attcttataa      914
tcatgttata gaatgtaaat gttttcttct ctctcctgct cttgttgga gacacctgcct      974
tgatttagaa tactaggcca tatgtcatat aaatatTTTT tctggaaaaa aaaaaaa      1031
```

<210> 226

<211> 1283

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 91..459

<221> sig_peptide

<222> 91..330

<223> Von Heijne matrix

score 7.69999980926514

seq LVLFLSLALLVTP/TS

<221> polyA_site

<222> 1271..1281

<400> 226

```
tattccttgg agttccacga ctgaattaag actgttgtgg grdccataat tttcaaatac      60
ttgccctata ttcgtgttga ggggttcacac atg agc aca tgg tat ttg gca ctt      114
                                   Met Ser Thr Trp Tyr Leu Ala Leu
                                   -80                               -75
aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg      162
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu
                                   -70                               -65                               -60
tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat      210
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn
                                   -55                               -50                               -45
tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt      258
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe
                                   -40                               -35                               -30                               -25
ggg ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta      306
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu
                                   -20                               -15                               -10
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata      354
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile
                                   -5                               1                               5
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac      402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp
                                   10                               15                               20
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt      450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu
                                   25                               30                               35                               40
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct      499
His Gln Leu
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaaag      559
ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatttt      619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgctct      679
gtttttggaat tgaattagct ttcaggccas cagggcactg ttttggtaaat tgctttttcc      739
agtactagca tgtttttctc ctccatagcc tctgttagct tctgagcttg taacctccag      799
ggaaavatga gaatattcac ccttttaata tgtgtagaga ccatgcaaga ccattgtctt      859
ctaataatta gaaatactta gccagattct ctatagtaaa cccggagatt gggagggctg      919
ctttctactt ggtgcatect tctgcgcttc taatgatttt taaaaatctg ttaataattg      979
atgtttttctg gctgggcaca gtggctcacg cctgtaatcc cagcactttg ggaggccaag      1039
gagggcagat catgaggtca ggagattgar accatcctgg ctaacacggt gaaaccccgt      1099
ctctactaaa aatacaaaaar aattakccgg gcatggtagt gggcgctgt gtacccagct      1159
actggggagg ctgaggcarg araatcgctt gaacctggga ggcggaggtt gcastragct      1219
gagatggtgc caccgcactc tagcctgggt gacagagcga gacttcattt caaaaaaaaaa      1279
aamc                                                                1283
```

<210> 227

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..327

<221> sig_peptide

<222> 70..147

<223> Von Heijne matrix

score 9.60000038146973

seq WLIALASWSWALC/RI

<221> polyA_signal

<222> 1741..1746

<221> polyA_site

<222> 1763..1774

<400> 227

```
agcccggttt cgtgcccgcg gccgactgcg casctgtccg cgagtctgag atacttacag      60
agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg      111
      Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
      -25                      -20                      -15
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt      159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
      -10                      -5                      1
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt      207
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu
      5                      10                      15                      20
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat      255
Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp
      25                      30                      35
gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat      303
Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp
      40                      45                      50
tcc cat gcc cac tgg cmt tgc rca taaaaaaatt ttcatacagaa ccaaagatgg      357
Ser His Ala His Trp Xaa Ser Xaa
      55                      60
aatacgtctg aatcttattt tgatacgata cactggagac aattcacctt attccccaac      417
tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac      477
ttatgtttgg taacctcaaa gttaaccttt tgctggttga ttatcgagga tatggaaaaa      537
gtgaaggaga agcaagtga gaaggactct acttagattc tgaagctgtg ttagactacg      597
tgatgactag acctgacctt gataaaaaca aaatttttct ttttggccgt tccttgggtg      657
garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatggtgg      717
agaacacatt ttaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc      777
gttaccttcc tttatggtgc taaaaaata aatttttgtc ctacagaaaa atctctcagt      837
gtagaatgcc ttcacttttc atctctggac tctcagatca attaattcca ccagtaatga      897
tgaaacaact ttatgaactc tccccatctc ggactaagan attagccatt tttccagatg      957
ggactcacia tgacacatgg cagtgccaa gctatttcac tgcacttgaa cagttcatca      1017
aagaagtcgt aaagagccat tctcctgaag aaatggcaaa aacttcatct aatgtaacaa      1077
ttatataatg tttccctttt tgattattgc attgtatttt aatttgtgca gaatgataaa      1137
gaatgttctt tttagaagtg tgttatgtct gtacctgtct gaagagtgc attaaacttt      1197
gaaaggactt cactgctcct ttacgatatt ccaaatagtt ttttacattg gaaaaactaa      1257
ttcttgggat tctttcatac attttcatca aaactttcag tgtgattatg tattcatatc      1317
ttcagtttaa tatgtcagta taatagatat tgttcaaaag tttcttggtg ctaaaagtggt      1377
gtaatctgtt acacagatga atagctagat gtggaaagag atatgtaaac aagaaacctt      1437
tgggtattgt ttcttaagta aatattggga caatcatggt aagcaaactt agttctgtaa      1497
ctgcattttt caccttaaaa gttaaatagaa atgcatgatg gtattttatt ccttgaatta      1557
tgcaatgcaa cattttacat gtaaatagca ctggtcatat actgatgtat atggttatct      1617
gggttatatc tatttttatg taaactctat ttttgttttt ggcaagaagt gaaattgaga      1677
cttatgtgca ggttgccatt gaattttgct ctggtgaatg ctgagatcca gctttttctt      1737
acaaataaat gggaccctgt tttccaaaaa aaaaaaamcm      1777
```

<210> 228

<211> 970

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..497

<221> sig_peptide
<222> 12..104
<223> Von Heijne matrix
score 5.5
seq LVGVLFVSVTTG/PW

<221> polyA_signal
<222> 935..940

<221> polyA_site
<222> 955..967

<400> 228
aggtctccaa g atg gcg gcc gcc tgg ccg tct ggt ccg kct gct ccg gag 50
Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
-30 -25 -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act 98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
-15 -10 -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg 146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
1 5 10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca 194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
15 20 25 30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca 242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
35 40 45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc 290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
50 55 60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag 338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
65 70 75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg 386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
80 85 90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg 434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
95 100 105 110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg 482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
115 120 125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca 537
Asn Trp Glu Pro Asn
130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact 597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt 657
gagcctcctt gatttttaata gagaacttct agtgtatgga tttaaagatt tctctttttc 717
attcatatac cattttatga gttctgtata attttttgtg gtttttgttt tgttgagtta 777
aagtatatta ttgtgagatt tatttaatat gacttccttt gaaagctgta taatagtgtt 837
tctcgggcctt ctgtctctat gagagatagc ttattactct gatactcttt aatcctttac 897
aaaggcaagt tgccacttgt catttttggt tctgaaaaat aaaagtataa cttattcaca 957
aaaaaaaaa mms 970

<210> 229
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..383

<221> sig_peptide
 <222> 90..200
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFNVHS/AV

<221> polyA_signal
 <222> 609..614

<221> polyA_site
 <222> 632..643

<400> 229
 atctctgccc ccctgcgagg gcatacctggg ctttctccca ccgctttccg agcccgtttg 60
 cacctcggcg atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg 113
 Met Ala Ser Leu Leu Cys Cys Gly
 -35 -30
 ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc 161
 Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
 -25 -20 -15
 atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg 209
 Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
 -10 -5 1
 att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car 257
 Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln
 5 10 15
 aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct 305
 Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala
 20 25 30 35
 gca ggc ctt tac ctc ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg 353
 Ala Gly Leu Tyr Leu Leu Gly Gly Phe Ser Phe Cys Gln Xaa Arg
 40 45 50
 ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccg gcgcgtttcc 403
 Leu Asn Lys Arg Lys Glu Tyr Met Val Arg
 55 60
 ccgctccagc ccctcctcta tttaaaract ccctgcaccg tktcaccag gtcgcgtccc 463
 acccttgccg gcgcctctctg tgggactggg tttcccgggc rararactga atcccttctc 523
 ccattctctgg catccggccc ccgtggarar ggctgaggct ggggggctgt tccgtctctc 583
 cacccttcgc tgtgtcccg atctcaataa agagaatctg ctctcttcaa aaaaaaaaaa 643
 my 645

<210> 230
 <211> 773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..541

<221> sig_peptide

<222> 332..376
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLPCCLLWSVFNP/ES

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 761..773

<400> 230
 aaaacaattc atgcctttca tagtttatta ttattaaagt ctaaacaaaa ttgcaatttc 60
 ttaggtaacc ttatatattac aataaatgaa gattaccctc aaatgctaga agctgtctag 120
 gtccgtccgg tgtgtcagat tttcctcaga ttagatgtgc caataaccaa gtttattcag 180
 taaacaactt gtacttggtt catctgggtt tattactctc acccataaac agtaatgact 240
 ctctgaccct ctggaaatat gtaatgcttc caatcttgct ttgtgtatct catttaattt 300
 gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt 352
 Met Arg Phe Leu Pro Cys Cys
 -15 -10
 ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt 400
 Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe
 -5 1 5
 ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca 448
 Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser
 10 15 20
 ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac 496
 Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
 25 30 35 40
 ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act 541
 Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
 45 50 55
 tgaaaagaaa gtgttttatt ttcaaactctg gtccatattt acatttctagt tcagagccaa 601
 gcctttaaact gtacagaatt tccactgtaa ttaaaactat ttagtgtag ttataaatag 661
 ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggatgaatgt 721
 atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa 773

<210> 231
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..222

<221> sig_peptide
 <222> 43..177
 <223> Von Heijne matrix
 score 4
 seq ENFLSLLSKSCSA/DP

<221> polyA_signal
 <222> 530..535

<221> polyA_site
 <222> 555..566

<400> 231
 aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt 54
 Met His Ser Leu

09978360-101501

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..384

<221> sig_peptide
<222> 232..300
<223> Von Heijne matrix
score 3.70000004768372
seq FFLCAAFPLGAGV/KM

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 662..673

<400> 233
atttggcttg cagactgcct tctatcccag aacagctgag aaatctatga agctgagatt 60
ctgaaggacc cagcttaggt tcttccactt aggcctcaat tcccttcctt ttccaggggc 120
agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttcctttc ccagaagcca 180
ctggccccc atagcaccca gtgcatacctt tttacaagtg gaagaactag g atg gct 237
Met Ala
ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc 285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
-20 -15 -10
ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca 333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
-5 1 5 10
ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg 381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
15 20 25
cct tagcttctgg gcctatcsgc tgccttcctt cttyttccta ccacctcttc 434
Pro
tgccttcctt trawctctgt tgggcttggg gatcttagtt ttcttttgtt tatttcccat 494
ctcatTTTTT tcttctgggc agTTTTTTT aggggggggtg ttgtggtttt ttgtttttgt 554
tttgcttctg aaaaarcatt tgcctttcct cctctcccaa cataacaatc gtggtaacag 614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa 673

<210> 234
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..427

<221> sig_peptide
<222> 143..286
<223> Von Heijne matrix
score 7.5
seq FVILLLFIFTVVS/LV

<221> polyA_signal
<222> 606..611

<221> polyA_site
<222> 628..639

tat gcc tcg ggt act tat ttc cta ata tat atc agc aca gta acg cct	439
Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro	
5 10 15 20	
agc tgg agg ctt tgt ctt gtt agt tgataaatta gtggtaacag gtagatttgg	493
Ser Trp Arg Leu Cys Leu Val Ser	
25	
ttacctccca aagtgctggg attrcagacg tgagccaccg cgcttgccg aaacaattct	553
tttgaaagag agaagtctcc ctgtgttgcg caggctggtc tcagactcct ggggtcaagt	613
gagcctcctg ctttcgcctc cttaaagtgt gggattacag gcgtgagcca ccgcacccgg	673
acagatgtgt tgattttaaa gtgggtatga ggcctgagcc ctggagtttg agaccagcct	733
ggacaacatg gcaagaccct gtctctccaa aaaaaaaaa	772
<210> 236	
<211> 840	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 162..671	
<221> sig_peptide	
<222> 162..398	
<223> Von Heijne matrix	
score 4.09999990463257	
seq QGVLFICFTCARS/FP	
<221> polyA_signal	
<222> 805..810	
<221> polyA_site	
<222> 830..840	
<400> 236	
aaaaactgag gcctgggagc aggaacctgt aggcagcgct tgagggtagc gggatagcag	60
ctgcaacgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg	120
atgtttcccg ggaagaactg ggataaaggg gtcccagcac c atg gag gac ccg aac	176
Met Glu Asp Pro Asn	
-75	
cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc	224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro	
-70 -65 -60	
cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc	272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr	
-55 -50 -45	
cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg	320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met	
-40 -35 -30	
aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc	368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val	
-25 -20 -15	
ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc	416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala	
-10 -5 1 5	
ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg	464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu	
10 15 20	
ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt	512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys	
25 30 35	
ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr	560

Gly	Lys	Thr	Phe	Gly	Gln	Ala	Val	Ser	Leu	Xaa	Arg	His	Xaa	Gln	Xaa		
40						45				50							
cat	gar	gtc	cgt	gcc	cct	cct	ggc	acc	ttc	gcc	tgc	aca	rad	tgc	ggg	608	
His	Glu	Val	Arg	Ala	Pro	Pro	Gly	Thr	Phe	Ala	Cys	Thr	Xaa	Cys	Gly		
55					60					65					70		
cag	gac	ttt	gct	car	gaa	rca	ggg	ctg	cat	caa	cac	tac	att	cgg	cat	656	
Gln	Asp	Phe	Ala	Gln	Glu	Xaa	Gly	Leu	His	Gln	His	Tyr	Ile	Arg	His		
				75				80						85			
gcc	cgg	ggg	gga	ctc	tgagttcagc	ttaagcctct	ccacggtgac	gggtggctct								711	
Ala	Arg	Gly	Gly	Leu													
				90													
gtggctggta	ggactcaccc	atgatatggg	gtgcaggaac	tctggggggc	ctgaaggatt											771	
tgcttccctc	ccctgggaag	gcagagggct	cttaataaag	aggacccaka	agattcttaa											831	
aaaaaaaa																840	

<210> 237
 <211> 840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..632

 <221> sig_peptide
 <222> 63..308
 <223> Von Heijne matrix
 score 4.40000009536743
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 808..813

 <221> polyA_site
 <222> 829..840

<400> 237																	
aacttccggt	cgcgccascg	cccgttgcca	gttctgcgcg	tgtcctgcat	ctccagtatg											60	
ga	atg	tat	gtd	tgg	ccc	tgt	gct	gtg	gtc	ctg	gcc	cag	tac	ctt	tgg	107	
Met	Tyr	Val	Trp	Pro	Cys	Ala	Val	Leu	Ala	Gln	Tyr	Leu	Trp				
		-80				-75						-70					
ttt	cac	aga	aga	tct	ctg	cca	ggc	aag	gcc	atc	tta	gag	att	gga	gct	155	
Phe	His	Arg	Arg	Ser	Leu	Pro	Gly	Lys	Ala	Ile	Leu	Glu	Ile	Gly	Ala		
		-65				-60						-55					
gga	gtg	agc	ctt	cca	gga	att	ttg	gct	gcc	aaa	tgt	ggg	gca	gaa	gta	203	
Gly	Val	Ser	Leu	Pro	Gly	Ile	Leu	Ala	Ala	Lys	Cys	Gly	Ala	Glu	Val		
		-50				-45						-40					
ata	ctg	tca	gac	agc	tca	gaa	ctg	cct	cac	tgt	ctg	gaa	gtc	tgt	cgg	251	
Ile	Leu	Ser	Asp	Ser	Ser	Glu	Leu	Pro	His	Cys	Leu	Glu	Val	Cys	Arg		
		-35				-30				-25				-20			
caa	agc	tgc	caa	atg	aat	aac	ctg	cca	cat	ctg	cag	gtg	gta	gga	cta	299	
Gln	Ser	Cys	Gln	Met	Asn	Asn	Leu	Pro	His	Leu	Gln	Val	Val	Gly	Leu		
			-15						-10					-5			
aca	tgg	ggg	cat	ata	tct	tgg	gat	ctt	ctg	gct	cta	cca	cca	caa	gat	347	
Thr	Trp	Gly	His	Ile	Ser	Trp	Asp	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Asp		
		1				5					10						
att	atc	ctt	gca	tct	gat	gtg	ttc	ttt	gaa	cca	gaa	rat	ttt	gaa	gac	395	
Ile	Ile	Leu	Ala	Ser	Asp	Val	Phe	Phe	Glu	Pro	Glu	Xaa	Phe	Glu	Asp		
		15				20					25						
att	ttg	gct	aca	ata	tat	ttt	ttg	atg	cac	aar	aat	ccc	aag	gtc	caa	443	
Ile	Leu	Ala	Thr	Ile	Tyr	Phe	Leu	Met	His	Lys	Asn	Pro	Lys	Val	Gln		

30	35	40	45	
ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct	491			
Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala				
50 55 60				
tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct	539			
Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser				
65 70 75				
ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga	587			
Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg				
80 85 90				
cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc	632			
His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu				
95 100 105				
tgaattatac ctacaacctg ttctgggaca gtatcaatac tgatgagcaa cctggcacac	692			
aaactatgag cagaccactt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg	752			
tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa	812			
aatacgtatt acaagcaaaa aaaaaaaa	840			

<210> 238

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..362

<221> sig_peptide

<222> 21..200

<223> Von Heijne matrix

score 4.80000019073486

seq LVILSLKSQTLDA/ET

<221> polyA_signal

<222> 821..826

<221> polyA_site

<222> 838..849

<400> 238

agtaagtccc cccgcctcgc atg atg gct gcg gtg ccg ccg ggc ctg gag ccg	53
Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro	
-60 -55 -50	
tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca	101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr	
-45 -40 -35	
gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att	149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile	
-30 -25 -20	
aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat	197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp	
-15 -10 -5	
gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga	245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg	
1 5 10 15	
atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt	293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys	
20 25 30	
tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg	341
Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu	
35 40 45	

ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt 392
Phe Glu Leu Phe Ser Ser Lys

50

ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga ttkctctakg ctygckggtg 452
gaatataacc aattataccw cagctgtaka aatwttgttt taatgtgggg taccygggtg 512
ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt 572
catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga 632
gcttaaagca agtcttcact tgaaaaactgc tatagaaatg ctttataattt aaaaatgaaa 692
gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc 752
tctgtgcttc ttctgccata ccttgcccta tgcactctctt tgtttcaatc ctttgtcata 812
tcctttataa taaactggta aatgtaaaaa aaaaaaa 849

<210> 239

<211> 1344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..503

<221> sig_peptide

<222> 21..344

<223> Von Heijne matrix

score 5.30000019073486

seq ACMTLTASPGVFP/SL

<221> polyA_signal

<222> 1305..1310

<221> polyA_site

<222> 1330..1341

<400> 239

aaacaactcc ggaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag 53
Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln

-105

-100

tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca 101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
-95 -90 -85

atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc 149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
-80 -75 -70

aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt 197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
-65 -60 -55 -50

tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct 245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
-45 -40 -35

aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag 293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
-30 -25 -20

gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc 341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
-15 -10 -5

ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg 389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
1 5 10 15

cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa 437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
20 25 30

CCCTTGTGATC

```

aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg      485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
      35              40              45
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag      533
Glu Lys Ser Ile Met Leu
      50
atgatgaccg ttcatthaata aatttgcac tcatgcacac cagttacttc ctctttgtga      593
tgggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga      653
gcaatcctga attttgtccc gagaagggtgg ctttggctga agcctaattc cacagctcct      713
tggtttttga gagagactga gagaaccata atccttgccg gctgaaccca gcctgggcct      773
ggatgctctg tgaatacatt atcttgcgat gttgggttat tccagccaaa gacatttcaa      833
gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg      893
cacgtgcttt gccctgggta cagccagagc ccttcaaccc caccttggac ttgaggacct      953
acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac     1013
gatgttttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttggtttgg     1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacctt tgatacggta     1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg cttaataatc     1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaaacata ccttaagttt     1253
tttttgtttt gttttgtttt ttttgttttt tgttttcctt tatgaagaaa aaataaaaata     1313
gtcacatttt aatacyaaaa aaaaaaaamc h                                     1344

```

```

<210> 240
<211> 671
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 1..201

<221> sig_peptide
<222> 1..63
<223> Von Heijne matrix
      score 5.09999990463257
      seq LLLKIWLLQRPES/QE

```

```

<221> polyA_signal
<222> 637..642

```

```

<221> polyA_site
<222> 660..671

```

```

<400> 240
atg ctg gga ggt gac cat agg gct ctg ctt tta aag ata tgg ctg ctt      48
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
      -20              -15              -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg      96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
      -5              1              5              10
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt     144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
      15              20              25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca     192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
      30              35              40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtcttttg      241
Leu Arg Met
      45
ctcagttcat ttaaaaaaga tatctatttg aaagttctca rarttgtaca tatgtttcac     301
agtacaggat ctgtacataa aagttttcttt cctaaaccat tcaccaagag ccaatatcta     361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcctc cttgttattt     421

```



```

ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac      584
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
135          140          145          150
atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att      632
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
          155          160          165
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr      680
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser
          170          175          180
cca gct gcc tcc ttc tgc cgg ggc ctg ctc agc cag ccg ggg ccc tca      728
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser
          185          190          195
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg      776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr
          200          205          210
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc ttc tat gac cag      824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln
          215          220          225          230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag      872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln
          235          240          245
ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct      920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser
          250          255          260
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag      968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu
          265          270          275
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga      1016
Asp Phe Ala Val Leu Gly Glu Gly Leu Val Gln Thr Val Glu Ala Arg
          280          285          290
agt gag agg tgg act gtg tgateccagc tctggagcaa gctgtagacg      1064
Ser Glu Arg Trp Thr Val
          295          300
gacagcagga cattggacct ctagagcaag atgtcagtag gatgacctcc accctccttg      1124
gacatgaatc ctccatggag ggccctgctgg ctgaacatgc tgaatcatct ccaacaaaac      1184
ccagcccaaa ctttctctct gatgctccag cattggggca ggggcatggt ggcccatgta      1244
gtctcctggg cctcaccatc ccagaagagg agtgggagcc agctcagaga aggaactgaa      1304
cccaggagat ccatccacct attagccctg ggccctggacc tccctgcgat ttcccactcc      1364
tttcttagtc ttcttccaga aacagagaag gggatgtgtg cctgggagag gctctgtctc      1424
cttcctgctg ccaggacctg tgccctagact tagcatgccc ttcaactgcag tgtcaggcct      1484
ttagatggga ccagcgaaaa atgtggccct tctgagtcac atcaccgaca ctgagcagtg      1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gcaaaaaaaaa aaamcch      1601

```

<210> 242
 <211> 1206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..263

<221> sig_peptide
 <222> 69..125
 <223> Von Heijne matrix
 score 3.90000009536743
 seq ALSMSSFHSSS/CS

<221> polyA_signal
 <222> 1173..1178

<221> polyA_site

<222> 1196..1205

<400> 242

acatttgtga ctttaccaat accctcccag ttcttgatag acagctgtag gttgctgggt 60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt 110

Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser

-15

-10

ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc 158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser

-5

1

5

10

aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta 206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu

15

20

25

gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa 254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys

30

35

40

att gtg ggc tgatttggtc ttctctctct cctcccactg ttactgccct 303
Ile Val Gly

45

gcagcccttg ttcaggtgta cagaccctta ttctggcctc tagtgtcctt gtctgtcatg 363

acacaccctt ccgccccaat acctctgacc ccaaggctgg aatggggctg gtaggarata 423

agtttgctta ctcatartca tgtcctttct cttaggcacct gcttccctgc ggtgtcctca 483

aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt 543

gtattattat taagggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa 603

aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt 663

cctgaggcag tggctgccac cccttttcar atgttttagtc ctgcaaatac catctttctt 723

gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat 783

caakttgagt ttttttccag caggggttar gggagggtact csctgttgat atttgacact 843

araaagtaat cttttttaca aaactgtttt tctagggtggg tggaaagtga aactgccaca 903

tccttggttg tttagtccaa raratcattt gcaacaacag taratgtccg ggttttgttt 963

ctgtcttttt attatgaaaa actatgttaa gggggaaaat gtggattatg gtaaccarag 1023

gaatccctas cctgttttct cttaraarac ttgttttagtg ttttatcara cgtctgttgt 1083

agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgtttttgca 1143

caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gttttaccat ttaaaaaaaaa 1203

aat 1206

<210> 243

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..285

<221> sig_peptide

<222> 115..204

<223> Von Heijne matrix

score 3.70000004768372

seq SMMLLTIVYGGYLC/SV

<221> polyA_signal

<222> 505..510

<221> polyA_site

<222> 525..536

<400> 243

acgagtgtctg cgttcggtctg tgctgggaag ttgcgtagac agtggcctcg agaccctgcc 60

tgcttgagga ggcctcggtt ggatgcgaag gagctgcagc atccagggga caag atg 117

```

Met
-30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc 165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
-25 -20 -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga 213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
-10 -5 1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa 261
Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
5 10 15
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcctgagcar 315
Glu Gln Lys Xaa Ser Gly Ile Met
20 25
asakgccccaa ggcattgctgt ggagagactt cacctgccac catttccagg tcaacaggac 375
tagagcgttg atggttttca aaccctgttg gaagaaagtg cccatggttt ctctggttct 435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca 495
cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a 536

<210> 244
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..344

<221> sig_peptide
<222> 90..140
<223> Von Heijne matrix
score 8.19999980926514
seq LLLITAILAVAVG/FP

<221> polyA_signal
<222> 500..505

<221> polyA_site
<222> 515..527

<400> 244
aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca 60
gagagaaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc 113
Met Lys Lys Val Leu Leu Leu Ile
-15 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile
40 45 50 55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414

```

caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc 529

<210> 245
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..311

<221> sig_peptide
<222> 57..107
<223> Von Heijne matrix
score 8.19999980926514
seq LLLITAILAVAVG/FP

<221> polyA_signal
<222> 467..472

<221> polyA_site
<222> 482..493

<400> 245
aacttgccat ttctcataac agcgtcagag agaaagaact gactgaaacg tttgag atg 59
Met
aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt 107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
-15 -10 -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac 155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
1 5 10 15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca 203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
20 25 30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga 251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
35 40 45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt 299
Arg Asn Phe Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
50 55 60
ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga 351
Pro Ser Glu Lys
65
aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaa gaaaaacaaa 411
tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 471
acatgaaagc aaaaaaaaaa aa 493

<210> 246
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..302

<221> sig_peptide
<222> 96..182
<223> Von Heijne matrix

score 5
seq ELSLLPSSLWVLA/TS

<221> polyA_site
<222> 501..514

<400> 246
aagagacgtc accggtgctg cccttcagta tcgcggacgg aagatggcgt ccgccacccg 60
tctcatccag cggctgcgga actgggcgtc cgggc atg acc tgc agg gga agc 113
Met Thr Cys Arg Gly Ser
-25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca 161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
-20 -15 -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca 209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
-5 1 5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt 257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10 15 20 25
crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg 302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Xaa Ala Leu Leu
30 35 40
tagctgccac tgaaaaraag gcggtgactc cagctcctcc cataaagagg tgggagctgt 362
cctcggacca gccttacctg tgacactgca ccctcacggc caccgacta ctttgccctcc 422
ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gctcaggtat 482
cacttctagt ttacttttaa aaaataaaaa aatagagac 521

<210> 247
<211> 811
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..526

<221> sig_peptide
<222> 161..328
<223> Von Heijne matrix
score 4.19999980926514
seq XSPLLTLALLGQC/SL

<221> polyA_site
<222> 799..811

<400> 247
aaaaaattgc agtgcgtgaag aactggacc cgcaaaaggc tgtccctccc aaacctggga 60
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagtag 120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc 175
Met Val Pro Trp Pro
-55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc 223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
-50 -45 -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct 271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35 -30 -25 -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg 319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
-15 -10 -5

09986010501

```

ggg cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa      367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
          1          5          10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg      415
Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
          15          20          25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa      463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
          30          35          40          45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt      511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
          50          55          60
caa ttt ttt tta ggg tgaatggagg garagtgggg gactgaaaaa ccttcaaara      566
Gln Phe Phe Leu Gly
          65
caatgttatt acagcaktct ccccttatcc aaaktttctt tttcctgadt ttcagttagc      626
tatgggtcaac cgcttggaac atakttgaac acagtacaat aarataatgtt gaggtctgga      686
ktgggtggctc atgcctgtta taatcccagg actttgtgar accaaktttg aaggatcact      746
tgaaccaggg aktttgarac caccctgggc aacatrgtra gacctcatct ctacaaaaaa      806
aaaaa      811

<210> 248
<211> 625
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..332

<221> sig_peptide
<222> 210..299
<223> Von Heijne matrix
      score 8.10000038146973
      seq ITCLLAFWVPASC/IQ

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 613..625

<400> 248
acaggtcsmc ttaacatctc ttgatttgag ccactccac tgtcatcagc tttcacctgg      60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccctaaaa      120
atgcattgca tagttgatca agtcactctc tggcctaaaa ccttccttgg ctccctgctg      180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc      233
                                Met Ala Cys Glu Thr His Gly Val
                                -30          -25
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc      281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
          -20          -15          -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca      329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
          -5          1          5          10
ctc tgattcctcc tttcttttgg tcacagagaa aggggtacttt ctctgtcaaa      382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc      442
accctggcat actacacara tcactctggg ctcaacttgc tgccaatagg tcatctcccc      502
agtaaaactgt aagctccttg agggcaagga ttgtgttgga atttttgtat taacagtgcc      562
tggcttggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa      622

```

aaa

625

<210> 249
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..361

<221> sig_peptide
<222> 212..319
<223> Von Heijne matrix
score 4.09999990463257
seq HWLFLASLSGIKT/YQ

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 673..684

<400> 249
atccccawns cactctctca cagagactgt tcttttcctt ctgagaccct actccagctt 60
gtagttctaa atctgtgatt atgcactgtc tgtcttcctc ttgaggtcag gggccatttc 120
ttttgtttctc tgctatgctc aggaccacaga tcaaaggagc tcagtaacta tttacaggcg 180
tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc 232
Met Ala Pro His Thr Ala Ser
-35 -30
ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag 280
Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
-25 -20 -15
cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc 328
His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
-10 -5 1
tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra 381
Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile
5 10
aggtgttaat ggtggtaatg gcataktatt tattacccca ggggaccak aacggtgta 441
tcaaaacata tcattcccca gtggttttaa actctggtag ctttccargg aatccaaagt 501
ggaatccagt ctcccttagct gawttcacag ggccccgtct gcacaacttg gcttctgtcg 561
gcttccctan ccctgacttc ccaagcctta gtcacaccc tctctccac ccaggggtca 621
gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcac yaaaaaaaaa 681
aaa 684

<210> 250
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 75..482

<221> sig_peptide
<222> 75..128
<223> Von Heijne matrix
score 3.59999990463257
seq KMLISVAMLGAXA/GV

<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

<400> 250
aagtgagacc gcgcggcaac agcttgccgc tgcggggagc tcccgtgggc gctccgctgg 60
ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
-15 -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg 158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
-5 1 5 10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg 206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
15 20 25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg 254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
30 35 40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg 302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
45 50 55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac 350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
60 65 70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc 398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
75 80 85 90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg 446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
95 100 105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg 492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
110 115
tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaaggtccg caaggcgggc 552
cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc 612
cammcaaaaa aaaaah 628

<210> 251
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..631

<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
score 8
seq LTLIGCLVTGVES/KI

<221> polyA_signal
<222> 777..782

<221> polyA_site
<222> 801..812

<400> 251

```

aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                   Met Gln Asp
                                   -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
      -60                               -55                               -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
      -45                               -40                               -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
      -30                               -25                               -20                               -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
      -10                               -5                               1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
      5                               10                               15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
      20                               25                               30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
      35                               40                               45                               50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
      55                               60                               65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
      70                               75                               80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
      85                               90                               95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
      100                               105                               110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc      631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
      115                               120                               125
taaactggaa ctggaccag gatgctttgc ascaacgccc tagggtttgc agtgaatgtc      691
caaatgcctg tgtcatcttg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg      751
gaaaattaag ctatactttt aagaaaataa atatttccat ttaaatgtca amaaaaaaaa      811
ah                                                                813

```

<210> 252
 <211> 778
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..576

<221> sig_peptide
 <222> 154..360
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF

<221> polyA_signal
 <222> 737..742

<221> polyA_site

<222> 763..775

<400> 252

```
agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                               Met Thr Ser Gln Pro Val Pro
                               -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
                               -60                               -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
                               -45                               -40                               -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
                               -30                               -25                               -20                               -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                               -10                               -5                               1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
                               5                               10                               15
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg      462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
                               20                               25                               30
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct      510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
                               35                               40                               45                               50
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa      558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
                               55                               60                               65
tct tgt tct cct gtc ggg targataaca ggggttgctt rattttagat      606
Ser Cys Ser Pro Val Gly
                               70
caattttctta tcagactcaa ataaacattt cttttgaaaa tcatcttatt cttcacatta      666
tcatcttgag ctatgatgga aactagtgas ktctctccag gttaggcga aaaaaaaatc      726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaaah cc      778
```

<210> 253

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..897

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix

score 4.80000019073486

seq MMVLSLGIILASA/SF

<221> polyA_signal

<222> 1017..1022

<221> polyA_site

<222> 1044..1054

```

<400> 253
agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                               Met Thr Ser Gln Pro Val Pro
                               -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
                               -60 -55 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
                               -45 -40 -35
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
                               -30 -25 -20 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                               -10 -5 1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
                               5 10 15
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc      462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
                               20 25 30
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt      510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val
                               35 40 45 50
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg      558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu
                               55 60 65
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg      606
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu
                               70 75 80
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat      654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His
                               85 90 95
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct      702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala
                               100 105 110
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa      750
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa
                               115 120 125 130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc      798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
                               135 140 145
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm      846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly
                               150 155 160
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act      894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
                               165 170 175
tct taagaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata      947
Ser
tggaagagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agcttttaaa      1007
gtaatgaaca ttaaaaaaaa ccattatttc actgtcaaaa aaaaaaamcc nkt      1060

<210> 254
<211> 444
<212> DNA
<213> Homo sapiens

```

<220>
 <221> CDS
 <222> 146..292

<221> sig_peptide
 <222> 146..253
 <223> Von Heijne matrix
 score 5.5
 seq FTSMCILFHCLLS/FQ

<221> polyA_signal
 <222> 395..400

<221> polyA_site
 <222> 433..444

<400> 254
 aacttgggac aagaratcaa acttttaaaga tggctctaaag cccctcttaa aggtctgact 60
 gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120
 ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg 172
 Met Gln Val Pro His Leu Arg Val Trp
 -35 -30
 aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca 220
 Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
 -25 -20 -15
 agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa 268
 Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
 -10 -5 1 5
 aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt 322
 Lys Lys Arg Lys Leu Xaa Leu Phe
 10
 tattgttggt ttgtcttttc tgccttcaaa ctactccac aggccaaata tavctggctg 382
 cttctttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa 442
 aa 444

<210> 255
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..383

<221> sig_peptide
 <222> 126..167
 <223> Von Heijne matrix
 score 7.5
 seq VALNLILVPCCAA/WC

<221> polyA_signal
 <222> 726..731

<221> polyA_site
 <222> 743..754

<400> 255
 aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaacttct 60
 gtcggtttac actgcacatt gaatacaggt aactaattgg wwgagaggg gaggtcactc 120
 ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg 170


```

      10      15      20
ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc 350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser
      25      30      35
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg 398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu
      40      45      50
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac 446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn
      55      60      65
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc 494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg
      70      75      80      85
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct 547
Ser
ccatccttg gctgakanc ccctcccccac aactcagtgt ccttcaaata tacaatgacc 607
acccttcttc aaaaaaaaaa aa 629

<210> 257
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..411

<221> sig_peptide
<222> 49..96
<223> Von Heijne matrix
      score 10.1000003814697
      seq LVLTLCTLPLAVA/SA

<221> polyA_signal
<222> 732..737

<221> polyA_site
<222> 750..763

<400> 257
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg 57
                                     Met Glu Arg
                                     -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc 249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro
      40      45      50
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg 297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro
      55      60      65
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc 345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly
      70      75      80

```

cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg 393
 Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
 85 90 95
 ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga 441
 Gly Glu His Pro Xaa Xaa
 100 105
 agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tctactgaatt tacaaaraca 501
 gcaggaacrs ackggtgggg atgggcagct gttcrargcr atggggtkac tgcccttcct 561
 ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaatcgat 621
 acagtgtatg acaatgtcat atagtataac acaacataat gaatataacg tgtatattgc 681
 aacttaatat aatacgatgt aatataatgc tacataatac aacataatat aataaaatag 741
 aatgcaacac aaaaaaaaaa aacc 765

 <210> 258
 <211> 623
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 49..534

 <221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCTLPLAVA/SA

 <221> polyA_signal
 <222> 593..598

 <221> polyA_site
 <222> 612..623

 <400> 258
 aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgctc atg gag agg 57
 Met Glu Arg
 -15
 ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
 Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
 -10 -5 1
 tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
 Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
 5 10 15
 gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
 Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
 20 25 30 35
 caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
 Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
 40 45 50
 cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
 Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
 55 60 65
 atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc 345
 Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
 70 75 80
 agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
 Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
 85 90 95
 gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg 441
 Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser


```

100          105          110          115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
          120          125          130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
          135          140          145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa      594
taaactotca tgcccccaaa aaaaaaaaaa      623

<210> 259
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 86..415

<221> sig_peptide
<222> 86..145
<223> Von Heijne matrix
      score 9.80000019073486
      seq FTIGLTLLLGXQA/MP

<221> polyA_signal
<222> 540..545

<221> polyA_site
<222> 560..571

<400> 259
aaaaactcac ccagtgagtg tgagcattta agaagcatcc tctgccaaga ccaaaggaa      60
agaagaaaaa bggccaaaag ccaaaa atg ara ctg atg gta ctt gtt ttc acc      112
                        Met Xaa Leu Met Val Leu Val Phe Thr
                        -20                        -15
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc      160
Ile Gly Leu Thr Leu Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg
      -10      -5      1      5
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt      208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu
          10          15          20
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat      256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp
          25          30          35
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc      304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe
          40          45          50
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat      352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp
          55          60          65
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct      400
Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser
      70          75          80          85
ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt      455
Gly Glu His His Ser
          90
tctagtttct atagagtgca atagagcata gattctataa attcttactt gtctaagaaa      515
gtaaatctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa      571

<210> 260

```

<211> 612
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..268

<221> sig_peptide
<222> 56..100
<223> Von Heijne matrix
score 4.59999990463257
seq LLTHNLLSSHVRG/VG

<221> polyA_signal
<222> 584..589

<221> polyA_site
<222> 601..612

<400> 260
ctaatacgaaa aggggggattt tccggttccg gcctggcgag agtttgtgcg gcgac atg 58
Met
-15
aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg 106
Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
-10 -5 1
tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc 154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
5 10 15
cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg 202
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
20 25 30
gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag 250
Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
35 40 45 50
gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct 298
Val Pro Arg Arg Ala Gly
55
gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccc tgcagtgccc 358
ggaatctgga cgtatgttcc ccacagcccg cgggatcccc aacatgctgc tgagtgaaga 418
ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg 478
ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac 538
accaaacaca gtgtttttga gctcgggtatt atatattttt ttctcattaa aggtttaaaa 598
c caaaaaaaaa aaaa 612

<210> 261
<211> 539
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..328

<221> sig_peptide
<222> 32..103
<223> Von Heijne matrix
score 4.59999990463257
seq FFIFCSLNTLLLG/GV

<221> polyA_signal
<222> 508..513

<221> polyA_site
<222> 528..539

<400> 261
aacaactatc ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga 52
Met Lys Ser Ala Lys Leu Gly
-20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg 100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
-15 -10 -5
ggt ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat 148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
1 5 10 15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt 196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
20 25 30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc 244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
35 40 45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt 292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg
50 55 60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg 338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg
65 70 75
tgaactcatg aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcaractg 398
atttwgaaat ctttgttwta tttccmymak ggcgwktaag cttccatatg tttgctatgt 458
tcctgaccct agttttgtct ttccctggaaa ttaactgtat gakcattasa atgaaagagt 518
ctttctgtca aaaaaaaaaa a 539

<210> 262
<211> 964
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..527

<221> sig_peptide
<222> 21..95
<223> Von Heijne matrix
score 8.5
seq LKVLLLPLAPAAA/QD

<221> polyA_signal
<222> 921..926

<221> polyA_site
<222> 953..963

<400> 262
agggcgatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca 53
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
-25 -20 -15
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat 101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
-10 -5 1

```

tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac      149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr
      5      10      15
caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc      197
Gln Arg Phe Phe Ala Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr
      20      25      30
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag      245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln
      35      40      45      50
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc      293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys
      55      60      65
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act      341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr
      70      75      80
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt      389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys
      85      90      95
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa      437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu
      100      105      110
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc      485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Leu Pro His Leu Thr
      115      120      125      130
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc      527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala
      135      140
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgctccc tgggaggcca      587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca      647
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagagggaac aggaagagga      707
gggaaagcag gaagaaggac aggggactaa ggagggacgg gaggctgtgt ctcagctgca      767
gacagactca gagcccaagt ttactctga atctctatct tctaaccctt cctcttttgc      827
tcccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat      887
tcgatcagcc caggaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag      947
aaacccaaaaa aaaaaaak      964

<210> 263
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..647

<221> sig_peptide
<222> 147..374
<223> Von Heijne matrix
      score 3.5
      seq LASASELPLGSRP/AP

<221> polyA_site
<222> 668..681

<400> 263
aacttcctgt gagcccggcg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg      60
acgacttctc ctrgrarmcc ccgactgagg cggagacgaa ggtgctgcag gcgcgacggg      120
agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac      173
      Met Gly Asp Tyr Leu Leu Arg Gly Tyr
      -75      -70
cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa      221

```

Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln	
-65 -60 -55	
gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca	269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser	
-50 -45 -40	
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc	317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser	
-35 -30 -25 -20	
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc	365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly	
-15 -10 -5	
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag	413
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu	
1 5 10	
gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct	461
Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala	
15 20 25	
gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg	509
Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu	
30 35 40 45	
caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg	557
Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa	
50 55 60	
gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg	605
Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg	
65 70 75	
ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc	647
Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro	
80 85 90	
tgagaaaaac ctctagaaaa acaaaaaaaaaaaa aaaaccc	684
<210> 264	
<211> 693	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 262..471	
<221> sig_peptide	
<222> 262..306	
<223> Von Heijne matrix	
score 3.5	
seq LCFLLPHHRLQEA/RQ	
<221> polyA_signal	
<222> 663..668	
<221> polyA_site	
<222> 682..693	
<400> 264	
atttcgcggc gctcgcbgma cyhsgwtgtt cagcaccttc ggtccggttg aggttgtcaa	60
gtcggmccaa acagggttggtt tctctgcagt ttccaacatg gcagggmsgt ttaatagaca	120
tggataagaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggta	180
aacacaaaacg aaagaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat	240
cagtgcagtc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat	291
Met Ile Leu Cys Phe Leu Leu Pro His His	
-15 -10	
cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg	339

Gly	Glu	Thr	Met	Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro		
			80					85						90			
aat	att	gtt	tgt	agc	aaa	rat	tac	ttt	gtc	aca	gca	aac	tcc	aac	cta	493	
Asn	Ile	Val	Cys	Ser	Lys	Xaa	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu		
			95					100					105				
gtg	att	atc	aca	gca	ggt	gca	cgc	caa	raa	aag	gga	gaa	acg	cgc	ctt	541	
Val	Ile	Ile	Thr	Ala	Gly	Ala	Arg	Gln	Xaa	Lys	Gly	Glu	Thr	Arg	Leu		
			110					115					120				
aat	tta	stc	cag	cga	aat	gtg	gcc	atc	ttc	aag	tta	atg	att	tcc	agt	589	
Asn	Leu	Xaa	Gln	Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser		
			125				130						135				
att	gtc	cag	tac	agc	ccc	cac	tgc	aaa	ctg	att	att	gtt	tcc	aat	cca	637	
Ile	Val	Gln	Tyr	Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro		
							145						150		155		
gtg	gat	atc	tta	act	tat	gta	gct	tgg	aag	ttg	agt	gca	ttt	ccc	aaa	685	
Val	Asp	Ile	Leu	Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys		
							160						165		170		
aac	cgt	att	att	gga	agc	ggc	tgt	aat	ctg	ata	mhg	gct	cgt	ttt	cgt	733	
Asn	Arg	Ile	Ile	Gly	Ser	Gly	Cys	Asn	Leu	Ile	Xaa	Ala	Arg	Phe	Arg		
							175						180		185		
ttc	ttg	att	gga	caa	aag	ctt	ggt	atc	cat	tct	gaa	agc	tgc	cat	gga	781	
Phe	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly		
							190						200				
tgg	atc	ctc	gga	gag	cat	gga	gac	tca	agt	gtt	cct	gtg	tgg	agt	gga	829	
Trp	Ile	Leu	Gly	Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly		
							205						210		215		
gtg	aac	ata	gct	ggt	gtc	cct	ttg	aag	gat	ctg	aac	tct	gat	ata	gga	877	
Val	Asn	Ile	Ala	Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly		
							220						225		230		
act	gat	aaa	gat	cct	gag	caa	tgg	aaa	aat	gtc	cac	aaa	gaa	gtg	act	925	
Thr	Asp	Lys	Asp	Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr		
							240						245		250		
gca	act	gcc	tat	gag	att	att	aaa	atg	aaa	ggt	tat	act	tct	tgg	gcc	973	
Ala	Thr	Ala	Tyr	Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala		
							255						260		265		
att	ggc	cta	tct	gtg	gcc	gat	tta	aca	gaa	agt	att	ttg	aag	aat	ctt	1021	
Ile	Gly	Leu	Ser	Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu		
							270						275		280		
agg	aga	ata	cat	cca	gtt	tcc	acc	ata	act	aag	ggc	ctc	tat	gga	ata	1069	
Arg	Arg	Ile	His	Pro	Val	Ser	Thr	Ile	Thr	Lys	Gly	Leu	Tyr	Gly	Ile		
							285						290		295		
rat	gaa	gaa	gta	ttc	ctc	agt	att	cct	tgt	atc	ctg	gga	gag	aac	ggt	1117	
Xaa	Glu	Glu	Val	Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly		
							300						305		310		
att	acc	aac	ctt	ata	aag	ata	aag	ctg	acc	cct	gaa	gaa	gag	gcc	cat	1165	
Ile	Thr	Asn	Leu	Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His		
							320						325		330		
ctg	aaa	aaa	agt	gca	aaa	aca	ctc	tgg	gaa	att	cag	aat	aag	ctt	aag	1213	
Leu	Lys	Lys	Ser	Ala	Lys	Thr	Leu	Trp	Glu	Ile	Gln	Asn	Lys	Leu	Lys		
							335						340		345		
ctt	taa	agt	tggc	taaa	act	tacc	att	ccg	aaat	tatt	gaag	ag	at	cat	agata	1266	
Leu																	
cagg	att	tata	taac	gaa	att	ttga	ata	aaac	ttga	att	ccct	aaa	agat	gga	aac	agg	1326
tag	g	att	ttt	ctc	tata	ttt	att	tttag	ctt	ccag	ctc	tttt	att	gag	cat	ccac	1386
ctg	g	ac	gata	ctt	att	taca	att	cka	agt	att	ttt	tggt	cct	ctg	at	gag	1446
gcc	at	gtt	at	atat	at	gtag	tt	gr	mat	ttg	gtt	ccca	aaa	ag	tag	gat	1506
tgt	gtt	ctag	aa	att	ccg	ac	tctt	ttc	at	at	at	at	at	gc	tatt	ttct	1566
gtt	tata	cct	at	gtt	cat	tt	at	gt	ctg	tata	aaaa	ag	tag	at	gtt	ctt	1626
aata	aat	gt	ata	ca	aaaa	aaaa	aa	am	cm								1656

<211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..164

<221> sig_peptide
 <222> 48..89
 <223> Von Heijne matrix
 score 4
 seq YYMVCLFFRLIFS/EH

<221> polyA_signal
 <222> 482..487

<221> polyA_site
 <222> 505..517

<400> 266
 aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac 56
 Met Tyr Tyr
 atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att 104
 Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
 -10 -5 1 5
 ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca 152
 Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
 10 15 20
 aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt 204
 Thr Ser Ala Gly
 25
 taaaatgggtt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctgggtg 264
 atttatatgg ctcttcacaa ggtgttattt tggggatatca aggtatggat gcttaaatca 324
 gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg 384
 gtccttccac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct 444
 acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg 504
 aaaaaaaaaa aaa 517

<210> 267
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..334

<221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSYASSALSPCLT/AP

<221> polyA_signal
 <222> 355..360

<221> polyA_site
 <222> 392..405

<400> 267

09973360.101501


```

atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccttc tctgacctg      60
cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct      120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg      180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg      229
      Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
            -35                -30                -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
            -20                -15                -10
ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
            -5                1                5                10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a      405

```

```

<210> 268
<211> 1087
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 195..347

<221> sig_peptide
<222> 195..272
<223> Von Heijne matrix
      score 7.09999990463257
      seq LASLQWSLTLAWC/GS

```

```

<221> polyA_signal
<222> 1037..1042

```

```

<221> polyA_site
<222> 1071..1082

```

```

<400> 268
aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt      60
acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg      120
gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgacct agttgctggc      180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg      230
            Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg
            -25                -20                -15
cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc      278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser
            -10                -5                1
ggc agc cac tgg aca gag aga cca akt cag akt tca ccg tgg akt tct      326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser
            5                10                15
ctg tca gcg acc acc agg ggg tgatcacacg gaaggtgaac atccaggtcg      377
Leu Ser Ala Thr Thr Arg Gly
            20                25
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcattccctg      437
araatacacc agtgggggacg cccatcttca tcgtgaatgc cacagacccc gacttggggg      497
cagggggcag cgctcctctac tccttccagc cccctcccca attcttcgcc attgacagcg      557
cccgcggtat cktcacagtg atccgggagc tggactacga taccacrcmg gcctaccagc      617
tcwcggtcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaaacttg      677
ccatcatcat cacagatgtc caggacatgg accccatctt catcaacctg ccttacagca      737
ccaacatcta cgagcattct cctccgggca cgacggtgcg catcatcacc gccatagacc      797
aggataaagg acgtccccgg ggcattggct acaccatcgt ttcagggcat ctgtgtttac      857

```


ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg	641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu	
140 145 150	
gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc	689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile	
155 160 165 170	
cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg	737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly	
175 180 185	
acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta	785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu	
190 195 200	
ctg tac atc ctc arg ccc tct cgg cag ctg targgggtggg gaccgggggar	835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu	
205 210	
macctgcctg tagcccccac caraccctgc cccaagcacc atatggaaat aaagttcttt	895
cttacatcca aaaaaaaaaa a	916

<210> 270
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..513
 <221> sig_peptide
 <222> 52..231
 <223> Von Heijne matrix
 score 4
 seq LVRRTLVAALRA/WM

<221> polyA_signal
 <222> 553..558
 <221> polyA_site
 <222> 572..583

<400> 270	
aaggaaacag caaccagagg gagatgatca cctgaaccac tgctccaaac c atg ggc	57
	Met Gly
	-60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag	105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln	
-55 -50 -45	
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg	153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val	
-40 -35 -30	
aar gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc	201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg	
-25 -20 -15	
agg acc ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg	249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp	
-10 -5 1 5	
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg	297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu	
10 15 20	
ttr ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctc cag tcc	345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser	
25 30 35	

tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat	393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn	
40 45 50	
gct ctc tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act	441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr	
55 60 65 70	
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag	489
Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu	
75 80 85	
ttc cac att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg	543
Phe His Ile Glu Ile Leu Ser Ile	
90	
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa	583

<210> 271
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..438

 <221> sig_peptide
 <222> 172..354
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LLPCNLHCSWLHS/SP

<221> polyA_signal
 <222> 682..687

<221> polyA_site
 <222> 685..697

<400> 271	
agattggctg ggcagatggg ctgactggct gggcagatgg gtgggtgagt tccctctccc	60
cagagccatc ggccaggtac caaagctcag ctgtatggat tcccaacagg aggacctgcg	120
cttccctggg acccattggt gtactggatt aacaagcgac ggcgctacgg c atg aat	177
Met Asn	
-60	
gca gcc atc aac acg ggc cct gcc cct gct gtc acc aag act gag act	225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr	
-55 -50 -45	
gag gtc cag aat cca gat gtt ctg tgg gat ttg gac atc ccc gaa gcc	273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala	
-40 -35 -30	
agg agc cat gct gac caa gac agc aac ccc aag gcg gaa gcc ctg ctc	321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala Leu Leu	
-25 -20 -15	
ccc tgc aac ctg cac tgc agc tgg ctc cac agc agc ccc agg cca gat	369
Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg Pro Asp	
-10 -5 1 5	
ccc cat tcc cac ttc cca tct ktc agg agg tgc cct ttg ccc cac cct	417
Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro His Pro	
10 15 20	
tgt gca acc tac ccc ccs kgc tgaaccactc tgtctcctat cctttggcca	468
Cys Ala Thr Tyr Pro Pro Xaa	
25	
cctgtcctga aaggaatggt ctcttccatt cctcctgaa tctggcccag gaagaccata	528
gcttcaatgy caagcctttt ccttcaaaac tgtagcctcc tctcactgaa ggtgggagct	588

gcaggaatca ggtgcagagt aggaaatgga actaacctca ggaaggtggt attgacagag 648
gtcaggaccc acctggatgt catgctatga aacattaaaa gaaaaaaaaa 697

<210> 272
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..366

<221> sig_peptide
<222> 148..225
<223> Von Heijne matrix
score 5.5
seq LFTLLFLIMLVLK/LD

<221> polyA_signal
<222> 770..775

<221> polyA_site
<222> 792..803

<400> 272
aaatggggggg aaaagggcggg aaaaggacaa ggatccaaac tggcgaattt gctgatcttc 60
gcgctccctct ccgctttccg gccggcagcg ctgccagggt atatttcctt ttttccgatc 120
ctgcaacagc ctcttttaaac tgttttaa atg aga atg tcc ttg gct cag aga gta 174
Met Arg Met Ser Leu Ala Gln Arg Val
-25 -20
cta ctc acc tgg ctt ttc aca cta ctc ttc ttg atc atg ttg gtg ttg 222
Leu Leu Thr Trp Leu Phe Thr Leu Leu Phe Leu Ile Met Leu Val Leu
-15 -10 -5
aaa ctg gat gag aaa gca cct tgg aac tgg ttc ctc ata ttc att cca 270
Lys Leu Asp Glu Lys Ala Pro Trp Asn Trp Phe Leu Ile Phe Ile Pro
1 5 10 15
gtc tgg ata ttt gat act atc ctt ctt gtc ctg ctg att gtg aaa atg 318
Val Trp Ile Phe Asp Thr Ile Leu Leu Val Leu Leu Ile Val Lys Met
20 25 30
gct ggg cgg tgt aag tct ggc ttt gac ctc gac atg gat cac aca ata 366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile
35 40 45
taaaaaaaaa aacctggtac ctcatgtcac tgtkacttaa attasccttc tgccctgcac 426
tctgtgctaa actggaacag ttactacca tgaatctatc ctatgtcttc attcctttat 486
gggccttgct ggctggggct ttaacagaac tcggatataa tgtctttttt gtgaaagact 546
gacttctaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc 606
tgaatctgtc aagcttcaag aataccagag aactgagga aaataccaaa tgtagtttta 666
tactacttcc ataaaaacagg attggtgaat cacggacttc tagtcaacct acagcttaat 726
tattcagcat ttgagttatt gaaatcctta ttatctctat gtaaataaag tttgttttgg 786
acctcaaaaa aaaaaaa 803

<210> 273
<211> 823
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 175..336

<221> sig_peptide

<222> 175..276
 <223> Von Heijne matrix
 score 3.70000004768372
 seq SVLNVGHLLFSSA/CS

<221> polyA_site
 <222> 812..823

<400> 273
 aaggcgcgcg cgaccggcgg ctctttggcg cggattaggg ggtctcggcg agggagtcac 60
 caagcttttg tgtatgtgtt ggccggttct gaagtcttga agaagctctg ctgaggaaga 120
 ccaaagcagc actcgttgcc aattagggaa tggaccgttt gggttccttt agca atg 177
 Met
 atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg 225
 Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp
 -30 -25 -20
 agc ctt ata tca agt gtg ctg aat gtg ggc cac ctc ctt ttt tcc tct 273
 Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser
 -15 -10 -5
 gct tgc agt gtt tca ctc gag gct ttg agt aca aga aac atc aaa gcg 321
 Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala
 1 5 10 15
 atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac 376
 Ile Ile Leu Met Lys
 20
 tgctcaagaa raaatggccc ttttagaasc tgtgatggac tgtggctttg gaaattggca 436
 ggatgtagcc aatcaaattgt gcaccaarac caaggaggag tgtgagaagc actatatgaa 496
 gcatttcac aataaccyc tgtttgcac trscctgctg aacctgaaac aascagrgga 556
 agcaaaaact gctgacacag ccattccatt tcactctaca ratgaccctc cccgacckac 616
 ctttgactcc ttgctttctc gggacatggc cgggtacwtg ccmgctcgag cagatttcat 676
 tgaggaattt gacaattatg cagaatggga cttgagagac attgattttg ttgaagatga 736
 ctcggacatt ttacatgctc tgaagatggc tgtggtagat atctatcatt ccaggttaaa 796
 ggagagacaa agacgaaaaa aaaaaaa 823

<210> 274
 <211> 823
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 191..553

<221> sig_peptide
 <222> 191..304
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LAFLSCLAFLVLD/TQ

<221> polyA_signal
 <222> 766..771

<221> polyA_site
 <222> 804..817

<400> 274
 aactctgcag ggccctccaag gccaggtctc agggctggga ctcaagtctg aggcactggg 60
 gagccatgag gggctgtggc agggaggggc aggggtgtga aagactcccc tggggccatg 120
 gtggagatgt gctgaggctc tctccctgat cgtcttctcc tccctgctga ccgacggcta 180
 ccagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac 229
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn

```

                                -35                                -30
agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc      277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25                                -20                                -15                                -10
agc tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc      325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
                                -5                                1                                5
ggc acc cgc ttc aag aca gcc ttc cag ctc ctg gac ttc atc ctg gct      373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
                                10                                15                                20
gtt ctc tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac      421
Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
                                25                                30                                35
caa tgg cag cat tcg ccg ccc aaa gar kkc ctc ctg ggg agc agc agt      469
Gln Trp Gln His Ser Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
40                                45                                50                                55
gcc cag gca gcc atc ggc stt cac ctt ctt ctc cat cct tgt ctg gat      517
Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
                                60                                65                                70
att cca rgc cta cct ggc akk cca gga cct ccg aaa tgatgctcca      563
Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
                                75                                80
gtcccttaacm arcgcttcct ggatgaaggt ggcattggtgs kkaacaccct ccccttgccc      623
tctgccaaca gcctgtgaac atgcccacca ctggcccaaa cagcctgagt tatgctagct      683
ctgccctgtc cccctgtctg accgctcmaa agtccccccg gcttgctatg atgcctgaca      743
actaaatatc cttatccaaa tcaataaaga gagaatcctc cctccagaag ggtttctaaa      803
aacaataaaaa aaaahncctt      823

<210> 275
<211> 1112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..603

<221> sig_peptide
<222> 106..216
<223> Von Heijne matrix
score 4.30000019073486
seq LWEKLTLLSPGIA/VT

<221> polyA_site
<222> 1102..1112

<400> 275
agcgattgcg aatcctccgc tgaggtgatt tggatatccc tagaacgttg agggcacgag      60
tcgggtcctg agaccaggtc ctcagccagc agagccacgt tcctt atg agc acc gtg      117
                                Met Ser Thr Val
                                -35
ggt tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca      165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
                                -30                                -25                                -20
tgg gga ctc cgg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata      213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
                                -15                                -10                                -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg      261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
1                                5                                10                                15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac      309

```

```

Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe Val Lys Gly His
      20      25      30
ggt cca ggg ggc cag gca acc aac aaa acc agc aac tgc gtg gtg ctg      357
Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn Cys Val Val Leu
      35      40      45
aar mac atc ccc tca ggc atc gtt gta aag tgc cat cag aca aga tca      405
Lys Xaa Ile Pro Ser Gly Ile Val Lys Cys His Gln Thr Arg Ser
      50      55      60
gtt gat cag aac aga aag cta gct cgg aaa atc cta caa gag aaa gta      453
Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu Gln Glu Lys Val
      65      70      75
rat gtt ttc tac aat ggt gaa aac agt cct gtt cac aaa gaa aaa cga      501
Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg
      80      85      90      95
gaa gcg gcg aag aaa aaa car gaa agg aaa aaa aga gca aag gaa acc      549
Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg Ala Lys Glu Thr
      100      105      110
ctg gaa aaa aag aas ctm ctt aaa raa ctg tgg gag tca agt aaa aag      597
Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu Ser Ser Lys Lys
      115      120      125
gtc cac tgagaaaaga attagagatt ccaactgaca gaatctgcca gaagctccca      653
Val His
gggaataatg gtggcgagtt ccatcaccag cattattata gtgcttcaaa agaaatattt      713
ttgatgaact taaaagacaa caaatattatt taaatggtgc actaaactgt agtgaacaga      773
gacatgcacg attcaagaat aaaactcggc cgggcacggt ggacggtgcc tcacatctgt      833
aatcccagca ctttgggagg ccgaggcggg cggatcactt gaggtcagga gtttgagacc      893
agcctggcca acatggtgaa acccgtctc tactaaaaat acaaaaaatt agccaggcat      953
ggtggcgggc acctgtaatc ccagctactc gggaggccga ggcaggagaa ttgcgtgaac      1013
ctgggaggcg gaggttcag tgagctgaga tcgcgccact gcactcaagc ctgggcaaca      1073
cctgggtgac agagcaagac cccatcycaa aaaaaaaaaa      1112

<210> 276
<211> 1623
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..586

<221> sig_peptide
<222> 47..124
<223> Von Heijne matrix
      score 6.30000019073486
      seq GVGLVTLGLAVG/SY

<221> polyA_signal
<222> 1583..1588

<221> polyA_site
<222> 1614..1623

<400> 276
agggatctgt cggcttggtca ggtggtggag gaaaaggcgc tccgtc atg ggg atc      55
                                   Met Gly Ile
                                   -25
cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act      103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
      -20      -15      -10
ctg ctc ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg      151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg

```



```

-5      1      5
cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg      199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
10      15      20      25
cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc      247
Leu Asp Lys Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
30      35      40
ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc      295
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
45      50      55
tac ctc tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act      343
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
60      65      70
cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag      391
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys
75      80      85
gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aar atg      439
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met
90      95      100      105
tct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg      487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa
110      115      120
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att      535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile
125      130      135
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg      583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp
140      145      150
gaa tgattgccgg cgggacagga atcaccccaa tgctacagct gatccgggcc      636
Glu
atcctgaaag tccctgaaga tccaaccag tgctttctgc tttttgccaa ccagacagaa      696
aaggatatca tcttgcgga ggacttagag gaactgcagg cccgctatcc caatcgcttt      756
aagctctggt tcaacttgga tcatccccc aaagrttggg cctacagcaa gggctttgtg      816
actgccgacw tgatccggga acacctgccc gctccagggg atgatgtgct ggtactgctt      876
tgtggggccmc cccaatggt gcagctggcc tgccatccca acttggaaca actgggctac      936
tcacaaaaga tgcgattcac ctactgagca tctccagct tccctgggtgc tgttcgctgc      996
agttgttccc catcagtact caagcactak aagccttagr ktcctkctc cagagtttca      1056
ggttttttca gttrsatcka gagctgaaat ctggatagta cctgcaggaa caatattcct      1116
gtagccatgg aagagggcca aggcctagtc actccttgga tggcctccta aatctccccg      1176
tggcaacagg tccaggagag gcccatggag cagtctcttc catggagtaa gaaggaaggg      1236
agcatgtacg cttgggtccaa gattggctag ttccttgata gcatcttact ctcaccttct      1296
ttgtgtctgt gatgaaagga acagtctgtg caatgggttt tacttaaact tcaactgttca      1356
acctatgagc aaatctgtat gtgtgagtat aagttgagca tagcatactt ccagaggtgg      1416
tcttatggag atggcaagaa aggaggaaat gatttcttca gatctcaaag gagtctgaaa      1476
tatcatattt ctgtgtgtgt cdctctcagc ccctgcccad gctagaggga wacagctact      1536
gataatcgaa aactgctgtt tgtgggcarg aaccctggc tgtgcaaata atggggctga      1596
ngccctgtgt gatattgaaa aaaaaaa      1623

```

<210> 277
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..371

<221> sig_peptide
 <222> 99..290
 <223> Von Heijne matrix
 score 3.79999995231628

seq LFIVVCVICVTLN/FP

<221> polyA_signal

<222> 491..496

<221> polyA_site

<222> 513..524

<400> 277

attggattag tagaattgct tttgtcattc cattgttttc atatatttgt ttgggacatt 60
ttactttttt ctgttaacgc ttaccctagr aattagaa atg aca cca cgt att ctt 116
Met Thr Pro Arg Ile Leu

-60
agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg 164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg

-55 -50 -45
ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct 212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala

-40 -35 -30
gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att 260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile

-25 -20 -15
gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt 308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe

-10 -5 1 5
ctt tgt ctc tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt 356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val

10 15 20
cac att ccc tct ccc tararcacac tcccttgat ttcctcradt ggggtctgct 411
His Ile Pro Ser Pro

25
gcggtgaagc tttcccatTTt tatgtgcaga ttattttcag agggatatata gaattcaggc 471
agctgtttcg ttgttagcaca ttaaaaaatat tttcccactt caaaaaaaaa aaacc 526

<210> 278

<211> 989

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 44..814

<221> sig_peptide

<222> 44..112

<223> Von Heijne matrix

score 8.30000019073486

seq VRLLLXLLLLLLIA/LE

<221> polyA_site

<222> 978..989

<400> 278

aaatgtgtac acgcccagct tcttgctgt tactctccac agt atg cga aga ata 55
Met Arg Arg Ile

-20
tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg ctg ttg cta 103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Leu Leu Leu

-15 -10 -5
cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac 151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn

099330.1060

	1	5	10	
ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg				199
Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala				
15	20	25		
cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac				247
His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn				
30	35	40	45	
aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc				295
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr				
50	55	60		
agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac				343
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp				
65	70	75		
ctc agg atg ctc ctt tgt gac atc aaa ccc car ata aag acc agt gat				391
Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp				
80	85	90		
cct tcc act ctg caa gtc kar atk ttt tgt caa cgt gaa gca gaa cgg				439
Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg Glu Ala Glu Arg				
95	100	105		
tgc act ggt gca tcc tgg cag ttc gcc acc aat gga gag aaa tcc ctc				487
Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu				
110	115	120	125	
ctc ttt gac gca atg aac atg acc tgg aca gta att aat cat gaa gcc				535
Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile Asn His Glu Ala				
130	135	140		
agt wag atc aag gag aca tgg aag aaa gac aga ngg ctg gaa aak tat				583
Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa Leu Glu Xaa Tyr				
145	150	155		
ttc agg aag ctc tca aar gga gac tgc gat cac tgg ctc agg gaa ttc				631
Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp Leu Arg Glu Phe				
160	165	170		
tta ggg cac tgg gaa gca atg cca raa ccg ama gtg tcm cca rta aat				679
Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val Ser Pro Xaa Asn				
175	180	185		
gct tca raw atc cac tgg tct tct tct art cta cca raw ara tgg atc				727
Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro Xaa Xaa Trp Ile				
190	195	200	205	
atc ctg ggg gca ttc atc ctg tta vtt tta atg gga att gtt ctc atc				775
Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly Ile Val Leu Ile				
210	215	220		
tgt gtc tgg tgg caa aat ggc ara ara tcc acc tad arg tgataccacg				824
Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa Xaa				
225	230			
gcggcgcaaaa attgttcacc tgttggtctc gatcgctgac agccttggtt cccactgctg				884
tgtgttccct gagtcaagtg gagggcgagc ctgcaatgag cggaratcgc gcctctgcat				944
tccagtcttg gcaacagarc aagactccgt ctcaaaaaaa aaaaa				989

<210> 279

<211> 1017

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 3..581

<221> sig_peptide

<222> 3..182

<223> Von Heijne matrix

score 6.69999980926514

seq LWPFLTWINPALS/IC

<221> polyA_site

<222> 1006..1016

<400> 279

```
ac atg tgc cct agt ctg gaa gag gct ccc agt gtc aag ggg act ctg      47
Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu
-60 -55 -50
ccc tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc      95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile
-45 -40 -35 -30
cca cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc      143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val
-25 -20 -15
ctg tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac      191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp
-10 -5 1
ccc tta gga tcc tgc gga tgg cyw tgc cac acg gcc car gtc cct gcg      239
Pro Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala
5 10 15
ccc ctg car ttg cct act gcc tgt cct ccc ctc cca cat ggc acc cgg      287
Pro Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg
20 25 30 35
gct gta ggc ccc acg cca ggc ctc ctc cct gag gct gca gcc cca sgc      335
Ala Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa
40 45 50
acg tgc ggg gca ctg tcc tca cgc agc agg cac tgg tca tgt tcc att      383
Thr Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile
55 60 65
gtc arc tgc ctc cac ctg cac ara ctc ctg tct gtg gag acc aga arc      431
Val Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa
70 75 80
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt      479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val
85 90 95
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca      527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr
100 105 110 115
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct      575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro
120 125 130
tgg gaa tgagcctgtc ctctgtgtga aggagggggg ggttctcaaa ccaactgactc      631
Trp Glu
ttggtgctca ggagggggcct gctgctgtcc tgggcatggg gtgggtcattg ttcaagactg      691
aggcagactc agtcctttgaa aggggtgcaga ggccaggcgc ggtggctcac gcctgtaatt      751
ccagcacttt gggaggccaa ggtggacaga tcatgaggtc aggagttcga gaccagcctg      811
gccaatacgg tgaaaccgca tctctactaa rraatawcaw aaattagtcg ggcatgggtg      871
atgtgtgctt gtagtccag ctactcatga ggyctgaggc agaagaatca cctgaatctg      931
ggaggcagag gttgcagtga accaagatcg cagcactgta caccagcctg ggcgacagag      991
tgagactccg tctcaaaaaa aaaaam      1017
```

<210> 280

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 107..427

<221> sig_peptide

092360.101501

<222> 107..190
 <223> Von Heijne matrix
 score 3.79999995231628
 seq RFLSLSAADGSDG/SH

<221> polyA_signal
 <222> 499..504

<221> polyA_site
 <222> 516..529

<400> 280
 aaagtcagcg ctggagtcgg ctaggcggct ggaaacggcg gctgccgccg gtgactcagg 60
 gaggcgggag gccgmsggmg gagctcttcc tgcaggcggtg garacc atg gtg ctc 115
 Met Val Leu
 acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt 163
 Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
 -25 -20 -15 -10
 ctg tcc gca gcc gac ggc agc gat ggc agc cac gac agc tgg gac gtg 211
 Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val
 -5 1 5
 gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt 259
 Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
 10 15 20
 tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt 307
 Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe
 25 30 35
 gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt 355
 Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu
 40 45 50 55
 cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga 403
 Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg
 60 65 70
 aag tca cct gaa att tct tgg ggt taaccatctt tagttaaagt gaattttaat 457
 Lys Ser Pro Glu Ile Ser Trp Gly
 75
 ttaaattgacg ctttgctaatt tttaagtgtt aagcattttg cattaaaata ttcatataat 517
 aaaaaaaaaa aa 529

<210> 281
 <211> 1046
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..407

<221> sig_peptide
 <222> 45..83
 <223> Von Heijne matrix
 score 5.69999980926514
 seq MLVLRSAALTRALA/SR

<221> polyA_signal
 <222> 1008..1013

<221> polyA_site
 <222> 1032..1042

<400> 281

00936010501

```

aaaaggacac ggctggctgc ttttctcagc gccgaagccg cgcc atg ctc gtc ctc      56
                                   Met Leu Val Leu
                                   -10
aga agc gcc ctg act cgg gcg ctg gcc tca cgg acg ctg gcg cct cag      104
Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln
                                   -5      1      5
atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc      152
Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe
                                   10      15      20
tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc      200
Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe
                                   25      30      35
ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa      248
Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu
                                   40      45      50      55
ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg      296
Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val
                                   60      65      70
ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag      344
Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln
                                   75      80      85
aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca      392
Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro
                                   90      95      100
aat ttg gct ctc aat tgataaaca gatagtgaga ttacttatct ggtaccatgg      447
Asn Leu Ala Leu Asn
                                   105
tgcaaattag aaaaacctcc aaaagaagga gtctatgaac tggccacttt tcagatgaaa      507
cctggtgggc cagctctgtg ggggtgatgca tttaaaaggg cagttcatgc tcatgtcaat      567
ctaggctaca caaaactagt tggagtgttc cacacagagt acggagcact caacagagtt      627
catgttcttt ggtggaatga gagtgcagat agtcgtgcag ctgggagaca taagtcccat      687
gaggatccca gagttgtggc agctgttcgg gaaagtgtca actacctagt atctcagcag      747
aatatgcttc tgattcctac atcgttttca ccaactgaaat agttttctac tgaaatacaa      807
aacatttcat taactgctat aggatctgtc tgctaattgtt gcttaaattc tccaagagg      867
ttctcacttt tatttgaagg aggtggtaag ttaatttgct atgtttcttg cattatgaag      927
gctacatctg tgctttgtaa gtaccacttc aaaaaatakt tctgtttact ttctgcatgg      987
tatttcagtg tctgtcatac attaaaaata cttgtcactg tttyaaaaaa aaaaammcc      1046

<210> 282
<211> 880
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..332

<221> sig_peptide
<222> 201..251
<223> Von Heijne matrix
      score 7.80000019073486
      seq VLWLISFFTFDGDG/HG

<221> polyA_site
<222> 869..880

<400> 282
aattgctgat ggatcagtga gcctgtgttc atgccagtga gctgctgtgg ctgagatact      60
gatactttct ttccaaacag cataagaagt gattgancca caagtatact gaaggmargg      120
yhcccwsvr tyctggwtg amgagataaa tcaccagtca cagactatgc acccgactgc      180
tgctgttcag tccagggaaa atg aaa gtt gga gtg ctg tgg ctc att tct ttc      233

```

```

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe
-15 -10
ttc acc ttc act gac ggc cac ggt ggc ttc ctg ggg gtg agt tgg tgc 281
Phe Thr Phe Thr Asp Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys
-5 1 5 10
tat gtc tca tat ctc ttc tca act aac tct cct ctc tcg ttc cgg cgc 329
Tyr Val Ser Tyr Leu Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg
15 20 25
att tagaaccct cactctctag gggactgcaa ctgcataatt taatgtactt 382
Ile
gagatcagaa gtccctgagtt ctcgtttcaa cattaccaac attcactgtg tggccttgga 442
taagtragtc atttcatctc ttcggagctt agatgatcma actgcaarag gaggatcttt 502
gattamacta tcttagagat cttttccagt tcaacacatg ctgtactatg gcttctcgga 562
tgcagaaaaa tcacatggat ggacattagc aatccttara cactgtcttt cctgtctaca 622
ctcgcttgag tgatgckttc atctaggatc atggttttaa tattctctac atgctgatga 682
ctcccagctg tatagctcca tctcagaacc tctcccctgt ccacactcac atatccatta 742
cctacgtggt atttccagct gggaaatcca gcggaacctc ggnaacttca tttgnttcaa 802
aatcgnaacc caatccttct tgcctatctc agcaagtggg atcactatct ttccagctac 862
ttaggcaaaa aaaaaaaaa 880

<210> 283
<211> 1217
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 217..543

<221> sig_peptide
<222> 217..255
<223> Von Heijne matrix
score 6.40000009536743
seq MCLLTALVTQVIS/LR

<221> polyA_site
<222> 1206..1217

<400> 283
aatgccagtg tcagcttctc tccgaaaact gggtaatacag aaatgggtctt tattgggtgt 60
gaacactcga gctgagaaac attttaggat ctttgtgtct tttgtgatga tttgtttct 120
graagrwwga aasctgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca 180
gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg 234
Met Cys Leu Leu Thr Ala
-10
tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt 282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
-5 1 5
tta tgc aag agg aga tgg ccc tgg ngc ccc tcg ccc cgg atc tac tgc 330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
10 15 20 25
tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc 378
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala
30 35 40
cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg 426
Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro
45 50 55
ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc 474
Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu
60 65 70
cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt 522

```


Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala
70 75 80
tct cta aag aag tat ggc gtg ggg act tgt gga ccc tgt gga ttt tat 434
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr
85 90 95
ggc aca ttt gaa tgaaratgaa ggatcattga tttccttgtg tatggataat 486
Gly Thr Phe Glu
100
ccgggaacag gccaaactaaa tatttgatga atgtatgatt tcaaatacag tgaattccct 546
gggagtcatac aaaraagacg gcattttatg gttgttttta ttaagtgtat attcttttgc 606
cctgaaaatg ttattaaata attgtttagg ccgggcatgg tggctcatgc ctgtaatccc 666
agcactttca aaggctgagg caggcagatc acctgaggtc aggagttcaa aaccagcctg 726
gccaacatgc tgaaacctcg tctctactaa aaatacaaaa attagctggg cgtgggtggg 786
grtgctgtg gtcccagctr cgtgggaggc tgaggtggga gaattgcttc aacctgggag 846
gcgagggttg cagtgaagccg agatcatgcc actgcactcc agcctgggca acagagcaag 906
actgtctcaa aaataaataa ataaataaaa ttgtttaaat gaaaaaaaaa aaa 959

<210> 285
<211> 921
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..724

<221> sig_peptide
<222> 29..118
<223> Von Heijne matrix
score 3.90000009536743
seq VAHALSLPAESYG/NX

<221> polyA_signal
<222> 886..891

<221> polyA_site
<222> 910..920

<400> 285
aaggagccac gctttcggggg gttgcaag atg gcg gcc acc agt gga act gat 52
Met Ala Ala Thr Ser Gly Thr Asp
-30 -25
gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg ctt tct ctc 100
Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu
-20 -15 -10
cca gca gag tcg tat ggy aac grt yct gac att gag atg gct tgg gcc 148
Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala
-5 1 5 10
atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca 196
Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser
15 20 25
gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac 244
Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr
30 35 40
tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc 292
Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa
45 50 55
cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat 340
Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn
60 65 70
tct ttg cca ttg aaa ttg ctc gga acc ggg aag gct ata aca aag ctg 388

09978360.101501

```

Ser Leu Pro Leu Lys Leu Leu Gly Thr Gly Lys Ala Ile Thr Lys Leu
75      80      85      90
ttt ata tca gtg ttc agg aca aag aag gag aga aag gag tca aca atg      436
Phe Ile Ser Val Phe Arg Thr Lys Lys Glu Arg Lys Glu Ser Thr Met
      95      100      105
gag gag aaa aaa gag ctg aca gtg gag aag aag aga aca cca aga atg      484
Glu Glu Lys Lys Glu Leu Thr Val Glu Lys Lys Arg Thr Pro Arg Met
      110      115      120
gag gag aga aag gag ctg ata gtg gag aag aaa aag agg aag gaa tca      532
Glu Glu Arg Lys Glu Leu Ile Val Glu Lys Lys Lys Arg Lys Glu Ser
      125      130      135
aca gag aag aca aaa ctg aca aag gag gag aaa aag gga aag aag ctg      580
Thr Glu Lys Thr Lys Leu Thr Lys Glu Glu Lys Lys Gly Lys Lys Leu
      140      145      150
aca aag aaa tca aca aaa gtg gtg aaa aag cta tgt aag gta tac agg      628
Thr Lys Lys Ser Thr Lys Val Val Lys Lys Leu Cys Lys Val Tyr Arg
      155      160      165
gaa cag cac tct aga agc tat gac tca att gag act aca agt acc acg      676
Glu Gln His Ser Arg Ser Tyr Asp Ser Ile Glu Thr Thr Ser Thr Thr
      175      180      185
gtg cta ctt gca cag acc cct ttg gtt aaa tgt aaa ttc ttg tac aat      724
Val Leu Leu Ala Gln Thr Pro Leu Val Lys Cys Lys Phe Leu Tyr Asn
      190      195      200
tgaaggatac gcagaaggac atctttctag tctaacagtc aggagctgct ctgggtcattc      784
ccttgatatga actgggtctaa agactgttag tgggggtgtta gttgattttt cctgggtatac      844
tgtttcttgg ctgacactac tgggtcaagta agaaatttgt aaataaaattt ctttttggttc      904
ttattaamaa aaaaaaas      921

<210> 286
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 404..586

<221> sig_peptide
<222> 404..466
<223> Von Heijne matrix
      score 4.09999990463257
      seq SLMFFSMMATCTS/NV

<221> polyA_signal
<222> 1304..1309

<221> polyA_site
<222> 1334..1344

<400> 286
ataattttaat gcaaaatatac cttttatgaa tttcatgtta atattgtgaa atattaaaaat      60
aattccacaa tagttgagaa aaatgagcat ttttttccat ttttaaaaaa tgcataaaaa      120
agacaattttt aaaatcctgg gamccawatt tathtagaa tagctgttag taaaacatta      180
gaaaaggagt caggccatba gggtatttat nbnaatctct aagcaattag gntgaagtta      240
ttaagtcaag cctagaaaag ctgcctcctt gtaaggcttt catgacaatg tatagtaatc      300
brcagtgtcc aattcttcgc actcctcagg aatatcacta cctcagggtta cggtagacag      360
gctataattg atgatgatgt tcagataact gaagacacaa taa atg aca ttc aga      415
                                Met Thr Phe Arg
                                -20
cat cag gac aat tcc ctc atg ttc ttt tct atg atg gcc acc tgt acc      463
His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met Ala Thr Cys Thr

```

```

-15          -10          -5
agc aac gtg ggt ttc acc cac aca acg atg aac tgt tct ctt act tct      511
Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys Ser Leu Thr Ser
      1          5          10          15
cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg      559
Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
      20          25          30
tat gat aga aaa tcc aca atc aaa tct tgaaccaaata aacatatataa      606
Tyr Asp Arg Lys Ser Thr Ile Lys Ser
      35          40
attactaata ttttaagtgat ggaagacaca caaaaaactt aaaagcacga acaacctaac      666
ttgaaaaara attttaaaat atgattaacc tgaaraaaar araatcctaa ragccaaagc      726
tccttttttat ttagcttgga attttcctat tggttcctaa caaactgtcc caatgtcata      786
taaggaaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt      846
aagtagtaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt      906
attatctgta taaaaattgg cagggggaag ctaaaaggaa aggagattgg agatctcaat      966
tctatcatgg tgtatttcat acgcaaataca ragcatgcat tgttttttgt ttttggaaar     1026
avaarggaag tgtgtttctgc cccatgtttc cttccgtgtt tatagttcaa actctatata     1086
tacttcaggt attttttgtt tagcccttca ttataaatgg gcaggaaatt gtttatcaac     1146
ctagccagtt tattactagt gaccttgact tcagtatcct gagcattcct ttatatTTTT     1206
cttttattat cctgagtcctg taactaaaca attttgtcct caaatTTTTa tccaatatcc     1266
attgcaccac accaaataca gcttcttgat tttcaaaaat aaaaaggggg aaatacttac     1326
aacttgtaaa aaaaaaaaaa                                     1344

<210> 287
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 331..432

<221> sig_peptide
<222> 331..387
<223> Von Heijne matrix
      score 7
      seq AGLSSCLLPCLWL/ER

<221> polyA_signal
<222> 548..553

<221> polyA_site
<222> 573..585

<400> 287
aagcctaggt gtggcgcccc gaccggactt tcacttctgg ccagcccttt cccacactgg      60
gcgcggggass ggtgccagtc ttttaacaac ctctcgatgg gtcccacgaa gatgtttcca     120
gacccttgga atgccaaagt caagtttagc tatgtctcgc ggagaggccg gtggaagaag     180
caacgagaat gaagcacccc agttctctgc tgagcacatg ggcattctga ataaagattt     240
aatttccagc cttctcctga agctcggtat ggccacaaca cttaaattctg cccgaggaga     300
ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc      354
                                Met Phe Leu Lys Ser Gly Ala Gly
                                -15
ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat      402
Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
      -10          -5          1          5
ggc agg agg cca agc asc cat cct gga agg tgaaagcctc atactaagga      452
Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
      10          15
cgtcacaracag cgaaataara rctggggtcc ttgaccctgt aaasatctcc ctccccatcc      512

```

tggtctgtct gccttgactc ctttcatatg aaaaaaataa actttttaact tgcgtwaacc 572
 aaaaaaaaaa aaa 585

<210> 288
 <211> 914
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..703

<221> sig_peptide
 <222> 59..220
 <223> Von Heijne matrix
 score 5.09999990463257
 seq FLLSQMSQHQVHA/VQ

<221> polyA_signal
 <222> 886..891

<221> polyA_site
 <222> 903..914

<400> 288
 acaaatatca atgatgttta tgaatctagt gtgaaagtkt taatcacatc acaaggct 58
 atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak 106
 Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
 -50 -45 -40
 ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg 154
 Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
 -35 -30 -25
 tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca 202
 Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
 -20 -15 -10
 cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg 250
 Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
 -5 1 5 10
 caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc 298
 Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
 15 20 25
 abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg 346
 Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
 30 35 40
 cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc 394
 Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
 45 50 55
 agt ttc ctc gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac 442
 Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
 60 65 70
 aar ata aca aat gga gtc atc ttc gtg ggc cat tca aar aag ttc agt 490
 Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
 75 80 85 90
 gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta 538
 Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
 95 100 105
 tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct 586
 Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
 110 115 120
 aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat 634
 Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr

0936010501

125	130	135	
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata			682
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile			
140	145	150	
ata att agg aaa tgt ttt att tagcactttc aaactttttca cttttataaat			733
Ile Ile Arg Lys Cys Phe Ile			
155	160		
gacaagtgtt ttgaaatgca gaagttttatg tacagttgtg tatacagtat gacaagatgt			793
aaaataatat gtttttcatg cagttttaaaa tattactaac ttaagggttt ctatgtgctt			853
ttttaaatat tccttctttg atgttgacat caaataaagt atgtgggtta aaaaaaaaaa			913
a			914

<210> 289
 <211> 1161
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 672..752

<221> sig_peptide
 <222> 672..722
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LLYAHLSTSKRA/VV

<221> polyA_site
 <222> 1150..1161

<400> 289	
aagatatcac tgtcttgttt tcacttagat cctacttaca aagtgagggt tattaacaga	60
ataaagcctt cctttaaagc tttataataa tcatatttat taataatgct gttgtgcata	120
cttatagtat gcatatattc agcatatggt gcatgtsttc agaattacat aagatgaaat	180
ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctgggtg gaagaaatag	240
tattttcttct tctcagggtg tctccctgcc ttggcccctc ccagaagccc cggcttttaa	300
agtgaaaatg tttgaaacat gaaacatgtc tgtaggaagc atcagcatgg ccataagtgc	360
artgattttc atatatgctt ctgcccattt caaatatatt tttgacatga ataaatctaa	420
cagtatacar aataattcat gtaaraccct aacgtgtaca tgtgaaaaag catttctata	480
taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaattt	540
tcaaaataga gcsstgcaag ataactgcaa tcataccaaa aactatttga gtaaatggat	600
ttttaaagta atttttgttt aaaaaaattt atatttcaga agsagaaaaat gtcaaatgat	660
agtctttgtgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca	710
Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr	
-15 -10 -5	
tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt	752
Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe	
1 5 10	
tgaatgactt ggtcaagctg tgtgtaaaa atttaaccat aagtcaagta cagtgtacta	812
tgtttaataa agttacattt aatgcattta ttgcatatat gaatatatac atgaagaggc	872
tttatgtctt ctgggtatttg attttgaatg ttttttaagt cagtgggtgcc tttaggcaag	932
aactttcgaa attaatacatt ctttgtgttt tctgattttt caggtaacat gtacactatt	992
tagaaacat catagtttat tcaccttaaa aaattgattg tattatttta atatatcact	1052
tagatgggca tttcctataa ttaggatatt ccaaatagtt gctgaaatca attgtgccat	1112
tgaccaatgg atgcacttgg ttagccttaa ttttttyaaa aaaaaaaaaa	1161

<210> 290
 <211> 363
 <212> DNA
 <213> Homo sapiens


```

accttcttgt tatttatgct attctctttg tggctccatt cttctttcaa tcttctcagc      60
ttataaccgt ctttccctt atg cta agg ata gcc ctt aca ctc atc cca tct      112
               Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser
               -15               -10
atg ctg tca agg gct gct ggt tgg tgc tgg tac aag gag ccc act cag      160
Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln
-5               1               5               10
cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg aat aar aaa ggc      208
Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly
               15               20               25
aac gtt ttg cag ctt cca aat ttc tgaaraaact aatctcarat tggcagttaa      262
Asn Val Leu Gln Leu Pro Asn Phe
               30               35
agtcaaaatg ttgccaaata tttattcctt ttgcctaakt ttggctaccc ggttcaattg      322
ctttttatatt ttaatgtctt gactcttcar agttcgtacc tcaaaaraac aatgaraaca      382
tttgctttgc tttctgctga atccctaate tcaacaatct atacctggac tgtccagttc      442
tcctcctgtg ctatctttctc ttctatccaa gtaraatgta ygccaggarc tccttccctc      502
tarcaatttc tactaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat      562
ttattaattt gctaraatcc aktaaatacat tttggtagct ctggctgtgc tatcaataaa      622
aagatgaaag caaaaaaaaaaaa aaa      645

```

```

<210> 292
<211> 400
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 91..291

<221> sig_peptide
<222> 91..219
<223> Von Heijne matrix
      score 3.79999995231628
      seq LISVLYLIPKTLT/TN

```

```

<221> polyA_signal
<222> 367..372

```

```

<221> polyA_site
<222> 389..400

```

```

<400> 292
aacaaaaagga gagttttata attcacttta aaaggagatt tgatggtaaa gtttaaagat      60
taaaatattt tgttcttcaa ttacagagcg atg acc cca cag tat ctg cct cac      114
               Met Thr Pro Gln Tyr Leu Pro His
               -40
ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc      162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe
-35               -30               -25               -20
ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa      210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys
               -15               -10               -5
aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt      258
Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys
               1               5               10
atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga      311
Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln
               15               20
ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa      371
aattttattt cctaagyaaa aaaaaaaaaa      400

```

<210> 293
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 196..384

<221> sig_peptide
 <222> 196..240
 <223> Von Heijne matrix
 score 6.69999980926514
 seq ILSTVTALTTFARA/LD

<221> polyA_signal
 <222> 461..466

<221> polyA_site
 <222> 485..496

<400> 293
 aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcggtttag 60
 attagccgtg gcctaggccg tttaacgggg tgacacgagc htgcagggcc gagtccaagg 120
 cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag 180
 gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt 231
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
 -15 -10 -5
 gcc aga gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt 279
 Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
 1 5 10
 gag aag cac aga ctc gag aaa tgt agg gaa ctc gag agc agc cac tcg 327
 Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
 15 20 25
 gcc cca gga tca acc cag cac cga aga aaa aca acc aga aga aat tat 375
 Ala Pro Gly Ser Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
 30 35 40 45
 tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc 424
 Ser Ser Ala
 atatttaa at tggaagagtc aaattgasca ttattaaata aagcttggtt aatatgtctc 484
 aaacaaaaaa aa 496

<210> 294
 <211> 968
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..590

<221> sig_peptide
 <222> 54..227
 <223> Von Heijne matrix
 score 3.5
 seq GGILMGSFQGTIA/GQ

<221> polyA_site
 <222> 955..965


```

<400> 294
atatttgccc cttactttat cttgtgcctt gagaaattgc tggggagaga ggt atg      56
                                     Met
tcc act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc      104
Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser
      -55                    -50                    -45
cag cag cca ggt tcc ctc acc cca agc tca ccc act gtt ggg gag att      152
Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile
      -40                    -35                    -30
atc tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt      200
Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu
      -25                    -20                    -15                    -10
atg ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc      248
Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr
      -5                    1                    5
tcc att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct      296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala
      10                    15                    20
ggg ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag gdw atc tac      344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
      25                    30                    35
acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna      392
Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
      40                    45                    50                    55
dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat      440
Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
      60                    65                    70
gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc      488
Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
      75                    80                    85
cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc      536
Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
      90                    95                    100
cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa      584
Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
      105                    110                    115
gtc aat taacaattta tgcacaggta ctagttttat tgtattaccg ttccagggta      640
Val Asn
120
gctttgaaaa aagtatctca aaaaggcaac atggggccgag cgcagtggct cagcctgta      700
atcccagcac ttggggaggc caaggtgggc agatcgctg aggtctggag ttcaagacca      760
gcctggccaa cagggtgaaa cccgtctctt acaaaaatar gaaaattrgc caggtgtggt      820
ggcagacgtc tgrgtccca gctattcagg agactgaggc acgagaattc catgaacca      880
ggatgcgagg gttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag      940
tggtattctg tttcaaaaaa aaaaamcm      968

```

```

<210> 295
<211> 901
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 133..846

<221> sig_peptide
<222> 133..345
<223> Von Heijne matrix
      score 9.39999961853027
      seq VVSFLLLLLAGLIA/TY

```

<221> polyA_site

<222> 890..901

<400> 295

```
aagcagcttc caggatcctg agatccggag cagccggggt cggagcggct cctcaagagt      60
tactgatcta tnnatggcag agaaaaaaaa attgtgacca gagacgtgta gcaatgaaca      120
aggaacrtca ta atg rwn nnk ttc aca gac ccc tct tca gtg aat gaa aag      171
          Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
          -70                      -65                      -60

aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag      219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
          -55                      -50                      -45

ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg      267
Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu
          -40                      -35                      -30

aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct      315
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser
          -25                      -20                      -15

ttt tta ctg ctg ctt gct ggg ctt ata gct acg tat tat gtt gaa gga      363
Phe Leu Leu Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly
          -10                      -5                      1                      5

gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat      411
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr
          10                      15                      20

gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca      459
Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr
          25                      30                      35

ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt      507
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val
          40                      45                      50

aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc      555
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro
          55                      60                      65                      70

tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc      603
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr
          75                      80                      85

att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg      651
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met
          90                      95                      100

tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc      699
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala
          105                      110                      115

aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag      747
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln
          120                      125                      130

gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gta aga aca      795
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr
          135                      140                      145                      150

gtg ggg ata gaa aat aga aca ctt tac ttc ttc cta aag agg cta tta      843
Val Gly Ile Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu
          155                      160                      165

agg taaaattgtt agtagttact ctgaagaaga aaactgctaa agtaaaaaaa aaaaa      901
Arg
```

<210> 296

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..671

<221> sig_peptide

<222> 138..248

<223> Von Heijne matrix

score 3.5

seq LVFNFLILILT/IW

<221> polyA_signal

<222> 1319..1324

<221> polyA_site

<222> 1338..1347

<400> 296

aagaatgctt	gtgaagtagc	aactaaagtg	gcagtgtttc	ttctgaaatt	ctcaggcagt	60
cagactgtct	taggcaaadc	ttgataaaat	agcccttatc	caggttttta	tctaaggaat	120
cccaagaaga	ctgggga	atg gag aga	cag tca agg	ggt atg tca	gaa aag	170
		Met Glu Arg	Gln Ser Arg	Val Met Ser	Glu Lys	
		-35		-30		
gat gag tat	cag ttt caa	cat cag gga	gcg gtg gag	ctg ctt gtc	ttc	218
Asp Glu Tyr	Gln Phe Gln	His Gln Gly	Ala Val Glu	Leu Leu Val	Phe	
	-25	-20		-15		
aat ttt ttg	ctc atc ctt	acc att ttg	aca atc tgg	tta ttt aaa	aat	266
Asn Phe Leu	Leu Ile Leu	Thr Ile Leu	Thr Ile Trp	Leu Phe Lys	Asn	
	-10	-5	1	5		
cat cga ttc	cgc ttc ttg	cat gaa act	gga gga gca	atg gtg tat	ggc	314
His Arg Phe	Arg Phe Leu	His Glu Thr	Gly Gly Ala	Met Val Tyr	Gly	
	10	15	20			
ctt aya atg	gga cta att	tta csa tat	gct aca gca	cca act gat	att	362
Leu Xaa Met	Gly Leu Ile	Leu Xaa Tyr	Ala Thr Ala	Pro Thr Asp	Ile	
	25	30	35			
gaa agt ggr	rct gtc tat	gac tgt gta	aaa cta act	ttc agt cca	tca	410
Glu Ser Gly	Xaa Val Tyr	Asp Cys Val	Lys Leu Thr	Phe Ser Pro	Ser	
	40	45	50			
act ctg ctg	gtt aat atc	act gac caa	gtt tat gar	tat aaa tac	aar	458
Thr Leu Leu	Val Asn Ile	Thr Asp Gln	Val Tyr Glu	Tyr Lys Tyr	Lys	
	55	60	65	70		
aga gaa ata	agt cag cac	amc atc aat	cct cat cam	gga aat gct	ata	506
Arg Glu Ile	Ser Gln His	Xaa Ile Asn	Pro His Xaa	Gly Asn Ala	Ile	
	75	80	85			
ctt gaa aag	atg aca ttt	gat cca raa	atc ttc ttc	aat gtt tta	ctg	554
Leu Glu Lys	Met Thr Phe	Asp Pro Xaa	Ile Phe Phe	Asn Val Leu	Leu	
	90	95	100			
cca cca att	ata ttt cat	gca gga tat	agt cta aag	aag aga cac	ttt	602
Pro Pro Ile	Ile Phe His	Ala Gly Tyr	Ser Leu Lys	Lys Arg His	Phe	
	105	110	115			
ttt caa aac	tta gga tct	att tta acg	tat gcc ttc	ttg gga act	gcc	650
Phe Gln Asn	Leu Gly Ser	Ile Leu Thr	Tyr Ala Phe	Leu Gly Thr	Ala	
	120	125	130			
atc tcc tgc	atc gtc ata	ggg taagt	gacat tcggag	ctca agttg	caggt	701
Ile Ser Cys	Ile Val Ile	Gly				
	135	140				
ggctgtgggg	tcygtgatct	gtgtgaggga	tctaacactt	ccaggattct	tgctggckgg	761
gaaaattgtc	ttttttttar	tawatcacaw	atgtgtatgt	tttttcwgac	ttaattccac	821
ggcttckgam	aaatacaagg	cttcaaatac	aagcaacta	waggattgct	ggactttctc	881
tgtgagttct	ggacttctga	cttagggaat	gtggatcact	tgcccttgagt	tatgtgaagc	941
gcattgcatt	cttcttttag	tttgagtaat	scgatatgc	tcactgcatt	cttttttgc	1001
ttgtattgag	agaccttacc	tgtatttggc	aggagtgc	aaagtaactat	atgccaaagag	1061
ttttctttct	aaaggaaaagt	ttacaagaca	gcagtctgaa	acagatatgt	ccaaatatca	1121
acagagttgc	ttaatacagg	gatagctttt	cagttaatac	cctgtagaat	gcagactctt	1181

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 372..494

<221> sig_peptide
<222> 372..443
<223> Von Heijne matrix
score 5.30000019073486
seq RILLLHFYCLLR/SE

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..745

<400> 298
acatgaaatg tgcttgggtct gtgatctctt ggtcagatat ctgccttcca ggcgatcctt 60
tgaggttgtg taattcagct ggccctggct cctgggtccct gttactgagc tgggcagtcg 120
aaccgaaggc agatgagctc aagatcatgc cttgggaagc atgggtgctct aggggtgcct 180
ttttattcct ttcatgttat tatagactgt ttccaagttt atggtttagaa atggtaaagt 240
gggtctgggtg ttttgaggta gaaccagcc tagggcaaga tatgaactgt tcttgaggta 300
gaaatgtcta cagtcagttg tttcatctag cttgcatctt aaaacacaaa cccttcagtt 360
gctttcactt a atg cac aca ttt gcc aat gac aga ggg tta tac agg atc 410
Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile
-20 -15
ctt ctt tta cat ttc tat tgt ctg cta cgc tca tca gag tat att ttg 458
Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu
-10 -5 1 5
ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt 504
Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu
10 15
attgaaaadt aaktgccctt ccattccagg cctcctcata ttgtacttgt ttcctgccaa 564
atctggggga tcatttgtat ttttaactttg taatctatgg ctctgtactg ttgaaagstc 624
tcaattctgt ggggtctcct tagtatgtat gtgacttttc atgttgcaat atcacacgat 684
gggatggccc gacttttgcct cttaataaat aatctgaatg agtaagaraa aaaaaaaaaa 744
accc 748

<210> 299
<211> 1106
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 112..450

<221> sig_peptide
<222> 112..192
<223> Von Heijne matrix
score 7.19999980926514
seq SLLFFLLLEGGXT/EQ

<221> polyA_signal
<222> 1053..1058

<221> polyA_site
<222> 1095..1106

```

<400> 299
aagacctcgg aacgagagcg ccccggggag ctcgagcgcg gtgcacgcgt ggcavacgga 60
gaaggcavakk rcnnnnrctt gaaggttctg tcaccttttg cagtgggtcca a atg aga 117
                                     Met Arg

raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tcg ttg ttg ttc 165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
-25 -20 -15 -10
ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag 213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
-5 1 5
aca tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg 261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
10 15 20
cat cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc 309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
25 30 35
tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat 357
Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn
40 45 50 55
gtt cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc 405
Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg
60 65 70
tgc cca gaa gac tcc tta ccc cca gtg aac aat rwg gtg acc agc 450
Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr Ser
75 80 85
tagtcttgck agtacaatgg gacaacttac caacatggas agctgttcgt agctgrrggg 510
ctctttcaga atcggaacc cmatcaatgc acccagtgc gctgttcgga rggaaacktg 570
tattgtggtc tcaagacttg ccccaaatta acctgtgcct tcccagtcct tgttccarat 630
tctgtctgcc gggwtgagc argagatgga caactgtcat gggaacmttc tgatggtgat 690
atcttccggc aacctgcca cagagaagca agacattctt accaccgctc tcatatgat 750
cctccacca ggcgacaggc tggaggtctg tcccgctttc ctggggccag aagtcaccgg 810
ggagctctta tggattccca gcaagcatca ggaaccattg tgcaaattgt catcaataac 870
aaacacaagc atggacaagt gtgtgtttcc aatggaaaga cctattctca tggcgagtcc 930
tggcacccaa acctccgggc atttggcatt gtggagtgtg tgctatgtac ttgtaatgtc 990
accaagcaag agtgaagaa aatccactgc cccaatcgat acccctgcaa gtatcctcaa 1050
aaaatagacg gaaaatgctg caaggtgtgt ccaggtaaaa aagcaaaaaa aaaaaa 1106

<210> 300
<211> 1191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 117..866

<221> sig_peptide
<222> 117..170
<223> Von Heijne matrix
      score 10.6999998092651
      seq LILLALATGLVGG/ET

<221> polyA_signal
<222> 1159..1164

<221> polyA_site
<222> 1178..1190

<400> 300
aaaaccagc ctacctgctg tagctgccgc cactgccgtc tccgccgcca ctggwccccc 60

```

```

agagcbtnmag cccagagcc taggaacctg gggcccgtc ctccccctc caggcc atg 119
Met
agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 167
Arg Ile Leu Gln Leu Ile Leu Ala Leu Ala Thr Gly Leu Val Gly
-15 -10 -5
gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag 215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
1 5 10 15
ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg 263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
20 25 30
acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag 311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
35 40 45
ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag 359
Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
50 55 60
ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc 407
Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
65 70 75
ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg 455
Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
80 85 90 95
gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc 503
Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
100 105 110
acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc 551
Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
115 120 125
ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg 599
Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
130 135 140
cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc 647
Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
145 150 155
tac ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa 695
Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
160 165 170 175
ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt 743
Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
180 185 190
aac cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg 791
Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
195 200 205
atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac 839
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
210 215 220
tgg atc cag gag acg atg aag aac aat tagactggac ccaccacca 886
Trp Ile Gln Glu Thr Met Lys Asn Asn
225 230
cagcccatca cctccattt ccacttggtg tttggttcct gttcactctg ttaataagaa 946
accctaagcc aagacctct acgaacattc tttgggcctc ctggactaca ggagatgctg 1006
tcacttaata atcaacctgg ggttcgaaat cagtgaagacc tggattcaaa ttctgccttg 1066
aaatattgtg actctgggaa tgacaacacc tggtttggtc tctgttgat cccagcccc 1126
aaakwcagct cctggccata tatcaaggtt tcaataaata tttgctaaat gaawaaaaaa 1186
aaaac 1191

```

<210> 301

<211> 1070

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 13..465

<221> sig_peptide
 <222> 13..75
 <223> Von Heijne matrix
 score 3.90000009536743
 seq PVAVTAAVAPVLS/IN

<221> polyA_signal
 <222> 1035..1040

<221> polyA_site
 <222> 1060..1070

<400> 301
 agagtcggga aa atg gct gcg agt acc tcc atg gtc ccg gtg gct gtg acg 51
 Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
 -20 -15 -10
 gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg 99
 Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
 -5 1 5
 cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag 147
 Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
 10 15 20
 cgg ggc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct 195
 Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
 25 30 35 40
 ctc cct gca ttg cct ctg gcc gag ctg caa ccg cct ccg cct att aca 243
 Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
 45 50 55
 gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac 291
 Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
 60 65 70
 ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc 339
 Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
 75 80 85
 aat gca aga aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg 387
 Asn Ala Arg Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
 90 95 100
 agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt 435
 Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
 105 110 115 120
 aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact 485
 Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
 125 130
 gaatgaatgt actttataca tagcaataat aaaaaaaaga tatcataaat aaagttaaaa 545
 aggatggtaa aaaaaaaaaat attccttagga atgactaaca ggataagtaa caacctgatt 605
 atttattttac tttaggttat ataagggttct tcatgcctgt gaattaatat tattgtgttaa 665
 gaattaagtt aaaaagcctg ggctgacttt taaattttata aattcattta tcatgtttat 725
 agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca 785
 agtaaaccaa cttaatactg tattgaataa taagtacaat ttattatttt actttgaaac 845
 attatgaatt tactttccta cttttttctta gttgttatct atataaattg attaaaaaaa 905
 cattttatgt actttctcatt tcctagtagca gggttaggat cccttatttg aagtgccttg 965
 gaccaaaagt gtttcagatt tcagattttt ttcagatttt ggtatatattg cattataactt 1025
 actggttgaa ataaaaaatg ctgcagtgag tgtcaaaaaa aaaaa 1070

<210> 302
 <211> 1213

0998360.10501

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..718

<221> sig_peptide
<222> 2..76
<223> Von Heijne matrix
score 3.90000009536743
seq RVGLLLGGGGVYG/SR

<221> polyA_signal
<222> 1170..1175

<221> polyA_site
<222> 1203..1213

<400> 302
a atg ccc cgg aag cgg aag tgc gat ctt cgg gct gtc aga gtt ggt ctg 49
Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-25 -20 -15 -10
tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt 97
Leu Leu Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
-5 1 5
cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga vtg cag aga cga 145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
10 15 20
agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt 193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
25 30 35
atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg 241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
40 45 50 55
gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg gaa aaa 289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
60 65 70
cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag tca gct 337
Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
75 80 85
ggt cga caa cag aaa aar aaa ata gag aga cdd kaa kas amc ctg arg 385
Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
90 95 100
aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg ttt gct 433
Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
105 110 115
att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc ata ttt 481
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120 125 130 135
gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct tas rtc 529
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
140 145 150
sra gga ctg tct cat cga aat ctg ctg gga gat gac acc aca gac tgt 577
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
155 160 165
tcc ttc att ttc ctg taw att ctc tgt act atg tcg att cga cag aac 625
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
170 175 180
att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc aag cag 673
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln

09978360.101501

185	190	195	
gca ggt gga ttt ctt ggc cca cca cct cct tct	ggg aag ttc tct	718	
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser	Gly Lys Phe Ser		
200	205	210	
tgaactcaag aactctttat tttctakcat tctttctaga	cacacacaca tcagactggc	778	
aactgttttg tascaagagc cataggtagc cttackactt	gggcctcttt ctagttttga	838	
attatttcta agccttttgg gtatkattag agtgaaaatg	gcagccagca aacttgatag	898	
tgcttttggt cctagatgat ttttatcaaa taagtggatt	gattagttaa gttcaggtaa	958	
tgtttatgta atgaaaaaca aatagcatcc ttcttgtttc	atttacataa gtattttctg	1018	
tgggaccgac tctcaaggca ctgtgtatgc cctgcaagtt	ggctgtctat gagcatttag	1078	
agatttagaa gaaaaattta gtttgtttaa cccttgtaac	tgtttgtttt gttgttgttt	1138	
ttttttcaag ccaatacat gacataarat caataaarag	gccaaatfff tasctgtttt	1198	
atgtaaaaaa aaaaa		1213	
<210> 303			
<211> 978			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 86..709			
<221> sig_peptide			
<222> 86..361			
<223> Von Heijne matrix			
score 6.30000019073486			
seq LLMSILALIFIMG/NS			
<221> polyA_signal			
<222> 943..948			
<221> polyA_site			
<222> 963..973			
<400> 303			
aaagcatcct tccctaggac tgctgtaagc tttgagcctc	tagcaggaga catgcctcgg	60	
ggacgaaaga gtcggcgccg ccgta atg cga gag ccg	cag aag aga acc gca	112	
	Met Arg Glu Pro Gln Lys Arg Thr Ala		
	-90 -85		
aca atc gca aaa tyc rrg gcs tva gag ggc ctc	cga gac ccc tat ggc	160	
Thr Ile Ala Lys Xaa Xaa Ala Xaa Glu Gly Leu Arg Asp	Pro Tyr Gly		
	-80 -75 -70		
cgc ctc tgt ggt agc gag cac ccc cga aga cca	cct gag cgg ccc gag	208	
Arg Leu Cys Gly Ser Glu His Pro Arg Arg Pro	Pro Glu Arg Pro Glu		
	-65 -60 -55		
gaa gac ccg agc act cca gag gag gcc tct acc	acc cct gaa gaa gcc	256	
Glu Asp Pro Ser Thr Pro Glu Ala Ser Thr	Thr Pro Glu Glu Ala		
	-50 -45 -40		
tcg agc act gcc caa gca caa aag cct tca gtg	ccc cgg agc aat ttt	304	
Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val	Pro Arg Ser Asn Phe		
	-35 -30 -25 -20		
cag ggc acc aag aaa agt ctc ctg atg tct ata	tta gcg ctc atc ttc	352	
Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile	Leu Ala Leu Ile Phe		
	-15 -10 -5		
atc atg ggc aac agc gcc aag gaa gct ctg gtc	tgg aaa gtg ctg ggg	400	
Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val	Trp Lys Val Leu Gly		
	1 5 10		
aag tta gga atg cag cct gga cgt cas cac agc	atc ttt gga gat ccg	448	
Lys Leu Gly Met Gln Pro Gly Arg Xaa His Ser	Ile Phe Gly Asp Pro		
	15 20 25		

```

aag aar atc gtc aca gaa ran ttt gtg cgc aga ggg tac ctg att tat      496
Lys Lys Ile Val Thr Glu Xaa Phe Val Arg Arg Gly Tyr Leu Ile Tyr
30                      35                      40                      45
ara ccg gtg ccc cgt abc agt ccg gtg gag tat gas ttc ttc tgg ggg      544
Xaa Pro Val Pro Arg Xaa Ser Pro Val Glu Tyr Xaa Phe Phe Trp Gly
                      50                      55                      60
ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg      592
Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val
                      65                      70                      75
gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac      640
Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp
                      80                      85                      90
tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt      688
Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly
                      95                      100                      105
gct arg ggt tat tcc gcc cct taagtaratc tgaggcagac ccttgggggt      739
Ala Xaa Gly Tyr Ser Ala Pro
110                      115
gtaaaagaga gtcacaggta ccccaaggag tagatgccag ggtcctaagt tgaaaatgmt      799
gtcgattggg ggcgggggac actgtatttg atatttgta tcagtgatca ttgttcaact      859
gcgaaataga gtgtttgctt ttgataatgg aaaattgtat tcgtttttaa attccgtttg      919
ttgagaataa caatatgttt aaaaatataa ttgaacaaat tttaaaaaaaa aaamcccy      978

<210> 304
<211> 810
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..320

<221> sig_peptide
<222> 63..179
<223> Von Heijne matrix
      score 3.90000009536743
      seq VLAIGLLHIVLLS/IP

<221> polyA_signal
<222> 771..776

<221> polyA_site
<222> 799..810

<400> 304
agggaaccga tcccggggccg ttgatcttcg gccccacacg aacagcagag aggggcatca      60
gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg      107
      Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
                      -35                      -30                      -25
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt      155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
                      -20                      -15                      -10
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc      203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
                      -5                      1                      5
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc      251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
                      10                      15                      20
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag      299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
25                      30                      35                      40

```

gcg agg ctg cta acc cac tgg tgagcagatg gattatggggg tccagttcac 350
Ala Arg Leu Leu Thr His Trp

45

ggcctctcgg aaktttcttga ccatcacacc catcgtgctg tacttctctca ccagcttcta 410
cactaaktac raccaaattcc attttgtgct caacaccgtg tccctgatra gcgtgcttat 470
ccccaaagctg ccccgactcc acggaktccg gatttttggg atcaataakt actgaaaktg 530
cascccccttc ccctgcccag ggtggcaggg gaggggtagg gtaaaaaggca tktgctgcaa 590
chctgaaaac araaaraara rscctctgga cactgccara ratgggggtt gagcctctgg 650
cctaatttcc cccctcgctt cccccagtag ccaacttgga gtagcttgta ytggggttgg 710
ggtaggcccc ctgggctctg accttttctg aattttttga tcttttcctt ttgctttttg 770
aatararact ccatggagtt ggcatggaa aaaaaaaaaa 810

<210> 305

<211> 771

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 299..418

<221> sig_peptide

<222> 299..379

<223> Von Heijne matrix

score 3.59999990463257

seq LTLILLITPSPSPL/LF

<221> polyA_signal

<222> 739..744

<221> polyA_site

<222> 762..771

<400> 305

accttgggct ccaaattcta gtcataaag atgcaagtkt tgcaatttcc tataaatggt 60
taagaaaaga gcaagctgtc cagagagtga gaagtttgaa aagagaggtg cataagagag 120
aaatgatgtc catttgagcc ccaccacgga gggtatgtgg tcccaaaagg aatgatggcc 180
aagcaattaa tttttcctcc tagttcttag cttgcttctg cattgattgg ctttacacaa 240
ctggcattta gtctgcatta cacaaataga cactaattta tttggaacaa gcagcaaa 298
atg aga act tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act 346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
-25 -20 -15
ctg ctt cta atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt 394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
-10 -5 1 5
ctg tcc ctc aga tca gca atg tct tagccccctct cctctcttcc attccttctc 448
Leu Ser Leu Arg Ser Ala Met Ser

10

gttggtactc atttcttcta actttttaata aacatttagg tataatacat tacagtaagt 508
gctattttaga tacaaactta aaacatacta tatatttttaa ggatctaaga atcctttara 568
rrrggcacat gactgaagta cctcagctgc gcagcctgta accagttttt ttaatgtaaa 628
agtaaraatg ccagccttaa cctabccctg carataaaag ctaactttta ttaataccag 688
ccctgaataa tggcactaat ccacactctt ccttaragtg atgctggaaa aataaaatca 748
ggggcttcag attaaaaaaaa aaa 771

<210> 306

<211> 409

<212> DNA

<213> Homo sapiens

<220>


```

Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
-40 -35 -30
ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt 206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25 -20 -15 -10
ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc 254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
-5 1 5
tgc aca gag ttc atg gca gcc ctg gtg ckm tgg ctg gag ttg tct gaa 302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
10 15 20
gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa 350
Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
25 30 35
gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa 398
Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
40 45 50 55
gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa 446
Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
60 65 70
gga tgg gca cta tgacscceg gccagagtcc tcgtttgcc catgacctcc 498
Gly Trp Ala Leu
75
ctgctccaag tgcccttgga ggagctggat gtccttgaaa agatgttcct ggagagcctg 558
aaggaaatca aagaagagga atctgaaatg gccgaggcat ccraaaaaa aaaaa 613

<210> 308
<211> 986
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..638

<221> sig_peptide
<222> 12..263
<223> Von Heijne matrix
score 4.19999980926514
seq ITMLQMLALLGYG/LF

<221> polyA_signal
<222> 951..956

<221> polyA_site
<222> 975..985

<400> 308
accctatcaa g atg gtc aac ttc ccc cag aaa att gca ggt gaa ctc tat 50
Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr
-80 -75
gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg 98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
-70 -65 -60
atg aag acg tct gac act att atc cgg gag ggc acc ctg atg ggc aca 146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
-55 -50 -45 -40
gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att 194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
-35 -30 -25
tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg 242

```

```

Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
-20 -15 -10
ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc 290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
-5 1 5
atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg 338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
10 15 20 25
ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct 386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
30 35 40
cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct 434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
45 50 55
gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa 482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
60 65 70
dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc 530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
75 80 85
atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg 578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
90 95 100 105
ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc 626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
110 115 120
ctg cag tca cac tgacccacc tgaaattctt ggccagtcct ctttcccgca 678
Leu Gln Ser His
125
gctgcagaga ggargaasac tattaaagga cagtcctgat gacatgtttc gtagatgggg 738
tttgtagctg ccaactgagct gtagctgcgt aagtacctcc ttgatgcctg tcggcacttc 798
tgaaaggcac aaggccaaga actcctggcc aggactgcaa ggctctgcag ccaatgcaga 858
aaatgggtca gtccttttga gaaccctcc ccacctacc cttccttcct ctttatctct 918
ccacatttgt cttgctaaat atagacttgg taattaaaat gttgattgaa gtctggaaaa 978
aaaaaaat 986

<210> 309
<211> 1447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 282..389

<221> sig_peptide
<222> 282..332
<223> Von Heijne matrix
score 3.5
seq RWWCFHLQAEASA/HP

<221> polyA_signal
<222> 1413..1418

<221> polyA_site
<222> 1437..1447

<400> 309
ataataatat ctaaaaagct aaatttttaa taccagcttt acataaatga ttgtkgactc 60
tggtctgtkt ctgacacctt tccagaaaaa agtcaattgt tcagggtacac caaagaggaa 120
gaagagctgt ggaggccacc ctctacaaag ctttatagaa cttctggatc taactcacia 180

```

```

acaagcttcc agaagagact agagacctta ggccaggaga tgaaggagtt cagtagcaaa 240
gtcacacctg tccaattccc tgagctttgc tcaactcagct a atg gga tgg caa agg 296
                                         Met Gly Trp Gln Arg
                                         -15
tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa 344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
-10 -5 1
ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt 389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys
5 10 15
taacaaadga aaacgtcttg gtggcggcag casctttgct ctgagtgcct acaaagctaa 449
tgcttggtgc tagaaacatc atcattatta aacttcagaa aagcagcagc catgttcagt 509
caggctcatg ctgcctcact gcttaagtgc ctgcaggagc cgcttgccaa rctccccctc 569
ctacacctgg cacactgggg tctgcacaag gctttgtcaa ccaaaracag cttcccccw 629
ttgattgcct gtagactttg gagccaaraa acactctgtg tgactctaca cacacttcag 689
gtggtttggtg cttcaaagtc attgatgcaa cttgaaagga aacagtttta tgggtggaaat 749
gaactacat ttataacttc tgttttttta ttgagaaaat gattcacgaa kkccaaatca 809
gattgccagg aagaaatagg acgtgacggt actgggccct gtgattctcc cagcccttgc 869
agtccgctag gtgagaggaa aagctcttta cttccgcccc tggcagggac ttctgggtta 929
tgggagaaac cagagatggg aatgaggaaa atatgaacta cagcagaagc ccctgggcag 989
ctgtgatgga gcccctgaca ttactcttct tgcactctgc ctgccttctt tccctctgcg 1049
aggcagtggg gtgggattca gagtgcctag tctgctcact gggagaagaa gagttcctgc 1109
gcatgcaagc cctgctgtgt ggctgtcgtt tacatttggg aggtgtcctg tatgtctgta 1169
cgttggggac tgcctgtatt tggaagattt aaaaacctag catcctgttc tcaccctcta 1229
agctgcattg agaaatgact cgtctctgta tttgtattaa gccttaaacac ttttcttaag 1289
tgcattcggt gccaacattt tttagagctg taccaaaaca aaaagcctgt actcacatca 1349
camtgtcatt ttgataggag cgtttttgta tttttacaag gcagaatggg gtgtaacagt 1409
tgaattaaac ttagcaatca cgtgctcaaa aaaaaaaaa 1447

<210> 310
<211> 1641
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 208..339

<221> sig_peptide
<222> 208..294
<223> Von Heijne matrix
      score 5.59999990463257
      seq LFLQLLVSHIVC/AT

<221> polyA_site
<222> 1631..1641

<400> 310
agaaccgtga tgggaagatg gacaaggaag agaccaaaga ctggatcctt ccctcagact 60
atgatcatgc agaggcagaa gccaggcacc tgggtctatga atcagaccaa aacaaggatg 120
gcaagcttac caaggaggag atcgttgaca agtatgactt atttgttggc agccaggcca 180
cagatttttg ggaggcctta gtacggc atg atg agt tct gag cta cgg agg aac 234
                                         Met Met Ser Ser Glu Leu Arg Arg Asn
                                         -25
cct cat ttc ctc aaa agt aat tta ttt tta cag ctt ctg gtt tca cat 282
Pro His Phe Leu Lys Ser Asn Leu Phe Leu Gln Leu Leu Val Ser His
-20 -15 -10 -5
gaa att gtt tgc gct act gag act gtt act aca aac ttt tta aga cat 330
Glu Ile Val Cys Ala Thr Glu Thr Val Thr Thr Asn Phe Leu Arg His
1 5 10
gaa aag gcg taatgaaaac catcccgctc ccattcctcc tcctctctga 379

```


Glu Lys Ala

15

```

gggactggag ggaagccgtg cttctgagga acaactctaa ttagtacact tgtgtttgta 439
ratttacacw wtgtattatg tattaacatg gcgtgtttat ttttgtattt ttctctggtt 499
gggagtatka tatgaaggat caaratcctc aactcacaca tgtaracaaa cattascctc 559
ttactctttc tcaacccttt wtatgatttt aataattctc acttaactaa ttttgtaagc 619
ctgagatcaa taagaaatgt tcaggagaga ggaaagaaaa aaaatatatg ctccacaatt 679
tatatttaga gagagaacac ttagtcttgc ctgtcaaaaa gtccaacatt tcataggtag 739
tagggggccac atattacatt cagttgctat aggtccagca actgaacctg ccattacctg 799
ggcaaggaaa gatccctttg ctctaggaaa gcttggccca aattgatttt cttctttttc 859
cccctgtagg actgactggt ggctaatttt gtcaagcaca gctgtggtgg gaagagttag 919
ggccagtgtc ttgaaaatca atcaagtagt gaatgtgatc tctttgcara gctatagata 979
gaaacagctg gaaaactaaa ggaaaaatac aagtgttttc ggggcataca ttttttttct 1039
gggtgtgcat ctgttgaaat gctcaagact taattatttg ccttttgaaa tcaactgtaa 1099
tgcccccatc cggttcctct tcttcccarg tgtgccagg aattaatctt ggtttacta 1159
caattaaaat tcactccttt ccaatcatgt cattgaaagt gcctttaacg aaagaaatgg 1219
tcactgaatg ggaattctct taagaaaccc tgagattaaa aaaagactat ttggataact 1279
tataggaaaag cctagaacct ccagtagag tggggatttt tttcttcttc ctttctctt 1339
ttggacaata gttaaattag cagtattagt tatgagtttg gttgcagtgt tcttatcttg 1399
tgggctgatt tccaaaaacc acatgctgct gaatttacca gggatcctca tacctcacia 1459
tgcaaacacc ttactaccag gcctttttct gtgtccactg gagagcttga gctcacactc 1519
aaagatcaga ggacctacag agagggtctt ttggtttgag gaccatggct tacctttcct 1579
gcctttgacc catcacaccc catttctctc tctttccctc tccccgctgc caaaaaaaaa 1639
aa 1641

```

<210> 311

<211> 884

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..557

<221> sig_peptide

<222> 69..224

<223> Von Heijne matrix

score 4.69999980926514

seq LGLALGRLEGGSA/RH

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 870..883

<400> 311

```

attggctccg gatcgtgcgt gaggcggctt cgtgggcagc gagagtcaca gacaagacag 60
caagcagg atg gag cac tac cgg aaa gct ggc tct gta gag ctg cca gcg 110
      Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
      -50      -45      -40
cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc 158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
      -35      -30      -25
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg 206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
      -20      -15      -10
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg 254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
      -5      1      5      10
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc 302

```

```

Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
      15      20      25
ccg ggc ctg cac cag ctc acc aag cta ckt ttc ctt caa act gag gac 350
Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp
      30      35      40
agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg 398
Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val
      45      50      55
cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg 446
Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu
      60      65      70
gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg 494
Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu
      75      80      85      90
ggg tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct 542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala
      95      100      105
cra rac acc cga tgc tgaaaacctg ctgasccagc ctgttctccg ggcctraatg 597
Xaa Xaa Thr Arg Ser
      110
tctgggggtgc ttgtgccttt tctranaagc gttgtgaskg ctcaacatcc ccatcaaggt 657
ttgagtgccac aaaagtggac ctccctatca tgcttcccct tccctctagc atgtgggaag 717
ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt gctaaataag 777
ggcttcctct gccttctacc tacagtgcatt ttgaactgcc ttctgaaaga ggtccakgga 837
gggatttagg aaataaagtt tctacctatt tgaaaaaaaa aaaacac 884

<210> 312
<211> 729
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..325

<221> sig_peptide
<222> 134..274
<223> Von Heijne matrix
      score 5.90000009536743
      seq TWLGLLSFQNLHC/FP

<221> polyA_site
<222> 718..729

<400> 312
atcatttttct tatccctgct gatttcaaac cttcccatgg tttagaagca taacctgtaa 60
tgtaatgcaa gtcccttaac tccctgggtg ctaacattaa cttccttaag taataatcaa 120
tgaaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa 169
      Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
      -45      -40
tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt 217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
      -35      -30      -25      -20
ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac 265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
      -15      -10      -5
ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa 313
Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys
      1      5      10
gga ktc aac act tgagcctagg gtgggctaca acaaaaratt ctaatttacc 365
Gly Xaa Asn Thr

```



```

      110      115      120
gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct 638
Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro
      125      130      135
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac 686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp
      140      145      150
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag 731
Phe Ser Gly His Pro Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
      155      160      165
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaatattaca 791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc 851
tttctcttag ttataaaaa gaaaaagacc tcttgcatga aaatagtagc ttgcaggaag 911
aaattgtcat gctaaractg gaactagack taatgaaaca tcagagccag ctaaraaaa 971
aaaaatattt ggaggaaatt gaaagtgtgg aaaaaaaaaa aa 1013

<210> 314
<211> 973
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..693

<221> sig_peptide
<222> 46..90
<223> Von Heijne matrix
      score 7.59999990463257
      seq CVLVLAAAAGAVA/VF

<221> polyA_signal
<222> 937..942

<221> polyA_site
<222> 962..973

<400> 314
aagcggctgg tccccggaag ttggacgcat gcgccgtttc tctgc atg gtg tgc gtt 57
                                     Met Val Cys Val
                                     -15
ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg 105
Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
      -10      -5      1      5
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct 153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
      10      15      20
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc 201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
      25      30      35
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat 249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
      40      45      50
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt 297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe
      55      60      65
gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac 345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr
      70      75      80      85
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc 393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro

```

	90		95		100	
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta						441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu						
	105		110		115	
att cac agg gtg aag cca rat ttg gtg tgt aac gga cca gga aca						489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr						
	120		125		130	
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata						537
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile						
	135		140		145	
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs						585
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr						
	150		155		160	165
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att						633
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile						
	170		175		180	
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tcg gtg tac ctt						681
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu						
	185		190		195	
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa						733
Gly Arg Ile Val						
	200					
cagtartatg tactcaaatt ggggggaaaa aaaccctaca tgtttcttgt aaaggcgtct						793
gacagtcctg araattattg atggtaagga ataaaaaatg twcagatrac tcagtgaara						853
aactgaggct tctcttatga aacaaacatt gataaacgta actacyaaat gtttatgcct						913
ctgtaaacca aattttctttt ctarataaaa atatgtatta ctacctgcaa aaaaaaaaaa						973
<210>	315					
<211>	868					
<212>	DNA					
<213>	Homo sapiens					
<220>						
<221>	CDS					
<222>	126..527					
<221>	sig_peptide					
<222>	126..182					
<223>	Von Heijne matrix					
	score 3.90000009536743					
	seq ILFHGVFYAGGFA/IV					
<221>	polyA_signal					
<222>	834..839					
<221>	polyA_site					
<222>	856..867					
<400>	315					
actggaagaa ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt						60
gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc						120
gggtca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc						170
Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala						
	-15		-10		-5	
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg						218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg						
	1		5		10	
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag						266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu						
	15		20		25	
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc						314

Ala	Gln	Glu	Ala	Leu	Gly	Pro	Pro	Leu	Asn	Ile	His	Tyr	Leu	Lys	Leu		
30						35					40						
atc	gac	agg	gaa	aac	ttc	gtg	gac	att	gtt	rat	gcc	aag	ttg	aaa	att	362	
Ile	Asp	Arg	Glu	Asn	Phe	Val	Asp	Ile	Val	Xaa	Ala	Lys	Leu	Lys	Ile		
45					50					55				60			
cct	gtc	tct	gga	tcc	aaa	tca	gag	ggc	ctt	ctc	tac	gtc	cac	tca	tcc	410	
Pro	Val	Ser	Gly	Ser	Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser		
				65				70					75				
aga	ggg	ggc	ccc	ttt	cag	agg	tgg	cac	ctt	gac	gag	gtc	ttt	tta	gag	458	
Arg	Gly	Gly	Pro	Phe	Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu		
			80					85					90				
ctc	aag	gat	ggg	cag	cag	att	cct	gtg	ttc	aag	ctc	agt	ggg	gaa	aac	506	
Leu	Lys	Asp	Gly	Gln	Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn		
		95					100						105				
ggg	gat	gaa	gtg	aaa	aag	gag	tagagacgac	ccagaagacc	cagcttgctt							557	
Gly	Asp	Glu	Val	Lys	Lys	Glu											
110						115											
ctagtccatc	cttccctcat	ctctaccata	tggccactgg	ggggtgggcc	catctcagtg											617	
acagacactc	ctgcaaccca	gktttccagc	caccagtggg	atgatgggat	gtgccagcac											677	
atggtaattt	tgggtgtaatt	ctaacttggg	cacaacgaat	gctattttgtc	atttttaaac											737	
tgaatccgaa	agaaactcct	attataaatt	taagataatg	taatgtattt	gaaagtgtt											797	
tgtataaaaa	agcacatgat	aaaaggaatc	agaattaata	aaatgtttgt	tgatctttta											857	
aaaaaaaaaa	h															868	

<210> 316
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..320

<221> sig_peptide
 <222> 66..113
 <223> Von Heijne matrix
 score 3.5
 seq TALAAXTWLGWVG/VR

<221> polyA_signal
 <222> 490..495

<221> polyA_site
 <222> 508..519

<400> 316																	
aattagcgcg	taacgcasag	actgcttget	gcggcagaga	cgccagakgt	gcagctccag											60	
cagca	atg	gca	gtg	acg	gcg	ttg	gcg	gcg	mrg	acg	tgg	ctt	ggc	gtg	tgg	110	
	Met	Ala	Val	Thr	Ala	Leu	Ala	Ala	Xaa	Thr	Trp	Leu	Gly	Val	Trp		
	-15					-10						-5					
ggc	gtg	agg	acc	atg	caa	gcc	cga	ggc	ttc	ggc	tcg	gat	cag	tcc	gag	158	
Gly	Val	Arg	Thr	Met	Gln	Ala	Arg	Gly	Phe	Gly	Ser	Asp	Gln	Ser	Glu		
	1				5				10					15			
aat	gtc	gac	cgg	ggc	gcg	ggc	tcc	atc	cgg	gaa	gcc	ggg	ggg	gcc	ttc	206	
Asn	Val	Asp	Arg	Gly	Ala	Gly	Ser	Ile	Arg	Glu	Ala	Gly	Gly	Ala	Phe		
			20				25					30					
gga	aag	aga	gag	cag	gct	gaa	gag	gaa	cga	tat	ttc	cga	gca	cag	agt	254	
Gly	Lys	Arg	Glu	Gln	Ala	Glu	Glu	Arg	Tyr	Phe	Arg	Ala	Gln	Ser			
			35				40					45					
aca	gaa	caa	ctg	gca	rct	ttg	aaa	aaa	crc	cat	gaa	gaa	gar	atc	gtt	302	
Thr	Glu	Gln	Leu	Ala	Xaa	Leu	Lys	Lys	Xaa	His	Glu	Glu	Glu	Ile	Val		

50 55 60
cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca 350
His His Arg Glu Gly Asp

65
taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat 410
ggcacatgtc attgcccact tctgtgtaaa catggttctg gtttaactaa tatttgtctg 470
tgtgtacta acagattata ataaattgtc atcagtgtgaaa aaaaaaaaaa 519

<210> 317
<211> 1028
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..948

<221> sig_peptide
<222> 73..159
<223> Von Heijne matrix
score 4.40000009536743
seq IVLHLVLQGMVYT/EY

<221> polyA_site
<222> 1016..1028

<400> 317
agctttaaaag gcctggccag gggaggagca cagatatttt cctgtataat tccagaatgt 60
cttcagagag cc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac 111
Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
-25 -20
cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act 159
His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
-15 -10 -5
gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc 207
Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
1 5 10 15
ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt 255
Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe
20 25 30
ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca 303
Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala
35 40 45
aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt 351
Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe
50 55 60
cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga 399
Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg
65 70 75 80
tcc aas cac tgc akt gtg tgt aac tgg tgt gtg cac cgt ttc rac cat 447
Ser Xaa His Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His
85 90 95
cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc 495
His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa
100 105 110
ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc 543
Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala
115 120 125
att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta 591
Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu
130 135 140

099860 101501

```

tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac      639
Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp
145                      150                      155                      160
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc      687
Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val
                      165                      170                      175
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac      735
Phe Met Leu Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr
                      180                      185                      190
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag      783
Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu
                      195                      200                      205
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc      831
Trp Tyr Arg Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala
                      210                      215                      220
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat      879
Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His
225                      230                      235                      240
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt      927
Gly Leu Arg Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys
                      245                      250                      255
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta      978
His Glu Arg Lys Lys Gln Glu
                      260
gttcccgttt atttacacat gtggatcctc gttttccaaa aaaaaaaaaa      1028

```

```

<210> 318
<211> 452
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 69..434

<221> sig_peptide
<222> 69..236
<223> Von Heijne matrix
      score 4.90000009536743
      seq  FACVPGASPTTLA/FP

```

```

<221> polyA_signal
<222> 419..424

```

```

<221> polyA_site
<222> 441..452

```

```

<400> 318
acagcgtgas tcgcccgcc gaagaatatg aaaaagcaga gcganctcgg ttaaggga    60
gcgccgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cg    110
      Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg
      -55                      -50                      -45
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac    158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn
      -40                      -35                      -30
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt    206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys
      -25                      -20                      -15
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc    254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu
-10                      -5                      1                      5

```



```

aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
          10          15          20
ggt ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
          25          30          35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
          40          45          50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
55          60          65
aaaaaaaaa      452

<210> 319
<211> 875
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 628..804

<221> sig_peptide
<222> 628..711
<223> Von Heijne matrix
      score 4.19999980926514
      seq LMPVIPALQEAXA/GG

<221> polyA_site
<222> 864..875

<400> 319
aaagatggac accgcggagg aagacatatg tagagtgtgt cggtcagaag gaacacctga      60
gaaaccgctt tatcatcctt gtgtatgtac tggcagtatt aagttngtcc atcaagaatg      120
cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaattttatt ctccagatat gccttcacgg cttccaattc aagacatatatt      240
tgctggactg gttacaagta ttggcactgc aatacgaatg tggtttcatt atacacttgt      300
ggcctttgca tggttgggag ttgttcctct tacagcatgt gagtattcat gcctctgatt      360
ggagttatth aaacattgca taactactta atattataaa gcaatattgc atcatattat      420
tatttgactg atgttttagtt atttgatgtc agagtgtcat gtattaggaa agccttactt      480
araaratggt catcggaact aaraatgakt ttaacagggtc agttttttga gtgaatgtgg      540
gaaaraaacac agcatacaga atggctaacc atgaaagttc atgaaagcgt kgaaaaaatc      600
aatcaaatc ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa      654
                                Met Leu Xaa Leu Ser Arg Ala Thr Lys
                                -25                                -20

rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag      702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu
          -15          -10          -5
gcc gan gca ggc gga tca cga ggt cag gag ttt gaa act agc ctg gcc      750
Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala
          1          5          10
aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg      798
Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg
          15          20          25
ttg car tgaactgaga tcgcaccact gcaactccagc ttgggcaaca gagcaagact      854
Leu Gln
30
ttgtctcgca aaaaaaaaaa a      875

<210> 320

```

<211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

<221> polyA_signal
 <222> 496..501

<221> polyA_site
 <222> 521..531

<400> 320
 aagtggccat ggcggatata gcgactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaaatta 406
 Leu Gly Arg Gln Leu
 85
 ttttaratgt ctaactttat gttattgctc acgggtatatt gactgaattg ttgatttagg 466
 ataagtcaat tcctggaggg aaattaccaa ataaaatgat atgtatttct taccacaaaa 526
 aaaaa 531

<210> 321
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

09978360 "101501

<221> polyA_site

<222> 1233..1244

<400> 321

```
aagtggccat ggcggataca gcgactacag catcggcggc ggcggctagt gccgctagcg      60
cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga      111
      Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
      -10 -5 1
cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tgc acc ctc      159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
      5 10 15
gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc      207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
      20 25 30
tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
      35 40 45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
      50 55 60 65
cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
      70 75 80
ttg gga cgc caa ttg tagtcgggtct tctcttgccc aaccagacac tggcatccac      406
Leu Gly Arg Gln Leu
      85
tgtcttcttg cagtggctga accagagcca caatgcctgt gtcaactatg caaaccgcaa      466
tgcraccaag ccttcacctg catccaagtt catccaggga tacctgggag ctgtcatcag      526
cgccgtctcc attgctgtgg gccttatktc ctggttcaga aagccaacaa gttcacccca      586
gccacccgcc ttctcatcca gaggtttgtg ccgttccttg ctgtagccag tgccaatatc      646
tgcaatgtgg tctgtatgcg gtacggggag ctggaggaag ggattgatgt cctggacagc      706
gatggcaacc tcgtgggctc ctccaagatc gcagcccgac acgccctgct ggagacggcg      766
ctgacgcgag tggtcctgcc catgcccata ctgggtgctac ccccgatcgt catgtccatg      826
ctggagaaga cggctctcct gcaggcacgc ccccggtgc tctccctgt gcaaagcctc      886
gtgtgcctgg cagccttcgg cctggccctg ccgctggcca tcagcctctt cccgcaaatg      946
tcagagattg aaacatccca attagagccg gagatagccc aggccacgag cagccggaca      1006
gtggtgtaca acaaggggtt gtgagtgtgg tcagcggcct ggggacggag cactgtgcag      1066
ccggggagct gaggggcarg gccgtagact cagggtgcga cctgcaggga gcagcacgcc      1126
aaccccagca gtcctgggcc ccctgggaga gtgctcaacc tacagtggag ggagactgac      1186
ccattcacat tttaacatag gcaagaggag ttctaacaca ttcgtacaa aaaaaaaaa      1244
```

<210> 322

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..434

<221> sig_peptide

<222> 111..185

<223> Von Heijne matrix

score 3.90000009536743

seq WIAAVTIAAGTAA/IG

<221> polyA_site

<222> 618..631

<400> 322

```

aatcgcggag tcggtgcttt agtacccgc tggcaccttt actctcgccg gccgcgcgaa      60
cccgtttgag ctcggtatcc tagtgcacac gccttgcaag cgacggcgcc atg agt      116
                                         Met Ser
                                         -25
ctg act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc      164
Leu Thr Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
          -20                      -15                      -10
att gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt      212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
          -5                      1                      5
tat gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag      260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
10                      15                      20                      25
aaa gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga      308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly
          30                      35                      40
gat aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc      356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
          45                      50                      55
tgt gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg      404
Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val
          60                      65                      70
ggc cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc      454
Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
          75                      80
tgcaaatacag cttgtcgtga agttacctga ttgtttaatt araatagacta ccacctctgt      514
ctgattcacc ttcgctggat tctaaatgtg gtatatgtcm aactgcagct ttcacattta      574
tggcatttgt cttgttgaaa catcgtggtg cacatttgtt taaacaaaaa aaaaaaa      631

<210> 323
<211> 781
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 19..567

<221> sig_peptide
<222> 19..63
<223> Von Heijne matrix
      score 8.39999961853027
      seq AMWLLCVALAVLA/WG

<221> polyA_signal
<222> 749..754

<221> polyA_site
<222> 771..781

<400> 323
aagtgtctgct taccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                      Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                      -15                      -10                      -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
          1                      5                      10
atg aag agt cgg gag cag gga aga cgg ctg gga gcc gaa agc cgg acc      147
Met Lys Ser Arg Glu Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr
          15                      20                      25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      195

```

```

Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
 30          35          40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc    243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
 45          50          55          60
ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa    291
Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu
          65          70          75
ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg    339
Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met
          80          85          90
att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac    387
Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp
          95          100          105
aca rag cac gtg gcc ara gtc ctc ctt cag cac ata gaa gtg aat ggc    435
Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly
          110          115          120
atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc    483
Ile Asn Leu Val Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser
          125          130          135          140
aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att    531
Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile
          145          150          155
tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgtgt    577
Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu
          160          165
caatcagtgt gctccacct tcaccatctt cttcccctta ctctcacttc cgtcagtgtgt    637
tttatacaac tctcaaactt ttcttgagaga aggaggatat acatacataa tatgaaatgt    697
gtttgttctt cacagtcacc cgattttact gatattttatt tgcattttac caataaaaag    757
aaaatgcaag ctcaaaaaaa aaaa    781

<210> 324
<211> 931
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 19..312

<221> sig_peptide
<222> 19..63
<223> Von Heijne matrix
      score 8.39999961853027
      seq AMWLLCVALAVLA/WG

<221> polyA_signal
<222> 896..901

<221> polyA_site
<222> 921..931

<400> 324
aagtgtgtgt tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg    51
          Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
          -15          -10          -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga    99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
          1          5          10
atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc    147
Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr

```

15	20	25	
ctg ctg gtc ata gcg cac	cct gac gat gaa gcc	atg ttt ttt gct ccc	195
Leu Leu Val Ile Ala His	Pro Asp Asp Glu Ala	Met Phe Phe Ala Pro	
30	35	40	
aca gtg cta ggc ttg gcc	cgc cta agg cac tgg	gtg tac ctg ctt tgc	243
Thr Val Leu Gly Leu Ala	Arg Leu Arg His Trp	Val Tyr Leu Leu Cys	
45	50	55	60
ttc tct gca gtt ttc cgt	agg gag cta agt gaa	tac acc gaa rgt ctt	291
Phe Ser Ala Val Phe Arg	Arg Glu Leu Ser Glu	Tyr Thr Glu Xaa Leu	
65	70	75	
acc tct gaa ccc ctc ama	gcc tagggacagg arcggccggc	ttacctgggtg	342
Thr Ser Glu Pro Leu Xaa	Ala		
80			
ggttggggga cgtcggcagc	tcrcgtacta cgccagcagg	attganganc acagaaacag	402
ttgchsttgg ttgtattcag	tacctkcatt tccgttggga	actccaccwg tacttgttat	462
kctgtggaac ttttttttat	ttgtagaagg agcaagaata	ttgaccttac tatatagcac	522
acgaaacaat ctatgctgta	tcgtgcctgc tcaatcctta	aagttaactt ctaatgatag	582
taaaaracct tcctgctgcc	tttaaaatgc agcttgtgct	aktaacatgc atgtgtcaaa	642
ttgaaraatt agacatagat	gactaratar aaagtaattt	tgtaggtaat tttaragttc	702
aactccaccc agctttcakt	gaaggaacct ttcaaataat	aratTTTTgc ttaccatara	762
raaaaratca aatgacaaag	caaataattga ccattaagct	ggaatatggt gataattgaa	822
cagttgtata aatgaaktaa	ttgaattgta cacatacaat	gggtgaattt tatggcatgt	882
caaagtatac ctcaataaag	ctattttttt aaattgcmma	aaaaaaaaa	931
<210> 325			
<211> 849			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 64..612			
<221> sig_peptide			
<222> 64..234			
<223> Von Heijne matrix			
score 3.79999995231628			
seq QLWLVMFCGAGS/VT			
<221> polyA_site			
<222> 839..849			
<400> 325			
acatacgggc aagtttataa	gggtcgatcat gtcaaaacgg	gccagcttgc agccatcaag	60
ggt atg gat gtc aca ggg	gat gaa gag gaa gaa	atc aaa caa gaa att	108
Met Asp Val Thr Gly	Asp Glu Glu Glu Glu	Ile Lys Gln Glu Ile	
-55	-50	-45	
aac atg ttg aag aaa tat	tct cat cac cgg aat	att gct aca tac tat	156
Asn Met Leu Lys Lys Tyr	Ser His His Arg Asn	Ile Ala Thr Tyr Tyr	
-40	-35	-30	
ggt gct ttt atc aaa aag	aac cca cca ggc atg	gat gac caa ctt tgg	204
Gly Ala Phe Ile Lys Lys	Asn Pro Pro Gly Met	Asp Asp Gln Leu Trp	
-25	-20	-15	
ttg gtg atg gag ttt tgt	ggt gct ggc tct gtc	acc gac ctg atc aag	252
Leu Val Met Glu Phe Cys	Gly Ala Gly Ser Val	Thr Asp Leu Ile Lys	
-10	-5	1	5
aac aca aaa ggt aac acg	ttg aaa gag gag tgg	att gca tac atc tgc	300
Asn Thr Lys Gly Asn Thr	Leu Lys Glu Glu Trp	Ile Ala Tyr Ile Cys	
10	15	20	
msg gaa atc tta cgg ggg	ctg art cac ctg cac	cag cat aaa gtg att	348
Xaa Glu Ile Leu Arg Gly	Leu Xaa His Leu His	Gln His Lys Val Ile	


```

ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga      296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
      60      65      70
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc      344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val
      75      80      85
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc      392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
      90      95     100
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag      440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
     105     110     115     120
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata      488
Leu Trp Thr Ser Leu Tyr
      125
tcgaatatct agagctctaa acccccacat acttaaaagt ctaattgctg tcctgtgggt      548
tcattagtct gataggaaga tagggatttc ctgagtcaca gatgatattt tgaaggaaag      608
ctgcaataaa gccacaatga tttgaaaaaa aaaaaa      644

<210> 327
<211> 918
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..185

<221> sig_peptide
<222> 9..50
<223> Von Heijne matrix
      score 3.70000004768372
      seq AALVTVLFTGVRR/LH

<221> polyA_site
<222> 906..918

<400> 327
agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg      50
      Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg
           -10           -5
ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc      98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser
      1      5      10      15
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc      146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser
           20           25           30
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaaggcca      195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
           35           40           45
gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra kttgtactgc tgtcacagga      255
aatggacgct ggattacaas catggcasct caggcagcar aaktgtcagg aaraacaaag      315
gaagcaggaa aatgctctta aacccaaagg ggcttcactg aaaascccac ttccaaktca      375
ataaaaagca actcctgcct cccttcctca ccctgtctct ggatttcttt tctatcacct      435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaaar      495
agctgggacm ccaaraacaa gctgttarat cactgcctgg gaggcttggc ttartactct      555
catctctggt tccattccag ttcagctaag tcttgcttta aaatttttac ctccagctg      615
ggtgcggtgg ctccgcctg taatcccagc actttgggag gctgaggcgg gcagatcaca      675
agatcaggag ttcgagacca gcctggccaa cccagcctgg tcaacatggt gaaaccctgt      735
ccctactaaa gatacaaaaca attagccggg cgtgggtggg tgcgcttgta atcccagcta      795
ctcaggaggc tgaggcagga gaatcgctta aactcgggag gtagagggtg cagtgcagca      855

```


agggtcacacc attgcactcc aacctgggcg acagggcgag actctgtctc aaaaaaaaaa 915
 aaa 918

<210> 328
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..316

<221> sig_peptide
 <222> 14..121
 <223> Von Heijne matrix
 score 5.19999980926514
 seq PLRLLNLLILIEG/SV

<221> polyA_signal
 <222> 442..447

<221> polyA_site
 <222> 458..471

<400> 328
 attatataga gcc atg ggg cct tac aac gtg gca gtg cct tca gat gta 49
 Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
 -35 -30 -25
 tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta 97
 Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
 -20 -15 -10
 aat ctg ctc atc ctt att gag ggc agt gtc gtc ttc tat cag ctc tat 145
 Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
 -5 1 5
 tcc ttg ctg cgg tgc gag aag tgg aac cac aca ctt tcc atg gct ctc 193
 Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
 10 15 20
 atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt ctc cgg gac aga 241
 Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
 25 30 35 40
 wta kta tta ggc agg gca tac tcc tac cca ctc aac agt tat gaa ctc 289
 Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
 45 50 55
 aag gca aac twa gct gcc tct caw caa tgagggagaa ctcagataaa 336
 Lys Ala Asn Xaa Ala Ala Ser Xaa Gln
 60 65
 aatatttttca tacgtttctat ttttttcttg tgatttttat aaatatttaa gatattttat 396
 attttgtata ctattatggt ttgaaagtcg ggaagagtaa gggatattaa atgtatccgt 456
 aaacaaaaaa aaaaam 472

<210> 329
 <211> 1504
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..1092

<221> sig_peptide
 <222> 70..234

09978360 "101501

<223> Von Heijne matrix
 score 4.09999990463257
 seq AVCAALLASHPTA/EV

<221> polyA_signal
 <222> 1475..1480

<221> polyA_site
 <222> 1493..1504

<400> 329
 agaaatcgta ggacttccga aagcagcggc ggcgtttgct tcaactgcttg gaagtgtgag 60
 tgcgcgaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att 111
 Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
 -55 -50 -45
 ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat 159
 Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
 -40 -35 -30
 ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct 207
 Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
 -25 -20 -15 -10
 gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg 255
 Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
 -5 1 5
 gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag 303
 Asp Val Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys
 10 15 20
 caa agg ttt cag aga tta gac tgt ata tat cta aat gct ggg atc atg 351
 Gln Arg Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met
 25 30 35
 cct aat cca caa cta aat atc aaa gca ctt ttc ttt ggc ctc ttt tca 399
 Pro Asn Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser
 40 45 50 55
 aga aaa gtg att cat atg ttc tcc aca gct gaa ggc ctg ctg acc cag 447
 Arg Lys Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln
 60 65 70
 ggt gat aag atc act gct gat gga ctt cag gag gtg ttt gag acc aat 495
 Gly Asp Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn
 75 80 85
 gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctc ctc tgt 543
 Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys
 90 95 100
 cac agt gac aat cca tct cag ctc atc tgg aca tca tct cgc agt gca 591
 His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala
 105 110 115
 agg aaa tct aat ttc agc ctc gag gac ttc cag cac agc aaa ggc aag 639
 Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys
 120 125 130 135
 gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct 687
 Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala
 140 145 150
 ttg aac agg aac ttc aac cag cag ggt ctc tat tcc aat gtg gcc tgt 735
 Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys
 155 160 165
 cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct ccg ttt 783
 Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe
 170 175 180
 ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca 831
 Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala
 185 190 195
 aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg 879

```

Asn Ala Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp
200                205                210                215
ctt ttc cac caa aag cct gaa tct ctc aat cct ctg atc aaa tat ctg      927
Leu Phe His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu
                220                225                230
agt gcc acc act ggc ttt gga aga aat tac att atg acc cag aag atg      975
Ser Ala Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met
                235                240                245
gac cta gat gaa gac act gct gaa aaa ttt tat caa aag tta ctg gaa      1023
Asp Leu Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu
                250                255                260
ctg gaa aag cac att agg gtc act att caa aaa aca gat aat cag gcc      1071
Leu Glu Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala
                265                270                275
agg ctc agt ggc tca tgc cta taattccagc actttgggag gccaaaggcag      1122
Arg Leu Ser Gly Ser Cys Leu
280                285
aaggatcact tgagaccagg agttcaagac cagcctgaga aacatagtgga gcccttgtct      1182
ctacaaaaag aaataaaaat aatagctggg tgtgggtggca tgcgcatgta gtcccagcta      1242
ctcagaagga tgaggtggga ggatctcttg aggctgggag gcagagggtg cagtggagctg      1302
agattgtgcc actgcactcc agcctgggtg acagcgagac cctgtctcaa aatatgtata      1362
tatttaatat atatataaaa ccagagctga caatgacact ctggaacatt gcataccttc      1422
tgtacattct ggggtacatg gatttctact gagttggata atatgcattt gtaataaact      1482
atgaactatg aaaaaaaaaa aa                                1504

<210> 330
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 274..597

<221> sig_peptide
<222> 274..399
<223> Von Heijne matrix
      score 5.19999980926514
      seq LLFDLVCHEFCQS/DD

<221> polyA_signal
<222> 731..736

<221> polyA_site
<222> 754..765

<400> 330
accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttgtg cctgtatata ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatgtt tac atg cac att tta caa ctg ctt      294
                                Met His Ile Leu Gln Leu Leu
                                -40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                -30                -25                -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
-15                -10                -5
tgc cag tct gat gat cca gcc atc att ctt caa raa car aaa acr gtg      438

```

Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Xaa Gln Lys Thr Val
 1 5 10
 cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act 486
 Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
 15 20 25
 gag caa gak tat cta aar ata raa aaa gga gac ggt ggc tca ggg agt 534
 Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys Gly Asp Gly Gly Ser Gly Ser
 30 35 40 45
 aaa gga agg cca ktt gan caa aca gaa ktg ttc ctc tgc att tca aaa 582
 Lys Gly Arg Pro Xaa Xaa Gln Thr Glu Xaa Phe Leu Cys Ile Ser Lys
 50 55 60
 cct tct tcc ttt cta tagccctgtg gtggaagatt ttattaaaaat cctacgtgaa 637
 Pro Ser Ser Phe Leu
 65
 gttgataagg cgcttgctga tgacttgga aaaaacttcc caagtttgaa gggttcagact 697
 taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa 757
 aaaaaaaa 765

 <210> 331
 <211> 1041
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 230..469

 <221> sig_peptide
 <222> 230..307
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VLCTNQVLITARA/VP

 <221> polyA_signal
 <222> 1004..1009

 <221> polyA_site
 <222> 1027..1040

 <400> 331
 aacttccaag ttgtagtggt gttgttttca gcctgctgct gctgctgcta ttgcggctag 60
 gggaaccgtc gtggggaagg atggtgtgcg aaaaatgtga aaagaaactt ggtactgtta 120
 tcaactccaga tacatggaaa gatggtgcta ggaataccac agaaagtggg ggaagaaagc 180
 tgaatgaaaa taaagctttg acttcaaaaa aagccagaat tgatccata atg gaa gaa 238
 Met Glu Glu
 -25
 ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag 286
 Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
 -20 -15 -10
 gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga 334
 Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
 -5 1 5
 tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg 382
 Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
 10 15 20 25
 tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc 430
 Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
 30 35 40
 tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgkt 479
 Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
 45 50

099360 101501

taagataatt	aagtktaaac	cagaraat	ttt gattgttact	catttttgctc	tcatgkcta	539
aaacagcaac	agtgtacta	gtcttttg	gtt gtaa	atggtt	attttcctta	599
aaaaactaag	tggcaaattc	catgaaaata	tttctcagtt	ctgtatgcac	ttttatttaa	659
cattattcat	ataattctcc	ccccaccact	ttatttataa	atactgcaaa	aktgaraagg	719
agataataaa	tacttttgctc	tgaat	tttggc	atccaaagt	aacatttctc	779
cttgctggtg	tcatagttat	tagaatcagc	agcctcttaa	ctaattgcgg	tttcatagga	839
tatataaatg	tttcaagcca	ttattgctga	atggttcttt	agttattaac	ctagacccaa	899
atcaaagacc	agttggattt	atgatatttt	ttatttgctc	ttgcagccaa	agtgccagtt	959
tctttaatat	gtgaccaaga	acacaaggag	catccat	atg gccaaataaa	tacactgaat	1019
tttagaaaaa	caaaaaaaaa	ar				1041

<210> 332

<211> 1164

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 72..545

<221> sig_peptide

<222> 72..203

<223> Von Heijne matrix

score 5.5

seq ILFFTGWIMIDA/AV

<221> polyA_site

<222> 1151..1162

<400> 332

aaagtcggcg	tggacgtttg	aggaagctgg	gatacagcat	ttaatgaaaa	atttatgctt	60
aagaagtaaa	a	atg gca ggc ttc cta	gat aat ttt cgt tgg cca gaa tgt			110
		Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys				
		-40	-35			
gaa tgt att gac tgg agt gag aga aga aat gct gtg gca tct gtt gtc						158
Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val						
-30	-25	-20				
gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg att gat gca gct						206
Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala						
-15	-10	-5	1			
gtg gtg tat cct aag cca gaa cag ttg aac cat gcc ttt cac aca tgt						254
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys						
5	10	15				
ggt gta ttt tcc aca ttg gct ttc ttc atg ata aat gct gta tcc aat						302
Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn						
20	25	30				
gct cag gtg aga ggt gat agc tat gaa agc ggc tgt tta gga aga aca						350
Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr						
35	40	45				
ggt gct cga gtt tgg ctt ttc att ggt ttc atg ttg atg ttt ggg tca						398
Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser						
50	55	60	65			
ctt att gct tcc atg tgg att ctt ttt ggt gca tat gtt acc caa aat						446
Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn						
70	75	80				
act gat gtt tat ccg gga cta gct gtg ttt ttt caa aat gca ctt ata						494
Thr Asp Val Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile						
85	90	95				
ttt ttt agc act ctg atc tac aaa ttt gga aga acc gaa gag cta tgg						542
Phe Phe Ser Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp						
100	105	110				

```

acc tgagatcact tcttaagtca cattttcctt ttgttatatt ctgtttgtag      595
Thr
atagggttttt tatctctcag tacacattgc caaatggagt agattgtaca ttaaattgttt      655
tgttttcttta cattttttatg ttctgagttt tgaaatagtt ttatgaaatt tctttatttt      715
tcattgcata gactgttaat atgtatataa tacaagacta tatgaattgg ataattgagta      775
tcagttttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat      835
cttgtcattt tagaagtaac cactcttgct tctctggctg ggcacgggtg ctcattgctg      895
taatcccagc actttgggag gccgaggcgg gccgattgct tgagggtcaag tgtttgagac      955
cagcctggcc aacatggcga aaccccatct actaaaaata caaaaattag ccaggcatgg     1015
tggtgggtgc ctgtaatccc aactacctag gaggctgagg caggagaatc gcttgaaccc     1075
ggggggcaga gggtgyagtg agctgagttt gcgccactgc actctagcct ggggggagaaa     1135
gtgaaactcc ctctcaaaaa aaaaaaamc                                     1164

```

```

<210> 333
<211> 1250
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 36..425

```

```

<221> sig_peptide
<222> 36..119
<223> Von Heijne matrix
      score 11.6000003814697
      seq LLLLVQLLRFLRA/DG

```

```

<221> polyA_signal
<222> 1215..1220

```

```

<221> polyA_site
<222> 1240..1250

```

```

<400> 333
attttcttccc cccgagctgg gcgtgcgcgg ccgca atg aac tgg gag ctg ctg      53
                               Met Asn Trp Glu Leu Leu
                               -25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg gtg cag ctg      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Val Gln Leu
                               -20                               -10
ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta cta tgg gcc gag      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
                               -5                               1                               5                               10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
                               15                               20                               25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
                               30                               35                               40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag      293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
                               45                               50                               55
ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc aat tta aaa gaa      341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
                               60                               65                               70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc act ggt tcc cat      389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
75                               80                               85                               90
gaa agc ggc tac caa agc tgt tct cca gga att tgg tagaatcgac      435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp

```

	95		100			
attctcgtgca	acaatgtgga	aatgtcccag	cgttctctgt	gcatggatac	caacttggat	495
gtctacagaa	agctaagtga	agcttaacta	cttagggacg	gtgtccttga	caaaatgtgk	555
kctgcctcac	atgacgaga	ngaarcaagg	aaagattggt	actgtgaata	gcatcctggg	615
tatcatatct	gtacctcttt	ccattggata	ctgtgctagc	aagcatgctc	tccgggggktk	675
ktttaatggc	cttcracag	aacttgccac	ataccargt	ataatagttt	ctaactttg	735
cccaggacct	gtgcaatcaa	atattgtgga	aaattcccta	gctggagaag	tcacaaagac	795
tataggcaat	aatggagacc	agtcccacaa	gatgacaacc	agtcgttgtg	tgcggtgat	855
gttaatcagc	atggccaatg	atgtgaaaga	agtttggatc	tcagaacaac	ctttcttggt	915
agtaacatat	ttgtggcaat	acatgccaac	ctgggcctgg	tggtataacca	acaagatggg	975
gaagaaaagg	attgagaact	ttaagagtgg	tgtggatgca	gactcttctt	attttaaaat	1035
ctttaagaca	aaacatgact	gaaaagagca	cctgtacttt	tcaagccact	ggagggagaa	1095
atggaaaaca	tgaaaacagc	aatcttctta	tgcttctgaa	taatcaaaga	ctaatttgtg	1155
attttacttt	ttaatatgata	tgactttgct	tccaacatgg	aatgaaataa	aaaataaata	1215
ataaaagatt	gccatgaatc	ttgcaaaaaa	aaaaa			1250

<210> 334
 <211> 947
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 155..751

<221> sig_peptide
 <222> 155..340
 <223> Von Heijne matrix
 score 3.70000004768372
 seq SILGIISVPLSIG/YC

<221> polyA_signal
 <222> 912..917

<221> polyA_site
 <222> 937..947

<400> 334
 agtgaagaaga agatgcctag agaattggcaa tttaaaagaa aaagatatatac ttgttttgcc 60
 ccttgacctg accgacactg gttcccatga agcggctacc aaagctgttc tccaggagtt 120
 tggtagaatc gacattctgg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc 175
 Met Ser Gln Arg Ser Leu Cys
 -60
 atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac 223
 Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
 -55 -50 -45 -40
 tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag 271
 Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
 -35 -30 -25
 agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata 319
 Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
 -20 -15 -10
 tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg 367
 Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg
 -5 1 5
 ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata 415
 Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile
 10 15 20 25
 ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa 463
 Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu
 30 35 40

aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac	511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn	
45 50 55	
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc	559
Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile	
60 65 70	
agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct ttc	607
Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro Phe	
75 80 85	
ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg tgg	655
Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp Trp	
90 95 100 105	
ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt ggt	703
Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser Gly	
110 115 120	
gtg gat gcm rac tct tct tat ttt aaa atc ttt aag aca aaa cat gac	751
Val Asp Ala Xaa Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His Asp	
125 130 135	
tgaaaaganc acctgtactt ttcaagccac tggagggaga aatggaaaac atgaaaacag	811
caatcttctt atgcttctga ataatacaaag actaatttgt gattttactt tttaatagat	871
atgacttttgc ttccaacatg grrtgaaata aaaaataaat aataaaaagat tgccatgrrt	931
cttgcaaaaa aaaaaa	947

<210> 335

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..585

<221> sig_peptide

<222> 46..120

<223> Von Heijne matrix

score 6.30000019073486

seq AFSLSVMAALTFG/CF

<221> polyA_signal

<222> 584..589

<221> polyA_site

<222> 606..619

<400> 335

aactgggtgt gcgtrtggag tccggactcg tgggagacga tcgcg atg aac acg gtg	57
Met Asn Thr Val	
-25	
ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg gcs	105
Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met Ala	
-20 -15 -10	
gcg ctc acc ttc ggc tgc ttc atc ayy acc gcc ttc aaa gac agg agc	153
Ala Leu Thr Phe Gly Cys Phe Ile Xaa Thr Ala Phe Lys Asp Arg Ser	
-5 1 5 10	
gtc ccg gtg cgg ctg cac gtc tcg cga atc atg cta aaa aat gta gaa	201
Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val Glu	
15 20 25	
gat ttc act gga cct aga gaa aga agt gat ctg gga ttt atc aca ttt	249
Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly Phe Ile Thr Phe	
30 35 40	
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag	297


```

Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp Asn Val Lys Gln
 45          50          55
ttg ttt ctt tat tta tca gca gaa tat tca aca aaa aat aat gct ctg      345
Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu
60          65          70          75
aac caa ktt gtc cta tgg gac aag att gtt ttg aga ggt gat aat ccg      393
Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro
      80          85          90
aag ctg ctg ctg aaa gat atg aaa aca aaa tat ttt ttc ttt gac gat      441
Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp
      95          100          105
gga aat ggt ctc wag gga aac agg aat gtc act ttg acc ctg tct tgg      489
Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp
      110          115          120
aac gtc gta cca aat gct gga att cta cct ctt gtg aca gga tca gga      537
Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly
      125          130          135
cac gta tct gtc cca ttt cca gat aca tat gaa ata acg aag agt tat      585
His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr
      140          145          150          155
taaattattc tgaatttgaa acaaaaaaaaaaaa aaaahm      621

<210> 336
<211> 699
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..568

<220>
<221> sig_peptide
<222> 35..100
<223> Von Heijne matrix
      score 10.7
      seq LLTLALLGGPTWA/GK

<220>
<221> polyA_signal
<222> 667..672

<220>
<221> polyA_site
<222> 685..699

<400> 336
aaccagacgc ccagtcacag gcgagagccc tggg atg cac cgg cca gag gcc atg      55
                        Met His Arg Pro Glu Ala Met
                        -20
ctg ctg ctg ctc acg ctt gcc ctc ctg ggg ggc ccc acc tgg gca ggg      103
Leu Leu Leu Leu Thr Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala Gly
-15          -10          -5          1
aag atg tat ggc cct gga gga ggc aag tat ttc agc acc act gaa gac      151
Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp
      5          10          15
tac gac cat gaa atc aca ggg ctg cgg gtg tct gta ggt ctt ctc ctg      199
Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu
      20          25          30
gtg aaa agt gtc cag gtg aaa ctt gga gac tcc tgg gac gtg aaa ctg      247
Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu

```

35	40	45	
gga gcc tta ggt ggg aat acc cag gaa gtc acc ctg cag cca ggc gaa			295
Gly Ala Leu Gly Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu			
50	55	60	65
tac atc aca aaa gtc ttt gtc gcc ttc caa act ttc ctc cgg ggt atg			343
Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Thr Phe Leu Arg Gly Met			
	70	75	80
gtc atg tac acc agc aag gac cgc tat ttc tat ttt ggg aag ctt gat			391
Val Met Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp			
	85	90	95
ggc cag atc tcc tct gcc tac ccc agc caa gag ggg cag gtg ctg gtg			439
Gly Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val			
	100	105	110
ggc atc tat ggc cag tat caa ctc ctt ggc atc aag agc att ggc ttt			487
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe			
	115	120	125
gaa tgg aat tat cca cta gag gag ccg acc act gag cca cca gtt aat			535
Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn			
130	135	140	145
ctc aca tac tca gca aac tca ccc gtg ggt cgc taggggtgggg tatggggcca			588
Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg			
	150	155	
tccgagctga ggccatctgg gtggtggtgg ctgatggtac tggagtaact gagtcgggac			648
gctgaatctg aatccaccaa taaataaagg ttctgcaaaa aaaaaaaaaa a			699

<210> 337
 <211> 497
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..337

 <220>
 <221> sig_peptide
 <222> 68..124
 <223> Von Heijne matrix
 score 10
 seq LVLLGVSIPLVSA/QN

<220>
 <221> polyA_signal
 <222> 462..467

<220>
 <221> polyA_site
 <222> 482..497

<400> 337	
agcgccttgc cttctcttag gctttgaagc atttttgtct gtgctccctg atcttcaggt	60
caccacc atg aag ttc tta gca gtc ctg gta ctc ttg gga gtt tcc atc	109
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile	
	-15
ttt ctg gtc tct gcc cag aat ccg aca aca gct gct cca gct gac acg	157
Phe Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr	
-5	1
tat cca gct act ggt cct gct gat gat gaa gcc cct gat gct gaa acc	205
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr	
	15
act gct gct gca acc act gcg acc act gct gct cct acc act gca acc	253


```

agt gaa gag gaa act gag agt tgattgtgcc aggcgccagt ttttcttggt      443
Ser Glu Glu Glu Thr Glu Ser
      105                      110
atgactgtgt atttttgttg atctataccc tgtttccgaa ttctgccgtg tgtatcccca      503
acccttgacc caatgacacc aaacacagtg tttttgagct cggtattata tatttttttc      563
tcattaaagg tttaaaacca aaaaaaaaaa aaaaaa      598

<210> 339
<211> 1579
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 235..642

<220>
<221> sig_peptide
<222> 235..336
<223> Von Heijne matrix
      score 8.7
      seq HLLALLVFSVLLA/LR

<220>
<221> polyA_signal
<222> 1540..1545

<220>
<221> polyA_site
<222> 1564..1579

<400> 339
gtgggggcat ggcgtccgat cgaggcgggc gttcacgggc ggccagggtt gagtcccggg      60
tcggggcccg gggattgccg gcgcatacagg gccgagggct ggggctggcg gggccgctcg      120
ctgcctctcg ctgcgcagcag cggcggcagg cgcgggagag ggccacgggg agaggagacg      180
cagccccgcg ggtggcacgc tcggccgggc cccggcccgc gctcaacggg cgcg atg      237
                                         Met

ctc ttc tcg ctc cgg gag ctg gtg cag tgg cta ggc ttc gcc acc ttc      285
Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr Phe
      -30                      -25                      -20

gag atc ttc gtg cac ctg ctg gcc ctg ttg gtg ttc tct gtg ctg ctg      333
Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu
      -15                      -10                      -5

gca ctg cgt gtg gat ggc ctg gtc ccg ggc ctc tcc tgg tgg aac gtg      381
Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn Val
      1                      5                      10                      15

ttc gtg cct ttc ttc gcc gct gac ggg ctc agc acc tac ttc acc acc      429
Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr
      20                      25                      30

atc gtg tcc gtg cgc ctc ttc cag gat gga gag aag cgg ctg gcg gtg      477
Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val
      35                      40                      45

ctc cgc ctt ttc tgg gta ctt acg gtc ctg agt ctc aag ttc gtc ttc      525
Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val Phe
      50                      55                      60

gag atg ctg ttg tgc cag aag ctg gcg gag cag act cgg gag ctc tgg      573
Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu Trp
      65                      70                      75

ttc ggc ctc att acg tcc ccg ctc ttc att ctc ctg cag ctg ctc atg      621
Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu Met
      80                      85                      90                      95

```

```

atc cgc gcc tgt cgg gtc aac tagcctcacc gaggtgccgg agagggagcg      672
Ile Arg Ala Cys Arg Val Asn
                                100
ctggacaact agaatgttga cctcgagccg aggccctact tgcagcgcac cggaggagag      732
gctctctagt ctgaaggcac cgccggccttg cgccgagctg agtgccgggt ttccctattc      792
caatcctgtt tgaaatgggt tcttcagcag ggcttaaaag agcagccttc atcctgaaaa      852
tgtatttcct tttgtttaat gctttgagta gataatcctg aattgaggtc atgaggaggc      912
ccccaggcc agacagtcct gaacccctct gacacttgga aactgaatat aagtaaaatg      972
tccaggtgga ctctgagtat ttctgtgga tcttgggaaa gtactgttgc acaaaggctg     1032
caaagctgga ctcaggaatg tcctccaacc agcagcgcta acctaagagc tccctgtgcc     1092
gtctatccag accagacttc ggtagatgcc tttgttagat ctatcacatg taaacgagct     1152
tgtatctcct tccctgtgcc acgagagaga ttggcttttt attccagtct aggcagagac     1212
agaagaatgt tgaataagag cacgattaga gtctgtctct gttatctgtt gcccaagaaa     1272
agaactctgc tgtccaggca ctgcttggct tactatccca gcaaagactg cagttttgtg     1332
gacttttgac caccttgggc tggcactctt agcacacctg agacagattt aagcctccct     1392
aagagactga agagaggaac aggtgtcaga tactcatagg cactgagatc tacaaatggg     1452
aagcttgtga gtggcccatc tttgttggcc tacgaacttt ggtttgatgc cagtcagggt     1512
ccacatgaga acctttgctg agatgcaaat aaagtaagag aatgttttcc caaaaaaaaaa     1572
aaaaaaaaa
                                1579

<210> 340
<211> 893
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..755

<220>
<221> sig_peptide
<222> 42..200
<223> Von Heijne matrix
      score 5.8
      seq ILSLQVLLTTVTS/TV

<220>
<221> polyA_signal
<222> 860..865

<220>
<221> polyA_site
<222> 878..893

<400> 340
gcggttagtg gaccgggacc ggtaggggtg ctgttgccat c atg gct gac ccc gac      56
                                Met Ala Asp Pro Asp
                                -50
ccc cgg tac cct cgc tcc tcg atc gag gac gac ttc aac tat ggc agc      104
Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp Phe Asn Tyr Gly Ser
      -45                                -40                                -35
agc gtg gcc tcc gcc acc gtg cac atc cga atg gcc ttt ctg aga aaa      152
Ser Val Ala Ser Ala Thr Val His Ile Arg Met Ala Phe Leu Arg Lys
      -30                                -25                                -20
gtc tac agc att ctt tct ctg cag gtt ctc tta act aca gtg act tca      200
Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser
      -15                                -10                                -5
aca gtt ttt tta tac ttt gag tct gta cgg aca ttt gta cat gag agt      248
Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe Val His Glu Ser
1                                5                                10                                15
cct gcc tta att ttg ctg ttt gcc ctc gga tct ctg ggt ttg att ttt      296

```

```

Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe
      20      25      30
gcg ttg att tta aac aga cat aag tat ccc ctt aac ctg tac cta ctt      344
Ala Leu Ile Leu Asn Arg His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu
      35      40      45
ttt gga ttt acg ctg ttg gaa gct ctg act gtg gca gtt gtt gtt act      392
Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val Ala Val Val Val Thr
      50      55      60
ttc tat gat gta tat att att ctg caa gct ttc ata ctg act act aca      440
Phe Tyr Asp Val Tyr Ile Ile Leu Gln Ala Phe Ile Leu Thr Thr Thr
      65      70      75      80
gta ttt ttt ggt ttg act gtg tat act cta caa tct aag aag gat ttc      488
Val Phe Phe Gly Leu Thr Val Tyr Thr Leu Gln Ser Lys Lys Asp Phe
      85      90      95
agc aaa ttt gga gca ggg ctg ttt gct ctt ttg tgg ata ttg tgc ctg      536
Ser Lys Phe Gly Ala Gly Leu Phe Ala Leu Leu Trp Ile Leu Cys Leu
      100      105      110
tca gga ttc ttg aag ttt ttt tta tat agt gag ata atg gag ttg gtc      584
Ser Gly Phe Leu Lys Phe Phe Leu Tyr Ser Glu Ile Met Glu Leu Val
      115      120      125
tta gcc gct gca gga gcc ctt ctt ttc tgt gga ttc atc atc tat gac      632
Leu Ala Ala Ala Gly Ala Leu Phe Cys Gly Phe Ile Ile Tyr Asp
      130      135      140
aca cac tca ctg atg cat aaa ctg tca cct gaa gag tac gta tta gct      680
Thr His Ser Leu Met His Lys Leu Ser Pro Glu Glu Tyr Val Leu Ala
      145      150      155      160
gcc atc agc ctc tac ttg gat atc atc aat cta ttc ctg cac ctg tta      728
Ala Ile Ser Leu Tyr Leu Asp Ile Ile Asn Leu Phe Leu His Leu Leu
      165      170      175
cgg ttt ctg gaa gca gtt aat aaa aag taattaaag tatctcagct      775
Arg Phe Leu Glu Ala Val Asn Lys Lys
      180      185
caactgaaga acaacaaaaa aaatttaacg agaaaaaagg attaaagtaa ttggaagcag      835
tatatagaaa ctgtttcatt aagtaataaa gtttgaacca ataaaaaaaa aaaaaaaaa      893

<210> 341
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..340

<220>
<221> sig_peptide
<222> 23..235
<223> Von Heijne matrix
      score 3.9
      seq VAVYCSFISFANS/RS

<220>
<221> polyA_signal
<222> 611..616

<220>
<221> polyA_site
<222> 629..644

<400> 341
gtgatctggc cttcgactcg ct atg tcc act aac aat atg tcg gac cca cgg      52

```


Pro Gly Pro Glu Arg Arg Gln Ser Gln Gln Gly Leu Phe Arg Ala Ala
-20 -15 -10
tgg ctc ccc ggg tct cgg ccg tct ccc ctc ttc tgc gtc tgt tcc gtg 290
Trp Leu Pro Gly Ser Arg Pro Ser Pro Leu Phe Cys Val Cys Ser Val
-5 1 5
act tcg cct ggg tgg gat gta ccg cag gtg cat cgc gtc gag gtg ggg 338
Thr Ser Pro Gly Trp Asp Val Pro Gln Val His Arg Val Glu Val Gly
10 15 20 25
cac ggc cgc cgg caa gaa acc cac cct gtc cgg agg cgg gcg 380
His Gly Arg Arg Gln Glu Thr His Pro Val Arg Arg Arg Ala
30 35
tgagacaagc ccagcccgcg cgcgcctcatc tttcttcggt ttttgatcag tttattcaga 440
attgctctat aattttaccaa ttgtatgtat ttaacctatt cttgtggaaa aaaaaggtct 500
ttcattatat ctttatttct gcaaaaaaaaa aaaaaaaaa 538

<210> 343
<211> 752
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..232

<220>
<221> sig_peptide
<222> 8..154
<223> Von Heijne matrix
score 4.7
seq DTFLLSFLSTTWL/KT

<220>
<221> polyA_site
<222> 737..752

<400> 343
gggggtg atg ccg cgc ggt cgc agg ctt ggg atg gtg ttc gcg cct ccg 49
Met Pro Arg Gly Arg Arg Leu Gly Met Val Phe Ala Pro Pro
-45 -40
aga ccc gga cag agg caa gca ggg gcg ccg tgg gtg cca gag agg cgg 97
Arg Pro Gly Gln Arg Gln Ala Gly Ala Pro Trp Val Pro Glu Arg Arg
-35 -30 -25 -20
aag agg agg cct gat ggg gat acc ttc ctg ctg tcc ttc ctg agc aca 145
Lys Arg Arg Pro Asp Gly Asp Thr Phe Leu Leu Ser Phe Leu Ser Thr
-15 -10 -5
acc tgg ctg aaa acc tgg agg tca caa cag tac aaa gaa tca aag tca 193
Thr Trp Leu Lys Thr Trp Arg Ser Gln Gln Tyr Lys Glu Ser Lys Ser
1 5 10
aga tct tgt gcc aga gag caa atg aac tct tcc tct tgc tgagaaaacc 242
Arg Ser Cys Ala Arg Glu Gln Met Asn Ser Ser Ser Cys
15 20 25
caccctgctc acctaaaccc tggccttgcc tggtaatcc atccatgcgc ctggaaggcc 302
ccagacatca aggcctctgag gggccaggca cggggagaac ccagcagtgc cctgccctgc 362
agtctgagct accagattcc ttgtgaagat aatttgagga ccatgactca cccaaccaca 422
tttcctgggg cctcaaattg aaaattcagg atgggctttt ctatatgact ggctgatatc 482
caactatgcc atggtcttta catgccatga acattctttc ctgccagagt tctaagaatc 542
tgtgttctct gccttagacc ttctgcagat gagcccacag gaagctccac gtgtagctga 602
gctacatgca ccaggcctca gtttgcccca agtcccctgt gtactctctc atggcctgtg 662
gccaagaaat gtattctctc actttggact taggagtcca aagagaagcc cagaaacaaa 722
attgcttgaa cttgaaaaaa aaaaaaaaaa 752

<210> 344
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 183..422

<220>
<221> sig_peptide
<222> 183..302
<223> Von Heijne matrix
score 5.8
seq VLFALFVAFLLRG/KL

<220>
<221> polyA_signal
<222> 505..510

<220>
<221> polyA_site
<222> 523..537

<400> 344
agtatctcac catttctttc tctttctgaa ccacattggg tgccaacaga acttgctctc 60
tgttctcttt caaaattacc aacatggacc ccaccaatt cttcccttgg aactaaggaa 120
cgctgactg atcatctgat acagcagttc ctgagcagaa caaaacaaca aaaacaggac 180
ag atg gat gga ata ccc atg tca atg aag aat gaa atg ccc atc tcc 227
Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile Ser
-40 -35 -30
caa cta ctg atg atc atc gcc ccc tcc ttg gga ttt gtg ctc ttc gca 275
Gln Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala
-25 -20 -15 -10
ttg ttt gtg gcg ttt ctc ctg aga ggg aaa ctc atg gaa acc tat tgt 323
Leu Phe Val Ala Phe Leu Leu Arg Gly Lys Leu Met Glu Thr Tyr Cys
-5 1 5
tcg cag aaa cac aca agg cta gac tac att gga gat agt aaa aat gtc 371
Ser Gln Lys His Thr Arg Leu Asp Tyr Ile Gly Asp Ser Lys Asn Val
10 15 20
ctc aat gac gtg cag cat gga agg gaa gac gaa gac ggc ctt ttt acc 419
Leu Asn Asp Val Gln His Gly Arg Glu Asp Glu Asp Gly Leu Phe Thr
25 30 35
ctc taacaacgca gtagcatgtt agattgagga tgggggcatg acactccagt 472
Leu
40
gtcaaaataa gtcttagtag atttccttgt ttcataaaaa agactcactc aaaaaaaaaa 532
aaaaa 537

<210> 345
<211> 1602
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..1004

<220>
<221> sig_peptide
<222> 24..170

<223> Von Heijne matrix
 score 5.6
 seq ACLSLGFFSLLWL/QL

<220>

<221> polyA_site

<222> 1586..1602

<400> 345

atgcgcccgc gcctctccgc acg atg ttc ccc tcg cgg agg aaa gcg gcg cag	53
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln	
-45 -40	
ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc tcc ggc ggc ctc cct	101
Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro	
-35 -30 -25	
cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc tgc ctc tcg ctg ggc	149
Arg Lys Cys Ser Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly	
-20 -15 -10	
ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc tct ggg gac gtg gcc	197
Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala	
-5 1 5	
cgg gca gtc agg gga caa ggg cag gag acc tcg ggc cct ccc cgt gcc	245
Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala	
10 15 20 25	
tgc ccc cca gag ccg ccc cct gag cac tgg gaa gaa gac gca tcc tgg	293
Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp	
30 35 40	
ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc cgc gaa cgc ttc gag	341
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe Glu	
45 50 55	
gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc ttc ctg agc agg aag	389
Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser Arg Lys	
60 65 70	
aag atc cgg cac cac atc tac gtg ctc aac cag gtg gac cac ttc agg	437
Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp His Phe Arg	
75 80 85	
ttc aac cgg gca gcg ctc atc aac gtg ggc ttc ctg gag agc agc aac	485
Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu Glu Ser Ser Asn	
90 95 100 105	
agc acg gac tac att gcc atg cac gac gtt gac ctg ctc cct ctc aac	533
Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp Leu Leu Pro Leu Asn	
110 115 120	
gag gag ctg gac tat ggc ttt cct gag gct ggg ccc ttc cac gtg gcc	581
Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly Pro Phe His Val Ala	
125 130 135	
tcc ccg gag ctc cac cct ctc tac cac tac aag acc tat gtc ggc ggc	629
Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly	
140 145 150	
atc ctg ctg ctc tcc aag cag cac tac ccg ctg tgc aat ggg atg tcc	677
Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu Cys Asn Gly Met Ser	
155 160 165	
aac cgc ttc tgg ggc tgg ggc cgc gag gac gac gag ttc tac ccg cgc	725
Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg	
170 175 180 185	
att aag gga gct ggg ctc cag ctt ttc cgc ccc tcg gga atc aca act	773
Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr	
190 195 200	
ggg tac aag aca ttt cgc cac ctg cat gac cca gcc tgg ccg aag agg	821
Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro Ala Trp Arg Lys Arg	
205 210 215	
gac cag aag cgc atc gca gct caa aaa cag gag cag ttc aag gtg gac	869

```

Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp
    220                225                230
agg gag gga ggc ctg aac act gtg aag tac cat gtg gct tcc cgc act    917
Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr
    235                240                245
gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc ctc aac atc atg ttg    965
Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu
    250                255                260                265
gac tgt gac aag acc gcc aca ccc tgg tgc aca ttc agc tgagctggat    1014
Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
    270                275
ggacagtgag gaagcctgta cctacaggcc atattgctca ggctcaggac aaggcctcag    1074
gtcgtggggc cagctctgac aggatgtgga gtggccagga ccaagacagc aagctacgca    1134
attgcagcca cccggccgcc aaggcaggct tgggctgggc caggacacgt ggggtgcctg    1194
ggacgctgct tgccatgcac agtgatcaga gagaggctgg ggtgtgtcct gtccgggacc    1254
ccccctgcct tcctgtctcac cctactctga cctccttcac gtgcccaggc ctgtgggtag    1314
tggggagggc tgaacaggac aacctctcat caccctcact tttgttcctt cctgctgggc    1374
tgcctcgtgc agagacacag tgtagggggc atgcagctgg cgtaggtggc agttgggcct    1434
ggtgaggggt aggacttcag aaaccagagc acaagcccca cagaggggga acagccagca    1494
ccgctctagc tggttgttgc catgccgga tgtgggccta gtgttgccag atcttctgat    1554
ttttcgaaag aaactagaat gctggattct caaaaaaaaa aaaaaaaaaa    1602

<210> 346
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..784

<220>
<221> sig_peptide
<222> 80..139
<223> Von Heijne matrix
      score 4
      seq LLKVVFVVFASLC/AW

<220>
<221> polyA_signal
<222> 910..915

<220>
<221> polyA_site
<222> 933..948

<400> 346
cttcctgacc caggggctcc gctggctgcg gtcgctggg agctgccgcc agggccagga    60
ggggagcggc acctggaag atg cgc cca ttg gct ggt ggc ctg ctc aag gtg    112
              Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val
              -20                -15                -10
gtg ttc gtg gtc ttc gcc tcc ttg tgt gcc tgg tat tcg ggg tac ctg    160
Val Phe Val Val Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu
              -5                1                5
ctc gca gag ctc att cca gat gca ccc ctg tcc agt gct gcc tat agc    208
Leu Ala Glu Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser
              10                15                20
atc cgc agc atc ggg gag agg cct gtc ctc aaa gct cca gtc ccc aaa    256
Ile Arg Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys
              25                30                35
agg caa aaa tgt gac cac tgg act ccc tgc cca tct gac acc tat gcc    304

```

Arg	Gln	Lys	Cys	Asp	His	Trp	Thr	Pro	Cys	Pro	Ser	Asp	Thr	Tyr	Ala		
40					45					50					55		
tac	agg	tta	ctc	agc	gga	ggt	ggc	aga	agc	aag	tac	gcc	aaa	atc	tgc		352
Tyr	Arg	Leu	Leu	Ser	Gly	Gly	Gly	Arg	Ser	Lys	Tyr	Ala	Lys	Ile	Cys		
				60						65				70			
ttt	gag	gat	aac	cta	ctt	atg	gga	gaa	cag	ctg	gga	aat	gtt	gcc	aga		400
Phe	Glu	Asp	Asn	Leu	Leu	Met	Gly	Glu	Gln	Leu	Gly	Asn	Val	Ala	Arg		
			75					80					85				
gga	ata	aac	att	gcc	att	gtc	aac	tat	gta	act	ggg	aat	gtg	aca	gca		448
Gly	Ile	Asn	Ile	Ala	Ile	Val	Asn	Tyr	Val	Thr	Gly	Asn	Val	Thr	Ala		
			90				95					100					
aca	cga	tgt	ttt	gat	atg	tat	gaa	ggc	gat	aac	tct	gga	ccg	atg	aca		496
Thr	Arg	Cys	Phe	Asp	Met	Tyr	Glu	Gly	Asp	Asn	Ser	Gly	Pro	Met	Thr		
			105			110					115						
aag	ttt	att	cag	agt	gct	gct	cca	aaa	tcc	ctg	ctc	ttc	atg	gtg	acc		544
Lys	Phe	Ile	Gln	Ser	Ala	Ala	Pro	Lys	Ser	Leu	Leu	Phe	Met	Val	Thr		
					125					130							
tat	gac	gac	gga	agc	aca	aga	ctg	aat	aac	gat	gcc	aag	aat	gcc	ata		592
Tyr	Asp	Asp	Gly	Ser	Thr	Arg	Leu	Asn	Asn	Asp	Ala	Lys	Asn	Ala	Ile		
				140					145					150			
gaa	gca	ctt	gga	agt	aaa	gaa	atc	agg	aac	atg	aaa	ttc	agg	tct	agc		640
Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg	Asn	Met	Lys	Phe	Arg	Ser	Ser		
			155					160					165				
tgg	gta	ttt	att	gca	gca	aaa	ggc	ttg	gaa	ctc	cct	tcc	gaa	att	cag		688
Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly	Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln		
			170				175					180					
aga	gaa	aag	atc	aac	cac	tct	gat	gct	aag	aac	aac	aga	tat	tct	ggc		736
Arg	Glu	Lys	Ile	Asn	His	Ser	Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly		
			185			190					195						
tgg	cct	gca	gag	atc	cag	ata	gaa	ggc	tgc	ata	ccc	aaa	gaa	cga	agc		784
Trp	Pro	Ala	Glu	Ile	Gln	Ile	Glu	Gly	Cys	Ile	Pro	Lys	Glu	Arg	Ser		
					205					210					215		
tgacactgca	gggtcctgag	taaatgtgtt	ctgtataaac	aaatgcagct	ggaatcgctc											844	
aagaatctta	tttttctaaa	tccaacagcc	catatttgat	gagtattttg	ggtttggtgt											904	
aaaccaatga	acatttgcta	gttggtaccaa	aaaaaaaaaa	aaaa												948	

<210> 347
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..222

<220>
 <221> sig_peptide
 <222> 67..159
 <223> Von Heijne matrix
 score 5.8
 seq VLFSASSFPSISG/NI

<220>
 <221> polyA_site
 <222> 673..687

<400> 347
 tacaattgga aaatctttat acattgaaaa aagcaacttt tcttccccct ctcaataggt 60
 acaaga atg cgg gtt tat aaa agg aca cag ttg agg caa gag acc gga 108
 Met Arg Val Tyr Lys Arg Thr Gln Leu Arg Gln Glu Thr Gly
 -30 -25 -20

```

ccc aaa agt tat gtg ctc ttt agt gcc tca agt ttt cca agc atc tct      156
Pro Lys Ser Tyr Val Leu Phe Ser Ala Ser Ser Phe Pro Ser Ile Ser
      -15              -10              -5
ggg aac ata agg agt aga aat tat ttt caa aaa caa aat aat cac tgg      204
Gly Asn Ile Arg Ser Arg Asn Tyr Phe Gln Lys Gln Asn Asn His Trp
      1              5              10              15
ttc cag acc agt gat tat taaccctttt tgaattatga acccctttaa      252
Phe Gln Thr Ser Asp Tyr
      20
aacctaatga aattttaagga ccctctcccc caaaatatac atataaaaaa acaaggcagt      312
ctatggacct actgagtaac tctcaagata gtaagtaagg agagaaagat ctatgtttcc      372
ctctttgata agtatgaaat atttggagga gatgctaatt tttgcacgtt tatgatattt      432
gcaatctttc atttttgtag cagattatac tcaaaaattt gatccagaac ttggcccccta      492
ttcttttatc agcactttta cttgtaaact gaaaagttta ccatcatctg tatgacatcc      552
taatgaggtt aaaaagataa aatgcagtta tgattatgat aggtataact gtatccaggt      612
ttccacagca aaaacaaaac aaaacataca ccatgttctg gggttattga cagcctctc      672
aaaaaaaaaa aaaaaa      687

<210> 348
<211> 821
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..732

<220>
<221> sig_peptide
<222> 46..186
<223> Von Heijne matrix
      score 9.4
      seq LILLILCVGMVVG/LV

<220>
<221> polyA_signal
<222> 781..786

<220>
<221> polyA_site
<222> 806..821

<400> 348
gcaaagtcac tgaactctga gctcagttgc agtactcggg aagcc atg cag gat gaa      57
                        Met Gln Asp Glu
                        -45
gat gga tac atc acc tta aat att aaa act cgg aaa cca gct ctc gtc      105
Asp Gly Tyr Ile Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val
      -40              -35              -30
tcc gtt ggc cct gca tcc tcc ttc tgg tgg cgt gtg atg gct ttg att      153
Ser Val Gly Pro Ala Ser Ser Phe Trp Trp Arg Val Met Ala Leu Ile
      -25              -20              -15
ctg ctg atc ctg tgc gtg ggg atg gtt gtc ggg ctg gtg gct ctg ggg      201
Leu Leu Ile Leu Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly
      -10              -5              1              5
att tgg tct gtc atg cag cgc aat tac cta caa gat gag aat gaa aat      249
Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp Glu Asn Glu Asn
      10              15              20
cgc aca gga act ctg caa caa tta gca aag cgc ttc tgt caa tat gtg      297
Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val
      25              30              35

```

gta aaa caa tca gaa cta aag ggc act ttc aaa ggt cat aaa tgc agc	345
Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser	
40 45 50	
ccc tgt gac aca aac tgg aga tat tat gga gat agc tgc tat ggg ttc	393
Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe	
55 60 65	
ttc agg cac aac tta aca tgg gaa gag agt aag cag tac tgc act gac	441
Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp	
70 75 80 85	
atg aat gct act ctc ctg aag att gac aac cgg aac att gtg gag tac	489
Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr	
90 95 100	
atc aaa gcc agg act cat tta att cgt tgg gtc gga tta tct cgc cag	537
Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln	
105 110 115	
aag tcg aat gag gtc tgg aag tgg gag gat ggc tcg gtt atc tca gaa	585
Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu	
120 125 130	
aat atg ttt gag ttt ttg gaa gat gga aaa gga aat atg aat tgt gct	633
Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala	
135 140 145	
tat ttt cat aat ggg aaa atg cac cct acc ttc tgt gag aac aaa cat	681
Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His	
150 155 160 165	
tat tta atg tgt gag agg aag gct ggc atg acc aag gtg gac caa cta	729
Tyr Leu Met Cys Glu Arg Lys Ala Gly Met Thr Lys Val Asp Gln Leu	
170 175 180	
cct taatgcaaag aggtggacag gataacacag ataagggcctt tattgtacaa	782
Pro	
taaaagatat gtatgaatgc aacaaaaaaaa aaaaaaaaaa	821

<210> 349
 <211> 445
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..356

<220>
 <221> sig_peptide
 <222> 81..152
 <223> Von Heijne matrix
 score 6.2
 seq AILGSTWVALTTG/AL

<220>
 <221> polyA_signal
 <222> 406..411

<220>
 <221> polyA_site
 <222> 429..445

<220>
 <221> misc_feature
 <222> 1
 <223> n=a, g, c or t

<400> 349

```

ngaaaaaaaa catccgggcc gcgcggggaa ggggagacgt ggggtagagg ggagcattgc      60
ttccttctct cgcagtgacc atg acg aaa tta gcg cag tgg ctt tgg gga cta      113
                      Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu
                                -20                                -15
gcg atc ctg ggc tcc acc tgg gtg gcc ctg acc acg gga gcc ttg ggc      161
Ala Ile Leu Gly Ser Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly
                      -10                      -5                      1
ctg gag ctg ccc ttg tcc tgc cag gaa gtc ctg tgg cca ctg ccc gcc      209
Leu Glu Leu Pro Leu Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala
                      5                      10                      15
tac ttg ctg gtg tcc gcc ggc tgc tat gcc ctg ggc act gtg ggc tat      257
Tyr Leu Leu Val Ser Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr
20                      25                      30                      35
cgt gtg gcc act ttt cat gac tgc gag gac gcc gca cgc gag ctg cag      305
Arg Val Ala Thr Phe His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln
                      40                      45                      50
agc cag ata cag gag gcc cga gcc gac tta gcc cgc agg ggg ctg cgc      353
Ser Gln Ile Gln Glu Ala Arg Ala Asp Leu Ala Arg Arg Gly Leu Arg
                      55                      60                      65
ttc tgacagccta accccattcc tgtgcggaca gcccttcctc ccatttccca      406
Phe
ttaaagagcc agtttatattt ctaaaaaaaaa aaaaaaaaaa      445

```

```

<210> 350
<211> 1517
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 72..1346

<220>
<221> sig_peptide
<222> 72..140
<223> Von Heijne matrix
      score 5.9
      seq SCDCFVSVPPASA/IP

```

```

<220>
<221> polyA_signal
<222> 1482..1487

```

```

<220>
<221> polyA_site
<222> 1502..1517

```

```

<400> 350
atggggcggc cctggccaga agcggaggag gtggcaccgc ggaccgagct ggggtcttgg      60
aggaagagag g atg gcg tcg tcg agc cct gac tcc cca tgt tcc tgc gac      110
                      Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Cys Asp
                                -20                                -15
tgc ttt gtc tcc gtg ccc ccg gcc tca gcc atc ccg gct gtg atc ttt      158
Cys Phe Val Ser Val Pro Pro Ala Ser Ala Ile Pro Ala Val Ile Phe
-10                      -5                      1                      5
gcc aag aac tcg gac cga ccc ccg gac gag gtg cag gag gtg gtg ttt      206
Ala Lys Asn Ser Asp Arg Pro Arg Asp Glu Val Gln Glu Val Val Phe
10                      15                      20
gtc ccc gca ggc act cac act cct ggg agc ccg ctc cag tgc acc tac      254
Val Pro Ala Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr
25                      30                      35

```

att	gaa	gtg	gaa	cag	gtg	tcg	aag	acg	cac	gct	gtg	att	ctg	agc	cgt	302
Ile	Glu	Val	Glu	Gln	Val	Ser	Lys	Thr	His	Ala	Val	Ile	Leu	Ser	Arg	
40						45					50					
cct	tct	tgg	cta	tgg	ggg	gct	gag	atg	ggc	gcc	aac	gag	cat	ggt	gtc	350
Pro	Ser	Trp	Leu	Trp	Gly	Ala	Glu	Met	Gly	Ala	Asn	Glu	His	Gly	Val	
55					60					65					70	
tgc	att	ggc	aac	gag	gct	gtg	tgg	acg	aag	gag	cca	gtt	ggg	gag	ggg	398
Cys	Ile	Gly	Asn	Glu	Ala	Val	Trp	Thr	Lys	Glu	Pro	Val	Gly	Glu	Gly	
			75						80					85		
gaa	gcc	ctg	ctg	ggc	atg	gac	cta	ctc	agg	ctg	gct	ttg	gaa	cgg	agc	446
Glu	Ala	Leu	Leu	Gly	Met	Asp	Leu	Leu	Arg	Leu	Ala	Leu	Glu	Arg	Ser	
			90					95					100			
agc	tct	gcc	cag	gag	gcc	ttg	cat	gtg	atc	aca	ggg	tta	ctg	gag	cac	494
Ser	Ser	Ala	Gln	Glu	Ala	Leu	His	Val	Ile	Thr	Gly	Leu	Leu	Glu	His	
		105					110					115				
tat	ggg	cag	ggg	ggc	aac	tgc	ctg	gag	gat	gct	gcg	cca	ttc	tcc	tac	542
Tyr	Gly	Gln	Gly	Gly	Asn	Cys	Leu	Glu	Asp	Ala	Ala	Pro	Phe	Ser	Tyr	
	120				125						130					
cat	agc	acc	ttc	ctg	ctg	gct	gac	cgc	act	gag	gcg	tgg	gtg	ctg	gag	590
His	Ser	Thr	Phe	Leu	Leu	Ala	Asp	Arg	Thr	Glu	Ala	Trp	Val	Leu	Glu	
	135				140					145					150	
aca	gct	ggg	agg	ctc	tgg	gct	gca	cag	agg	atc	cag	gag	ggg	gcc	cgc	638
Thr	Ala	Gly	Arg	Leu	Trp	Ala	Ala	Gln	Arg	Ile	Gln	Glu	Gly	Ala	Arg	
			155					160						165		
aac	atc	tcc	aac	cag	ctg	agc	att	ggc	acg	gac	atc	tcg	gcc	caa	cac	686
Asn	Ile	Ser	Asn	Gln	Leu	Ser	Ile	Gly	Thr	Asp	Ile	Ser	Ala	Gln	His	
			170					175					180			
ccg	gag	ctg	cgg	act	cat	gcc	cag	gcc	aag	ggc	tgg	tgg	gat	ggg	cag	734
Pro	Glu	Leu	Arg	Thr	His	Ala	Gln	Ala	Lys	Gly	Trp	Trp	Asp	Gly	Gln	
		185				190						195				
ggt	gcc	ttt	gac	ttt	gct	cag	atc	ttc	tcc	ctg	acc	cag	cag	cct	gtg	782
Gly	Ala	Phe	Asp	Phe	Ala	Gln	Ile	Phe	Ser	Leu	Thr	Gln	Gln	Pro	Val	
	200					205					210					
cgc	atg	gag	gct	gcc	aag	gcc	cgc	ttc	cag	gca	ggg	cgg	gag	ctg	ctg	830
Arg	Met	Glu	Ala	Ala	Lys	Ala	Arg	Phe	Gln	Ala	Gly	Arg	Glu	Leu	Leu	
	215				220					225					230	
cgg	caa	cgg	caa	ggg	ggc	atc	acg	gca	gag	gtg	atg	atg	ggc	atc	ctc	878
Arg	Gln	Arg	Gln	Gly	Gly	Ile	Thr	Ala	Glu	Val	Met	Met	Gly	Ile	Leu	
			235					240						245		
aga	gac	aag	gag	agt	ggt	atc	tgt	atg	gac	tcg	gga	ggc	ttt	cgc	acc	926
Arg	Asp	Lys	Glu	Ser	Gly	Ile	Cys	Met	Asp	Ser	Gly	Gly	Phe	Arg	Thr	
		250					255						260			
acg	gcc	agc	atg	gtg	tct	gtc	ctg	ccc	cag	gat	ccc	acg	cag	ccc	tgc	974
Thr	Ala	Ser	Met	Val	Ser	Val	Leu	Pro	Gln	Asp	Pro	Thr	Gln	Pro	Cys	
		265				270						275				
gtg	cac	ttt	ctt	acc	gcc	acg	cca	gac	cca	tcc	agg	tct	gtg	ttc	aaa	1022
Val	His	Phe	Leu	Thr	Ala	Thr	Pro	Asp	Pro	Ser	Arg	Ser	Val	Phe	Lys	
		280				285					290					
cct	ttc	atc	ttc	ggg	gtg	ggg	gtg	gcc	cag	gcc	ccc	cag	gtg	ctg	tcc	1070
Pro	Phe	Ile	Phe	Gly	Val	Gly	Val	Ala	Gln	Ala	Pro	Gln	Val	Leu	Ser	
	295				300					305					310	
ccc	act	ttt	gga	gca	caa	gac	cct	gtt	cgg	acc	ctg	ccc	cga	ttc	cag	1118
Pro	Thr	Phe	Gly	Ala	Gln	Asp	Pro	Val	Arg	Thr	Leu	Pro	Arg	Phe	Gln	
			315						320					325		
act	cag	gta	gat	cgt	cgg	cat	acc	ctc	tac	cgt	gga	cac	cag	gca	gcc	1166
Thr	Gln	Val	Asp	Arg	Arg	His	Thr	Leu	Tyr	Arg	Gly	His	Gln	Ala	Ala	
			330					335					340			
ctg	ggg	ctg	atg	gag	aga	gat	cag	gat	cgg	ggg	cag	cag	ctc	cag	cag	1214
Leu	Gly	Leu	Met	Glu	Arg	Asp	Gln	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Gln	
		345				350						355				
aaa	cag	cag	gat	ctg	gag	cag	gaa	ggc	ctc	gag	gcc	aca	cag	ggg	ctg	1262


```

ccgcggcttc cttaagcctc tggcctgccc ggtccctggc gccaggtctg ttttccctgc 954
tcccttctct ctgatcctgc tttgggtctga gccgtgcctc tgggccccag cattgctggg 1014
ccgcattgtc gttttatttc tcttgtgtcg ttgcgtctag tgtaagacat tcagtggatc 1074
attgtggatg gtcattagtg gtccagagtg gaaagtgagg tcgttggttg tgggtgtacct 1134
acagtgcctg ttagggagct gttcctggtg ttgcccgta atattagact tgctcccag 1194
cctgcgccac agcccatccc tagcgactta gcgacagtgg ctgccaggtg cgggtggctg 1254
tgtcttgat acactgtgtg ggcagcccag ggccaggggc ctcttccttc catggcagcc 1314
tctgtctgca tcacagagat aaggccgcgg ctgccaccag gataaggagc cagcagctgc 1374
tctcggagga gccgcctga cccctcccca tcatgccgcc gtgggggtttc catgcagaat 1434
tttccttggg cagagttgct ttttgattct agtttttaaa aaaactgttc tttccatcat 1494
gataaaaaga aagacatgct catttcaaat agtttaggag atgtggaagc aaaaaaaaaa 1554
aaaaaa 1560

```

```

<210> 352
<211> 1066
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 48..494

<220>
<221> sig_peptide
<222> 48..347
<223> Von Heijne matrix
      score 3.7
      seq LASSFLFTMGGLG/FI

```

```

<220>
<221> polyA_signal
<222> 1031..1036

```

```

<220>
<221> polyA_site
<222> 1051..1066

```

```

<400> 352
gaggcgcgtg gggcttgagg ccgagaacgg cccttgctgc caccaac atg gag act 56
                                         Met Glu Thr
                                         -100

ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg aag ctg 104
Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu Lys Leu
-95                                -90                                -85

aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg tat gct 152
Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val Tyr Ala
-80                                -75                                -70

ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att tat gat 200
Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile Tyr Asp
-65                                -60                                -55                                -50

gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa cat ggg 248
Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu His Gly
-45                                -40                                -35

cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga caa tat 296
His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly Gln Tyr
-30                                -25                                -20

att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga ggt tta 344
Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly Gly Leu
-15                                -10                                -5

ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca aaa ctc 392
Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro Lys Leu

```

1	5	10	15	
aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta ttg agt				440
Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu Leu Ser				
	20	25	30	
ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc tat ctg				488
Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly Tyr Leu				
	35	40	45	
atg ggt tagagtgcct ttgagaagaa atcagtggat actggatttg ctctgtcaa				544
Met Gly				
tgaagtttta aaggctgtac caatcctcta atatgaaatg tggaaaagaa tgaagagcag				604
cagtaaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga ctagaatttc				664
ttcttggtat taaagagaca agttttatcac agaatttttt ttctgtctgg cctattgcta				724
taccaatgat gttgagtggc atttttctttt tagttttttca ttaaaatata ttccatatct				784
acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat tttttggaga				844
tgacattttct gatttttcaga aattaacata aaatccagaa gcaagattcc gtaagctgag				904
aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag agtgtgtgat				964
ggtagattat ttcagatatg tatgtaaaac tgtttctctga acaataagat gtatgaacgg				1024
agcagaaata aatacttttt ctaattaaaa aaaaaaaaaa aa				1066

<210> 353
 <211> 1061
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 111..671

<220>
 <221> sig_peptide
 <222> 111..215
 <223> Von Heijne matrix
 score 4.5
 seq SFTVSMaIGLVLG/GF

<220>
 <221> polyA_signal
 <222> 990..995

<220>
 <221> polyA_site
 <222> 1045..1061

<400> 353
 attattttttc tcttgctgta ctacaaagag atagaatcaa actgctttttt ttcgacatac 60
 tggttttttct ttctgtttttt cttctctttt ttctattttct tgtggatatt atg gct 116
 Met Ala
 -35
 aat aac aca aca agt tta ggg agt cca tgg cca gaa aac ttt tgg gag 164
 Asn Asn Thr Thr Ser Leu Gly Ser Pro Trp Pro Glu Asn Phe Trp Glu
 -30 -25 -20
 gac ctt atc atg tcc ttc act gta tcc atg gca atc ggg ctg gta ctt 212
 Asp Leu Ile Met Ser Phe Thr Val Ser Met Ala Ile Gly Leu Val Leu
 -15 -10 -5
 gga gga ttt att tgg gct gtg ttc att tgt ctg tct cga aga aga aga 260
 Gly Gly Phe Ile Trp Ala Val Phe Ile Cys Leu Ser Arg Arg Arg Arg
 1 5 10 15
 gcc agt gct ccc atc tca cag tgg agt tca agc agg aga tct agg tct 308
 Ala Ser Ala Pro Ile Ser Gln Trp Ser Ser Ser Arg Arg Ser Arg Ser
 20 25 30
 tct tac acc cac ggc ctc aac aga act gga ttt tac cgc cac agt ggc 356

```

Ser Tyr Thr His Gly Leu Asn Arg Thr Gly Phe Tyr Arg His Ser Gly
      35      40      45
tgt gaa cgt cga agc aac ctc agc ctg gcc agt ctc acc ttc cag cga      404
Cys Glu Arg Arg Ser Asn Leu Ser Leu Ala Ser Leu Thr Phe Gln Arg
      50      55      60
caa gct tcc ctg gaa caa gca aat tcc ttt cca aga aaa tca agt ttc      452
Gln Ala Ser Leu Glu Gln Ala Asn Ser Phe Pro Arg Lys Ser Ser Phe
      65      70      75
aga gct tct act ttc cat ccc ttt ctg caa tgt cca cca ctt cct gtg      500
Arg Ala Ser Thr Phe His Pro Phe Leu Gln Cys Pro Pro Leu Pro Val
      80      85      90      95
gaa act gag agt cag ctg gtg act ctc cct tct tcc aat atc tct ccc      548
Glu Thr Glu Ser Gln Leu Val Thr Leu Pro Ser Ser Asn Ile Ser Pro
      100      105      110
acc atc agc act tcc cac agt ctg agc cgt cct gac tac tgg tcc agt      596
Thr Ile Ser Thr Ser His Ser Leu Ser Arg Pro Asp Tyr Trp Ser Ser
      115      120      125
aac agt ctt cga gtg ggc ctt tca aca ccg ccc cca cct gcc tat gag      644
Asn Ser Leu Arg Val Gly Leu Ser Thr Pro Pro Pro Pro Ala Tyr Glu
      130      135      140
tcc atc atc aag gca ttc cca gat tcc tgagtagggg ggcttttggg      691
Ser Ile Ile Lys Ala Phe Pro Asp Ser
      145      150
ttttgtttct ttcttgtctt gtcttttatt gaaaggaaat caaaaatagg ctaaacagaa      751
ttttgagggc atggcccaaa taactcatga gttccaagtt gaaacatggg tgtgcaagtt      811
ggacattaca atgtaaaaca ctttttcttc aaacacgttt tcccttttgt ttcaaaaaat      871
gtaatatatt cccccaagcg ttttatattt atgtattttg tattcaatgt gagggcttatt      931
aaaaatagtg attctaattg aagaatcagc taagatgcat tatatatatt ttaattaaaa      991
ttaaaacttc agatatattg ggattacaat cctcatctac ttccaatgtg actaaaaaaaa      1051
aaaaaaaaaa                                     1061

<210> 354
<211> 2025
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..373

<220>
<221> sig_peptide
<222> 5..82
<223> Von Heijne matrix
      score 4
      seq SLFWFTVITLSFG/YY

<220>
<221> polyA_signal
<222> 1986..1991

<220>
<221> polyA_site
<222> 2010..2025

<400> 354
agcc atg gct acg gca gcc ggc gcg acc tac ttt cag cga ggc agt ctg      49
      Met Ala Thr Ala Ala Gly Ala Thr Tyr Phe Gln Arg Gly Ser Leu
      -25      -20      -15
ttc tgg ttc aca gtc atc acc ctc agc ttt ggc tac tac aca tgg gtt      97
Phe Trp Phe Thr Val Ile Thr Leu Ser Phe Gly Tyr Tyr Thr Trp Val

```

```

-10      -5      1      5
gtc ttc tgg cct cag agt atc cct tat cag aac ctt ggg ccc ctg ggc      145
Val Phe Trp Pro Gln Ser Ile Pro Tyr Gln Asn Leu Gly Pro Leu Gly
      10      15      20
ccc ttc act cag tac ttg gtg gac cac cat cac acc ctc ctg tgc aat      193
Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys Asn
      25      30      35
ggg tat tgg ctt gcc tgg ctg att cat gtg gga gag tcc ttg tat gcc      241
Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr Ala
      40      45      50
ata gta ttg tgc aag cat aaa ggc atc aca agt ggt cgg gct cag cta      289
Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln Leu
      55      60      65
ctc tgg ttc cta cag act ttc ttc ttt ggg ata gcg tct ctc acc atc      337
Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Thr Ile
      70      75      80      85
ttg att gct tac aaa cgg aag cgc caa aaa caa act tgaagttgtc      383
Leu Ile Ala Tyr Lys Arg Lys Arg Gln Lys Gln Thr
      90      95
tgaaagcttg ctctacactt ttacattcat cctcaccctt ttttttgttg ggtagaggag      443
gtgcagtaat ttactcagtg atcttttctac tttctagaaa ctgtccttca aagctcttta      503
agacccccctc gttagtcaagt tttttctctt atatgctctg gttgagcttg aatagaccag      563
ttgttactta agaaagaaac agagaaagat tttagctttt caatcctatt tggcagagga      623
cttcagctac cttcttacag tctttggctg tgttggtacc ctctgtgtgt ctgagctaag      683
ccacatacta aactgaacttt ttggtttgta tacccttgct cccgccttct gatgaaaaca      743
ccttaccctc acaaccacca tctttcctct cctttccaaa gctctttcca ccttgctgca      803
ctaagataaa gtgacacttc cactatatgt caattccaca cacatttatt aggtacctgt      863
gaggtaggat octatcctct caaacttcca tttctcatgc tacagagaaa gataaggaag      923
atgagcaagt gcctggaatg gggcaggctg agcagtcaca caggcataga ggcacgctga      983
gaacctggag gggagactgc agagtgcctt ccctgatgct gcagccggaa gtgatccttc      1043
cctccacctg gccctggga cactgtgctc tgcagtgtgc agggcctgat ggcactgcta      1103
gattgctcct tcagctcagg gccacagctt aaacagcttt acctttccc tcagcacctg      1163
tcccactatc ttgcacacag gtgctctaac catgtttatt gaacaaagga gggaaactga      1223
tttcactttc acttgttcat tatcattcca atttttatgt gaaaatggca caacccattt      1283
ggggtaccct cccccaaaa taaaagccca agtctacctt tgactggtac cacctttttt      1343
gtgggttctg ttgtgagaaa cctttatctt tttcatacct ttctattctc aatcacttct      1403
ccaaaagtgt gtctttccag ctctgattta ttcaaaacac aagcatttct gtttagagat      1463
tctagcccat gggttatctg gctagttatt acctctcctg ttcacttagt tatactttat      1523
tattgctcac aggtcgggga ggcagaatga ctctgtcacc actaggagcc attagggctt      1583
cttccctgga ggactgcctg cttgctttct ggggacacta gccctcattt cccttctgtg      1643
gtacagtggg gcaaatattt tgtattaagc aaacatttat gggaaacaac ccgctcccga      1703
aaacggagcc cccaagtaaa gcacaaccct gaaagattat gaactatgaa ttgtctctgg      1763
tagagataaa tttctgcaaa catatctcag tcttccctct gtttctctgg tgattaagaa      1823
gttccctttt ggtaaggaaa aggattttta accatagagt taggcatcat ggaaattcaa      1883
accagatttc ttaatacctg gtcttcctca aagagaaata ataacagtaa tagtggtgct      1943
gggaacaata tggcagatta ttgaatgaaa ttgattaact tgaataaaat gctgtgaatt      2003
ttctctaaaa aaaaaaaaaa aa
      2025

```

```

<210> 355
<211> 591
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 14..472

```

```

<220>
<221> sig_peptide
<222> 14..319
<223> Von Heijne matrix

```

score 4.9
seq VFFFGVSIILVLG/ST

<220>
<221> polyA_signal
<222> 555..560

<220>
<221> polyA_site
<222> 576..591

<400> 355
agcaccatct gtc atg gcg gct ggg ctg ttt ggt ttg agc gct cgc cgt 49
Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg
-100 -95
ctt ttg gcg gca gcg gcg acg cga ggg ctc ccg gcc gcc cgc gtc cgc 97
Leu Leu Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg
-90 -85 -80 -75
tgg gaa tct agc ttc tcc agg act gtg gtc gcc ccg tcc gct gtg gcg 145
Trp Glu Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala
-70 -65 -60
gga aag cgg ccc cca gaa ccg acc aca ccg tgg caa gag gac cca gaa 193
Gly Lys Arg Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu
-55 -50 -45
ccc gag gac gaa aac ttg tat gag aag aac cca gac tcc cat ggt tat 241
Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr
-40 -35 -30
gac aag gac ccc gtt ttg gac gtc tgg aac atg cga ctt gtc ttc ttc 289
Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe
-25 -20 -15
ttt ggc gtc tcc atc atc ctg gtc ctt ggc agc acc ttt gtg gcc tat 337
Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr
-10 -5 1 5
ctg cct gac tac agg atg aaa gag tgg tcc cgc cgc gaa gct gag agg 385
Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg
10 15 20
ctt gtg aaa tac cga gag gcc aat ggc ctt ccc atc atg gaa tcc aac 433
Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn
25 30 35
tgc ttc gac ccc agc aag atc cag ctg cca gag gat gag tgaccagttg 482
Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
40 45 50
ctaagtgggg ctcaagaagc accgccttcc ccaccacctg cctgccattc tgacctcttc 542
tcagagcacc taattaaagg ggctgaaagt ctgaaaaaaaa aaaaaaaaaa 591

<210> 356
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..217

<220>
<221> polyA_signal
<222> 489..494

<220>
<221> polyA_site
<222> 529..544

```

<400> 356
t cta cct gtg agt act agg atc atc aat cat atc tac agc ttc ccc tca      49
  Leu Pro Val Ser Thr Arg Ile Ile Asn His Ile Tyr Ser Phe Pro Ser
    1             5             10             15
ggt gat tta tgg ata gtt tgt att ttc act gta tct gtc tca cac ctt      97
Val Asp Leu Trp Ile Val Cys Ile Phe Thr Val Ser Val Ser His Leu
          20             25             30
ttt gaa aag gga aca ttg tat ggc tac ttt tat gtg att aac tcc tcc      145
Phe Glu Lys Gly Thr Leu Tyr Gly Tyr Phe Tyr Val Ile Asn Ser Ser
          35             40             45
atc aat tta tgt gtc aat gat tgc ctt cct gta atg gat tca att tct      193
Ile Asn Leu Cys Val Asn Asp Cys Leu Pro Val Met Asp Ser Ile Ser
          50             55             60
ctg tct cca ttg ttt ctt tct cac tagagaagtt ctttaaaatt ctatgaaaat      247
Leu Ser Pro Leu Phe Leu Ser His
  65             70
gaaactgtgc taaattaaaa atctactcat gataacagga gacactcaaa attatggggtt      307
tcagtttcag gcttctcacc atgtcctcag attgtactcc ctttctagcc cttctgcagc      367
aaataaacct ttgccatcag ttcaccaaaa gcactcatga gagggaaaaat ggcatatcac      427
taaatataga gttctttgtc acttcttgat ttcaaattta caactaatac tcaacacttt      487
aattaaatct ttcttttctc ttcttcctaa aacatacatg caaaaaaaaa aaaaaaa      544

<210> 357
<211> 1689
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..575

<220>
<221> sig_peptide
<222> 51..110
<223> Von Heijne matrix
      score 11.2
      seq AFLLLVALSYTLA/RD

<220>
<221> polyA_signal
<222> 1653..1658

<220>
<221> polyA_site
<222> 1674..1689

<400> 357
agaagcttgg accgcacacct agccgccgac tcacacaagg cagagttgcc atg gag      56
                                   Met Glu
                                   -20
aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac act      104
Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr Thr
          -15             -10             -5
ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca aag      152
Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr Lys
    1             5             10
gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt gac      200
Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp
  15             20             25             30
caa ctc atc tgg act cag aca tat gaa gaa gct cta tat aaa tcc aag      248

```

Gln	Leu	Ile	Trp	Thr	Gln	Thr	Tyr	Glu	Glu	Ala	Leu	Tyr	Lys	Ser	Lys		
				35					40					45			
aca	agc	aac	aaa	ccc	ttg	atg	att	att	cat	cac	ttg	gat	gag	tgc	cca		296
Thr	Ser	Asn	Lys	Pro	Leu	Met	Ile	Ile	His	His	Leu	Asp	Glu	Cys	Pro		
			50					55					60				
cac	agt	caa	gct	tta	aag	aaa	gtg	ttt	gct	gaa	aat	aaa	gaa	atc	cag		344
His	Ser	Gln	Ala	Leu	Lys	Lys	Val	Phe	Ala	Glu	Asn	Lys	Glu	Ile	Gln		
		65				70					75						
aaa	ttg	gca	gag	cag	ttt	gtc	ctc	ctc	aat	ctg	gtt	tat	gaa	aca	act		392
Lys	Leu	Ala	Glu	Gln	Phe	Val	Leu	Leu	Asn	Leu	Val	Tyr	Glu	Thr	Thr		
	80					85					90						
gac	aaa	cac	ctt	tct	cct	gat	ggc	cag	tat	gtc	ccc	agg	att	atg	ttt		440
Asp	Lys	His	Leu	Ser	Pro	Asp	Gly	Gln	Tyr	Val	Pro	Arg	Ile	Met	Phe		
	95				100					105					110		
gtt	gac	cca	tct	ctg	aca	gtt	aga	gcc	gat	atc	act	gga	aga	tat	tca		488
Val	Asp	Pro	Ser	Leu	Thr	Val	Arg	Ala	Asp	Ile	Thr	Gly	Arg	Tyr	Ser		
			115					120						125			
aat	cgt	ctc	tat	gct	tac	gaa	cct	gca	gat	aca	gct	ctg	ttg	ctt	gac		536
Asn	Arg	Leu	Tyr	Ala	Tyr	Glu	Pro	Ala	Asp	Thr	Ala	Leu	Leu	Leu	Asp		
		130					135				140						
aac	atg	aag	aaa	gct	ctc	aag	ttg	ctg	aag	act	gaa	ttg	taaagaaaaa				585
Asn	Met	Lys	Lys	Ala	Leu	Lys	Leu	Leu	Lys	Thr	Glu	Leu					
	145					150					155						
aaatctccaa	gcccttctgt	ctgtcaggcc	ttgagacttg	aaaccagaag	aagtgtgaga												645
agactggcta	gtgtggaagc	atagtgaaca	cactgattag	gttatggttt	aatgtttacaa												705
caactatttt	ttaagaaaaa	caagtttttag	aaatttggtt	tcaagtgtac	atgtgtgaaa												765
acaatattgt	atactaccat	agtgagccat	gattttctaa	aaaaaaaaata	aatgtttttgg												825
gggtgttctg	ttttctccaa	cttggtcttt	cacagtgggt	cgttttaccaa	ataggattaa												885
acacacacaa	aatgctcaag	gaagggacaa	gacaaaacca	aaactagttc	aatgatgaa												945
gaccaaagac	caagttatca	tctcaccaca	ccacaggttc	tcactagatg	actgtaagta												1005
gacacgagct	taatcaacag	aagtatcaag	ccatgtgctt	tagcataaaa	gaatattttag												1065
aaaaaacatcc	caagaaaatc	acatcactac	ctagagtcaa	ctctggccag	gaactctaag												1125
gtacacacttt	tcattttagta	attaaaatttt	agtcagatttt	tgcccaacct	aatgctctca												1185
gggaaagcct	ctggcaagta	gcttttctcct	tcagagggtct	aatttagtag	aaagggtcatc												1245
caaagaacat	ctgcactcct	gaacacaccc	tgaagaaatc	ctgggaattg	accttgtaat												1305
cgatttgtct	gtcaagggtcc	taaagtactg	gagtgaaata	aattcagcca	acatgtgact												1365
aattggaaga	agagcaaagg	gtggtgacgt	gttgatgagg	cagatggaga	tcagagggtta												1425
ctagggttta	ggaaacgtga	aaggctgttg	catcagggtta	ggggagcatt	ctgcctaaca												1485
gaaattagaa	ttgtgtgtta	atgtcttcac	tctatactta	atctcacatt	cattaatata												1545
tggaattcct	ctactgccca	gcccctactg	atttctttgg	cccctggact	atggtgctgt												1605
atataatgct	ttgcagtatc	tgttgcttgg	cttgattaac	ttttttggat	aaaacctttt												1665
ttgaacagaa	aaaaaaaaaa	aaaa															1689

<210> 358
 <211> 1111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..977

<220>
 <221> sig_peptide
 <222> 69..128
 <223> Von Heijne matrix
 score 5.3
 seq VLLGSGLTILSQP/LM

<220>
 <221> polyA_signal

<222> 1076..1081

<220>

<221> polyA_site

<222> 1096..1111

<400> 358

acctaggacc	gggtcaccgg	gtcgtttggg	gggtccgtct	gtctgtccgt	ccgcccgcgg	60
gtgccatc	atg gcg gac gcg gcc agt cag gtg ctc ctg ggc tcc ggt ctc	110				
Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu						
-20 -15 -10						
acc atc ctg tcc cag ccg ctc atg tac gtg aaa gtg ctc atc cag gtg	158					
Thr Ile Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val						
-5 1 5 10						
gga tat gag cct ctt cct cca aca ata gga cga aat att ttt ggg cgg	206					
Gly Tyr Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg						
15 20 25						
caa gtg tgt cag ctt cct ggt ctc ttt agt tat gct cag cac att gcc	254					
Gln Val Cys Gln Leu Pro Gly Leu Phe Ser Tyr Ala Gln His Ile Ala						
30 35 40						
agt atc gat ggg agg cgc ggg ttg ttc aca ggc tta act cca aga ctg	302					
Ser Ile Asp Gly Arg Arg Gly Leu Phe Thr Gly Leu Thr Pro Arg Leu						
45 50 55						
tgt tcg gga gtc ctt gga act gtg gtc cat ggt aaa gtt tta cag cat	350					
Cys Ser Gly Val Leu Gly Thr Val Val His Gly Lys Val Leu Gln His						
60 65 70						
tac cag gag agt gac aag ggt gag gag tta gga cct gga aat gta cag	398					
Tyr Gln Glu Ser Asp Lys Gly Glu Glu Leu Gly Pro Gly Asn Val Gln						
75 80 85 90						
aaa gaa gtc tca tct tcc ttt gac cac gtt atc aag gag aca act cga	446					
Lys Glu Val Ser Ser Ser Phe Asp His Val Ile Lys Glu Thr Thr Arg						
95 100 105						
gag atg atc gct cgt tct gct gct acc ctc atc aca cat ccc ttc cat	494					
Glu Met Ile Ala Arg Ser Ala Ala Thr Leu Ile Thr His Pro Phe His						
110 115 120						
gtg atc act ctg aga tct atg gta cag ttc att ggc aga gaa tcc aag	542					
Val Ile Thr Leu Arg Ser Met Val Gln Phe Ile Gly Arg Glu Ser Lys						
125 130 135						
tac tgt gga ctt tgt gat tcc ata ata acc atc tat cgg gaa gag ggc	590					
Tyr Cys Gly Leu Cys Asp Ser Ile Ile Thr Ile Tyr Arg Glu Glu Gly						
140 145 150						
att cta gga ttt ttc gcg ggt ctt gtt cct cgc ctt cta ggt gac atc	638					
Ile Leu Gly Phe Phe Ala Gly Leu Val Pro Arg Leu Leu Gly Asp Ile						
155 160 165 170						
ctt tct ttg tgg ctg tgt aac tca ctg gcc tac ctc gtc aat acc tat	686					
Leu Ser Leu Trp Leu Cys Asn Ser Leu Ala Tyr Leu Val Asn Thr Tyr						
175 180 185						
gca ctg gac agt ggg gtt tct acc atg aat gaa atg aag agt tat tct	734					
Ala Leu Asp Ser Gly Val Ser Thr Met Asn Glu Met Lys Ser Tyr Ser						
190 195 200						
caa gct gtc aca gga ttt ttt gcg agt atg ttg acc tat ccc ttt gtg	782					
Gln Ala Val Thr Gly Phe Phe Ala Ser Met Leu Thr Tyr Pro Phe Val						
205 210 215						
ctt gtc tcc aat ctt atg gct gtc aac aac tgt ggt ctt gct ggt gga	830					
Leu Val Ser Asn Leu Met Ala Val Asn Asn Cys Gly Leu Ala Gly Gly						
220 225 230						
tgc cct cct tac tcc cca ata tat acg tct tgg ata gac tgt tgg tgc	878					
Cys Pro Pro Tyr Ser Pro Ile Tyr Thr Ser Trp Ile Asp Cys Trp Cys						
235 240 245 250						
atg cta caa aaa gag ggg aat atg agc cga gga aat agc tta ttt ttc	926					
Met Leu Gln Lys Glu Gly Asn Met Ser Arg Gly Asn Ser Leu Phe Phe						

0978360 101501

```

                255                260                265
cgg aag gtc ccc ttt ggg aag act tat tgt tgt gac ctg aaa atg tta      974
Arg Lys Val Pro Phe Gly Lys Thr Tyr Cys Cys Asp Leu Lys Met Leu
                270                275                280
att tgaagatgtg gggcagggac agtgacattt ctgtagtccc agatgcacag      1027
Ile
aattatggga gagaatgttg atttctatac agtgtggcgc gcttttttaa taatcattta      1087
atcttggcaa aaaaaaaaaa aaaa      1111

<210> 359
<211> 554
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..238

<220>
<221> sig_peptide
<222> 44..160
<223> Von Heijne matrix
      score 3.9
      seq FKTIAFLLLYVSA/GP

<220>
<221> polyA_signal
<222> 443..448

<220>
<221> polyA_site
<222> 540..554

<400> 359
atcctcaaca gaataattgc tgacaaactc tcttgcccag aaa atg tct act gga      55
                                Met Ser Thr Gly
att atg gag tac aaa aaa act aca aaa gca atg aaa aaa aag aag gat      103
Ile Met Glu Tyr Lys Lys Thr Thr Lys Ala Met Lys Lys Lys Lys Asp
-35                -30                -25                -20
gtt tta ttt aca tcc tat ttc aaa acc att gct ttc ttg cta ttg tat      151
Val Leu Phe Thr Ser Tyr Phe Lys Thr Ile Ala Phe Leu Leu Leu Tyr
                        -15                -10                -5
gtc tct gca ggc cca ata tcg cga atc ttc ata aga agt tta gaa ttg      199
Val Ser Ala Gly Pro Ile Ser Arg Ile Phe Ile Arg Ser Leu Glu Leu
                        1                5                10
ttc ctt atg ttt cct tct aac aaa cac tgg tat att tca tgaaagtgtg      248
Phe Leu Met Phe Pro Ser Asn Lys His Trp Tyr Ile Ser
                        15                20                25
tattttattc acttccaaaa cagttagctc ataattcaga acattgaggt ttgcaaaatg      308
actgaaggaa actttaccta aacaatagtt gccagttctg ctgagaatta tcacgggccc      368
acaacggctg tgtgtttttc catacagata ttctaatttt tttattatgc agctaatttt      428
tttttagact cgcgataaaa atagcaagtc agtctgtgca taagcatatg tttaaatcta      488
ccaggagaaa tgtctggaat ctttttggtt attaaaatta aaattcagga taaaaaaaaa      548
aaaaaa      554

<210> 360
<211> 1773
<212> DNA
<213> Homo sapiens

<220>

```

<221> CDS
<222> 114..524

<220>
<221> sig_peptide
<222> 114..164
<223> Von Heijne matrix
score 5.2
seq ATLAVGLTIFVLS/VV

<220>
<221> polyA_signal
<222> 1739..1744

<220>
<221> polyA_site
<222> 1758..1773

<400> 360
gattttgctttt cttttttctcc aaaagggggag gaaattgaaa ctgagtgggc cacgatggga 60
agaggggaaaa gcccgaggggt acaggaggcc tctgggtgaa ggcagaggct aac atg 116
Met
ggg ttc gga gcg acc ttg gcc gtt ggc ctg acc atc ttt gtg ctg tct 164
Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu Ser
-15 -10 -5
gtc gtc act atc atc atc tgc ttc acc tgc tcc tgc tgc tgc ctt tac 212
Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu Tyr
1 5 10 15
aag acg tgc cgc cga cca cgt ccg gtt gtc acc acc acc aca tcc acc 260
Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser Thr
20 25 30
act gtg gtg cat gcc cct tat cct cag cct cca agt gtg ccg ccc agc 308
Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro Ser
35 40 45
tac cct gga cca agc tac cag ggc tac cac acc atg ccg cct cag cca 356
Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln Pro
50 55 60
ggg atg cca gca gca ccc tac cca atg cag tac cca cca cct tac cca 404
Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr Pro
65 70 75 80
gcc cag ccc atg ggc cca ccg gcc tac cac gag acc ctg gct gga gga 452
Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly Gly
85 90 95
gca gcc gcg ccc tac ccc gcc agc cag cct cct tac aac ccg gcc tac 500
Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala Tyr
100 105 110
atg gat gcc ccg aag gcg gcc ctc tgagcattcc ctggcctctc tggctgccac 554
Met Asp Ala Pro Lys Ala Ala Leu
115 120
ttggttatgt tgtgtgtgtg cgtgagtggt gtgcaggcgc gggttccttac gccccatgtg 614
tgctgtgtgt gtccaggcac gggttccttac gccccatgtg tgctgtgtgt gtctgtgctg 674
tatatgtggc ttcctctgat gctgacaagg tggggaacaa tccttgccag agtgggctgg 734
gaccagactt tgttctcttc ctcacctgaa attatgcttc ctaaaatctc aagccaaact 794
caaagaatgg ggtggtgggg ggcacctgt gaggtggccc ctgagaggtg ggggcctctc 854
cagggcacat ctggagttct tctccagctt accctagggg gaccaagtag ggctgtcac 914
accagggtag cgcagctttc tgtgtgatgc agatgtgtcc tggtttcggc agcgtagcca 974
gctgctgctt gaggccatgg ctcgtccccg gagttggggg taccggttgc agagccaggg 1034
acatgatgca ggcgaagctt gggatctggc caagttggac tttgatcctt tgggcagatg 1094
tcccattgct ccctggagcc tgtcatgcct gttggggatc aggcagcctc ctgatgccag 1154
aacacctcag gcagagccct actcagctgt acctgtctgc ctggactgtc ccctgtcccc 1214
gcatctcccc tgggaccagc tggaggggcca catgcacaca cagcctagct gccccaggg 1274

09978360 "10501

```

agctctgctg cccttgctgg ccctgccctt cccacaggtg agcagggctc ctgtccacca 1334
gcacactcag ttctcttccc tgcagtgttt tcattttatt ttagccaaac attttgctg 1394
ttttctgttt caaacatgat agttgatatg agactgaaac ccctgggttg tggagggaaa 1454
ttggctcaga gatggacaac ctggcaactg tgagtccttg cttcccgaca ccagcctcat 1514
ggaatatgca acaactcctg taccacagtc cacggtgttc tggcagcagg gacacctggg 1574
ccaatggggc atctggacca aagggtgggg gtggggccct ggatggcagc tctggcccag 1634
acatgaatac ctctgtgttc tcctccctct attactgttt caccagagct gtcttagctc 1694
aaatctgttg tgtttctgag tctagggctc gtacacttgt ttataataaa tgcaatcggt 1754
tgcaaaaaaa aaaaaaaaaa 1773

```

```

<210> 361
<211> 917
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 26..487

```

```

<220>
<221> sig_peptide
<222> 26..64
<223> Von Heijne matrix
      score 6.4
      seq MALLLSVLRVLLG/GF

```

```

<220>
<221> polyA_signal
<222> 883..888

```

```

<220>
<221> polyA_site
<222> 901..917

```

```

<400> 361
aaccacggt ggggggagcg cggcc atg gcg ctc ctg ctt tcg gtg ctg cgt 52
                               Met Ala Leu Leu Leu Ser Val Leu Arg
                               -10                               -5
gta ctg ctg ggc ggc ttc ttc gcg ctc gtg ggg ttg gcc aag ctc tcg 100
Val Leu Leu Gly Gly Phe Phe Ala Leu Val Gly Leu Ala Lys Leu Ser
                               1                               5                               10
gag gag atc tcg gct cca gtt tcg gag cgg atg aat gcc ctg ttc gtg 148
Glu Glu Ile Ser Ala Pro Val Ser Glu Arg Met Asn Ala Leu Phe Val
                               15                               20                               25
cag ttt gct gag gtg ttc ccg ctg aag gta ttt ggc tac cag cca gat 196
Gln Phe Ala Glu Val Phe Pro Leu Lys Val Phe Gly Tyr Gln Pro Asp
                               30                               35                               40
ccc ctg aac tac caa ata gct gtg ggc ttt ctg gaa ctg ctg gct ggg 244
Pro Leu Asn Tyr Gln Ile Ala Val Gly Phe Leu Glu Leu Leu Ala Gly
45                               50                               55                               60
ttg ctg ctg gtc atg ggc cca ccg atg ctg caa gag atc agt aac ttg 292
Leu Leu Leu Val Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu
                               65                               70                               75
ttc ttg att ctg ctc atg atg ggg gct atc ttc acc ttg gca gct ctg 340
Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu
                               80                               85                               90
aaa gag tca cta agc acc tgt atc cca gcc att gtc tgc ctg ggg ttc 388
Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe
                               95                               100                               105
ctg ctg ctg ctg aat gtc ggc cag ctc tta gcc cag act aag aag gtg 436
Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val

```

```

110      115      120
gtc aga ccc act agg aag aag act cta agt aca ttc aag gaa tcc tgg      484
Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp
125      130      135      140
aag tagagcatct ctgtctcttt atgccatgca gctgtcacag caggaacatg      537
Lys
gtagaacaca gagtctatca tcttgttacc agtataatat ccagggtcag ccagtgttga      597
aagagacatt ttgtctacct ggcactgctt tctcttttta gctttactac tcttttgtga      657
ggagtacatg ttatgcatat taacattcct catatcatat gaaaatacaa aataagcaga      717
aaagaaattht aaatcaacca aaattctgat gcccacaaata accactttta atgccttggt      777
gtaagtatac ctctgaactt ttttctgtgc ctttaaacag atatatattht tttttaaatg      837
aaaataaaaac catatatcct attttattttc ctctcttttaa aaccttataa actataaacac      897
tgcaaaaaaaa aaaaaaaaaaa      917

<210> 362
<211> 641
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..388

<220>
<221> sig_peptide
<222> 80..187
<223> Von Heijne matrix
      score 3.6
      seq RALSTFLFGSIRG/AA

<220>
<221> polyA_signal
<222> 609..614

<220>
<221> polyA_site
<222> 627..641

<400> 362
gccagtgcgc agacgcaggg gtcggcgccg ggtgagagcg tgcggccggg taagggcgtg      60
tggcgggatt caccacaac atg gca aat ctt ttt ata agg aaa atg gtg aac      112
              Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn
              -35              -30
cct ctg ctc tat ctc agt cgt cac acg gtg aag cct cga gcc ctc tcc      160
Pro Leu Leu Tyr Leu Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser
-25              -20              -15              -10
aca ttt cta ttt gga tcc att cga ggt gca gcc ccc gtg gct gtg gaa      208
Thr Phe Leu Phe Gly Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu
              -5              1              5
ccc ggg gca gca gtg cgc tca ctt ctc tca ccc ggc ctc ctg ccc cat      256
Pro Gly Ala Ala Val Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His
              10              15              20
ctg ctg cct gcg ctg ggg ttc aaa aac aag act gtc ctt aat aag cgc      304
Leu Leu Pro Ala Leu Gly Phe Lys Asn Lys Thr Val Leu Asn Lys Arg
              25              30              35
tgc aag gac tgt tac ctg gtg aag agg cgg ggt cgg tgg tac gtc tac      352
Cys Lys Asp Cys Tyr Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr
40              45              50              55
tgt aaa acc cat ccg agg cac aag cag aga cag atg tagacccttt      398
Cys Lys Thr His Pro Arg His Lys Gln Arg Gln Met
              60              65

```

```

ccctccagac tcacgcacat actcgtcatc gcatcacttg ggagaatggt tgtatcttat 458
ggaaggaatt atcacatcaa ggagtcaggg gaaagtgact ggaagcaaac gccctaaaag 518
ttacccatca cgttttcagt taaatgagta actatagaag acattgcgtt atcttatttc 578
caaaacgttc caactaaaaa acattttcct attaaaaatag accttccgaa aaaaaaaaaa 638
aaa 641

```

```

<210> 363
<211> 854
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 186..443

```

```

<220>
<221> sig_peptide
<222> 186..407
<223> Von Heijne matrix
      score 3.9
      seq ISCTCLLLYLTHC/IL

```

```

<220>
<221> polyA_signal
<222> 827..832

```

```

<220>
<221> polyA_site
<222> 839..854

```

```

<400> 363
aaatgttaat attagaaaga gtctcatagt gcttatgtga catcattctt tgcctaaagc 60
ctttgtacct actgtaatga agctaaactc cttggcacag gatataaggc tcacgatctg 120
gcctggactc atttttcaact ccatcttcag tcattcccta actccccac agtcagtccc 180
caaag atg cca tat gct ttc act tct cca tgc cct tgc tca ttt gtc tca 230
      Met Pro Tyr Ala Phe Thr Ser Pro Cys Pro Cys Ser Phe Val Ser
                        -70                        -65                        -60

ttg cct gaa ata tcc ttt tat ttc acc aaa ctg ctg ctc atc ctc aag 278
Leu Pro Glu Ile Ser Phe Tyr Phe Thr Lys Leu Leu Leu Ile Leu Lys
                        -55                        -50                        -45

gcc ctg cct gag tca cct ttc ctt ctt gct tcc tcc ccc ttg cct cct 326
Ala Leu Pro Glu Ser Pro Phe Leu Leu Ala Ser Ser Pro Leu Pro Pro
                        -40                        -35                        -30

ctc ccc act acc cta aga aaa ttc atc cct ccc cct tca tta ata tca 374
Leu Pro Thr Thr Leu Arg Lys Phe Ile Pro Pro Pro Ser Leu Ile Ser
                        -25                        -20                        -15

tgc aca tgc ttg tta tta tat tta aca cat tgt ata tta ggt att tgt 422
Cys Thr Cys Leu Leu Leu Tyr Leu Thr His Cys Ile Leu Gly Ile Cys
      -10                        -5                        1                        5

ttt gct tat cct ttt atc cta tgaaattgtg aacaatttgt tgaataattg 473
Phe Ala Tyr Pro Phe Ile Leu
      10

aataatcaca tatcaaatg tagagagggt atttgtctct tccctgtagg actccatttt 533
caggcagtgt ctgctaagaa tccccttgac ctgggattgg aagttgtttc tcccactgct 593
gagctccttt atattagctc ttcacctctc actcctttgt ttcttctctt ggcactttac 653
gtctttctac ccatttaatt tgataaatgt ctcatgtcat ctttaaaact gaaggtgaca 713
catgtctggg ttatctttat aactcaaaaa tgttgagctt aatgcagaat ggagaatagc 773
tacttagtaa atttttaaaa tacatgctac cattttttaag gggagaagaa gacaatatat 833
atgacaaaaa aaaaaaaaaa a 854

```

```

<210> 364

```

<211> 1568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..1259

<220>
 <221> sig_peptide
 <222> 75..1004
 <223> Von Heijne matrix
 score 4.4
 seq VLILLFSLALIIL/PS

<220>
 <221> polyA_signal
 <222> 1536..1541

<220>
 <221> polyA_site
 <222> 1553..1568

<400> 364
 agaaaagggtg tagtggtttgg ggcgggtcaac gggctatgct ggcttgacag ggctgggctc 60
 ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac gcg tgg 110
 Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp
 -310 -305 -300
 ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc ctg gag ctg 158
 Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu
 -295 -290 -285
 gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg cta cag gaa 206
 Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu
 -280 -275 -270
 cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt 254
 Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu
 -265 -260 -255
 caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat 302
 Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn
 -250 -245 -240 -235
 gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt ggc atc tct 350
 Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser
 -230 -225 -220
 gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt 398
 Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser
 -215 -210 -205
 tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc ctg gag agg 446
 Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg
 -200 -195 -190
 atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc atc cag cta 494
 Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu
 -185 -180 -175
 gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc atg gtc agt 542
 Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser
 -170 -165 -160 -155
 gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga gca ggc acc 590
 Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr
 -150 -145 -140
 gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa acc ctg ttc 638
 Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe
 -135 -130 -125

ctg	acc	gat	gag	gag	aag	cgt	ctg	ctg	ggg	cag	gaa	ggg	gtt	tcc	ctg	686	
Leu	Thr	Asp	Glu	Glu	Lys	Arg	Leu	Leu	Gly	Gln	Glu	Gly	Val	Ser	Leu		
			-120							-115				-110			
ccc	tct	cac	ctg	ccc	ctc	acc	aag	gca	gag	gag	agg	gtc	ctc	aag	aag	734	
Pro	Ser	His	Leu	Pro	Leu	Thr	Lys	Ala	Glu	Glu	Arg	Val	Leu	Lys	Lys		
			-105							-100				-95			
gtc	agg	agg	aaa	atc	cgt	aac	aag	cag	tca	gct	cag	gac	agt	cgg	cgg	782	
Val	Arg	Arg	Lys	Ile	Arg	Asn	Lys	Gln	Ser	Ala	Gln	Asp	Ser	Arg	Arg		
			-90				-85				-80				-75		
cgg	aag	aag	gag	tac	att	gat	ggg	ctg	gag	agc	agg	gtg	gca	gcc	tgt	830	
Arg	Lys	Lys	Glu	Tyr	Ile	Asp	Gly	Leu	Glu	Ser	Arg	Val	Ala	Ala	Cys		
			-70							-65				-60			
tct	gca	cag	aac	caa	gaa	tta	cag	aaa	aaa	gtc	cag	gag	ctg	gag	agg	878	
Ser	Ala	Gln	Asn	Gln	Glu	Leu	Gln	Lys	Lys	Val	Gln	Glu	Leu	Glu	Arg		
			-55							-50				-45			
cac	aac	atc	tcc	ttg	gta	gct	cag	ctc	cgc	cag	ctg	cag	acg	cta	att	926	
His	Asn	Ile	Ser	Leu	Val	Ala	Gln	Leu	Arg	Gln	Leu	Gln	Thr	Leu	Ile		
			-40							-35				-30			
gct	caa	act	tcc	aac	aaa	gct	gcc	cag	acc	agc	act	tgt	gtt	ttg	att	974	
Ala	Gln	Thr	Ser	Asn	Lys	Ala	Ala	Gln	Thr	Ser	Thr	Cys	Val	Leu	Ile		
			-25							-20				-15			
ctt	ctt	ttt	tcc	ctg	gct	ctc	atc	atc	ctg	ccc	agc	ttc	agt	cca	ttc	1022	
Leu	Leu	Phe	Ser	Leu	Ala	Leu	Ile	Ile	Leu	Pro	Ser	Phe	Ser	Pro	Phe		
			-10				-5				1				5		
cag	agt	cga	cca	gaa	gct	ggg	tct	gag	gat	tac	cag	cct	cac	gga	gtg	1070	
Gln	Ser	Arg	Pro	Glu	Ala	Gly	Ser	Glu	Asp	Tyr	Gln	Pro	His	Gly	Val		
			10							15				20			
act	tcc	aga	aat	atc	ctg	acc	cac	aag	gac	gta	aca	gaa	aat	ctg	gag	1118	
Thr	Ser	Arg	Asn	Ile	Leu	Thr	His	Lys	Asp	Val	Thr	Glu	Asn	Leu	Glu		
			25							30				35			
acc	caa	gtg	gta	gag	tcc	aga	ctg	agg	gag	cca	cct	gga	gcc	aag	gat	1166	
Thr	Gln	Val	Val	Glu	Ser	Arg	Leu	Arg	Glu	Pro	Pro	Gly	Ala	Lys	Asp		
			40				45				50						
gca	aat	ggc	tca	aca	agg	aca	ctg	ctt	gag	aag	atg	gga	ggg	aag	cca	1214	
Ala	Asn	Gly	Ser	Thr	Arg	Thr	Leu	Leu	Glu	Lys	Met	Gly	Gly	Lys	Pro		
			55				60				65				70		
aga	ccc	agt	ggg	cgc	atc	cgg	tcc	gtg	ctg	cat	gca	gat	gag	atg		1259	
Arg	Pro	Ser	Gly	Arg	Ile	Arg	Ser	Val	Leu	His	Ala	Asp	Glu	Met			
			75							80				85			
tgagctggaa	cagaccttcc			tggccctt			cctgatcaca			aggaatcctg			ggcttcttta			1319	
tggcttttctt	cccactggga			ttcctactta			ggtgtctgcc			ctcaggggtc			caaatcactt			1379	
caggacaccc	caagagatgt			cctttagtct			ctgcctgagg			cctagtctgc			atattgtttgc			1439	
atatatgaga	gggtacctca			aatacttctg			ttatgtatct			gtgatatttat			ttcttctttg			1499	
ggtatatgggt	tgaggggaaa			taagttttga													

<210> 365

<212> DNA

<220>

<221> CDS

<222> 98..376

<220>

```
<221> sig peptide
```

<222> 98..151

<223> Von Heijne matrix

```
score 12.3
```

seq HILFLLLLPVAAA/QT


```

<220>
<221> polyA_signal
<222> 471..476

<220>
<221> polyA_site
<222> 491..506

<400> 365
gacatccgct attgctactt ctctgctccc ccacagttcc tctggacttc tctggaccac      60
agtcctctgc cagacccctg ccagacccca gtccacc atg atc cat ctg ggt cac      115
                               Met Ile His Leu Gly His
                               -15
atc ctc ttc ctg ctt ttg ctc cca gtg gct gca gct cag acg act cca      163
Ile Leu Phe Leu Leu Leu Leu Pro Val Ala Ala Ala Gln Thr Thr Pro
          -10          -5          1
gga gag aga tca tca ctc cct gcc ttt tac cct ggc act tca ggc tct      211
Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr Pro Gly Thr Ser Gly Ser
5          10          15          20
tgt tcc gga tgt ggg tcc ctc tct ctg ccg ctc ctg gca ggc ctc gtg      259
Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro Leu Leu Ala Gly Leu Val
          25          30          35
gct gct gat gcg gtg gca tgc ctg ctc atc gtg ggg gcg gtg ttc ctg      307
Ala Ala Asp Ala Val Ala Ser Leu Leu Ile Val Gly Ala Val Phe Leu
          40          45          50
tgc gca cgc cca cgc cgc agc ccc gcc caa gaa tat ggc aaa gtc tac      355
Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln Glu Tyr Gly Lys Val Tyr
          55          60          65
atc aac atg cca ggc agg ggc tgaccctcct gcagcttga cctttgactt      406
Ile Asn Met Pro Gly Arg Gly
          70          75
ctgaccctct catcctggat ggtgtgtggt ggcacaggaa ccccgcccc aacttttga      466
ttgtaataaaa acaattgaaa caccaaaaaa aaaaaaaaaa      506

<210> 366
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..254

<220>
<221> sig_peptide
<222> 72..134
<223> Von Heijne matrix
      score 4.2
      seq LINLAASRTLSFC/IS

<220>
<221> polyA_signal
<222> 506..511

<220>
<221> polyA_site
<222> 528..542

<400> 366
gaccttaaga agagctaaac gggctgccac ctgtagctga agagtgcctt aacgccgagg      60

```

```

cccacggctc c atg cga gag atg cct gtt cct tct ctg ata aat ttg gca      110
      Met Arg Glu Met Pro Val Pro Ser Leu Ile Asn Leu Ala
            -20              -15              -10
gct tca cgt acc cta agt ttt tgc att tct gac aac cac gtg tcc tca      158
Ala Ser Arg Thr Leu Ser Phe Cys Ile Ser Asp Asn His Val Ser Ser
            -5              1              5
cct gga ccc gcc aac cca tcc tgt ggc ctc cac cct cac tgg ctt cgt      206
Pro Gly Pro Ala Asn Pro Ser Cys Gly Leu His Pro His Trp Leu Arg
            10              15              20
cca ctt aaa ctt tta acg tac aca tgt aga gag ctg aaa ctc cag ggg      254
Pro Leu Lys Leu Leu Thr Tyr Thr Cys Arg Glu Leu Lys Leu Gln Gly
            25              30              35              40
taacatggga caggtcctct tgatttaatg aaaacagaag atcaactgga ccgggtagca      314
agaaataagg cttaagaagc actggtttct ctgcagaaga cagcaagatg ccccgaggaa      374
tgtttgtgaa aaaggatgac tggatgggaa gcaagctgaa gaaaaagaag gaaagaaaga      434
gagaaatcag taaatcacca cacaagaggt ggagaagagg acttataaat attgtttcta      494
tgacatttga aaataaatgt tttactccat gctaaaaaaaa aaaaaaaaaa      542

```

<210> 367
 <211> 1629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 148..1140

 <220>
 <221> sig_peptide
 <222> 148..240
 <223> Von Heijne matrix
 score 10
 seq LVLILLVTRSPVNA/CL

<220>
 <221> polyA_signal
 <222> 1590..1595

<220>
 <221> polyA_site
 <222> 1614..1629

```

<400> 367
gtctgtgcc gccattgtgc ggcgctggtc ccctcagagg gttcctgctg ctgccggtgc      60
cttgaccct cccctcgtct tctcgttcta ctgcccagg agcccgcggt gtccgggact      120
cccgctccgtg ccgggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
                        Met Trp Leu Trp Glu Asp Gln Gly Gly
                        -30              -25
ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg      222
Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr
            -20              -15              -10
cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta      270
Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu
            -5              1              5              10
ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag      318
Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln
            15              20              25
gtg ctc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt ggc ggc      366
Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly
            30              35              40
agc cac gac gcg ccc gag aac acg ctg gcg gcc att ccg cag gca gct      414

```

Ser	His	Asp	Ala	Pro	Glu	Asn	Thr	Leu	Ala	Ala	Ile	Arg	Gln	Ala	Ala		
		45					50					55					
aag	aat	gga	gca	aca	ggc	gtg	gag	ttg	gac	att	gag	ttt	act	tct	gac		462
Lys	Asn	Gly	Ala	Thr	Gly	Val	Glu	Leu	Asp	Ile	Glu	Phe	Thr	Ser	Asp		
		60					65					70					
ggg	att	cct	gtc	tta	atg	cac	gat	aac	aca	gta	gat	agg	acg	act	gat		510
Gly	Ile	Pro	Val	Leu	Met	His	Asp	Asn	Thr	Val	Asp	Arg	Thr	Thr	Asp		
		75				80				85					90		
ggg	act	ggg	cga	ttg	tgt	gat	ttg	aca	ttt	gaa	caa	att	agg	aag	ctg		558
Gly	Thr	Gly	Arg	Leu	Cys	Asp	Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu		
			95						100					105			
aat	cct	gca	gca	aac	cac	aga	ctc	agg	aat	gat	ttc	cct	gat	gaa	aag		606
Asn	Pro	Ala	Ala	Asn	His	Arg	Leu	Arg	Asn	Asp	Phe	Pro	Asp	Glu	Lys		
			110						115				120				
atc	cct	acc	cta	atg	gaa	gct	gtt	gca	gag	tgc	cta	aac	cat	aac	ctc		654
Ile	Pro	Thr	Leu	Met	Glu	Ala	Val	Ala	Glu	Cys	Leu	Asn	His	Asn	Leu		
		125				130					135						
aca	atc	ttc	ttt	gat	gtc	aaa	ggc	cat	gca	cac	aag	gct	act	gag	gct		702
Thr	Ile	Phe	Phe	Asp	Val	Lys	Gly	His	Ala	His	Lys	Ala	Thr	Glu	Ala		
		140				145					150						
cta	aag	aaa	atg	tat	atg	gaa	ttt	cct	caa	ctg	tat	aat	aat	agt	gtg		750
Leu	Lys	Lys	Met	Tyr	Met	Glu	Phe	Pro	Gln	Leu	Tyr	Asn	Asn	Ser	Val		
					160					165					170		
gtc	tgt	tct	ttc	ttg	cca	gaa	gtt	atc	tac	aag	atg	aga	caa	aca	gat		798
Val	Cys	Ser	Phe	Leu	Pro	Glu	Val	Ile	Tyr	Lys	Met	Arg	Gln	Thr	Asp		
				175				180						185			
cgg	gat	gta	ata	aca	gca	tta	act	cac	aga	cct	tgg	agc	cta	agc	cat		846
Arg	Asp	Val	Ile	Thr	Ala	Leu	Thr	His	Arg	Pro	Trp	Ser	Leu	Ser	His		
			190					195					200				
aca	gga	gat	ggg	aaa	cca	cgc	tat	gat	act	ttc	tgg	aaa	cat	ttt	ata		894
Thr	Gly	Asp	Gly	Lys	Pro	Arg	Tyr	Asp	Thr	Phe	Trp	Lys	His	Phe	Ile		
		205					210					215					
ttt	gtt	atg	atg	gac	att	ttg	ctc	gat	tgg	agc	atg	cat	aat	atc	ttg		942
Phe	Val	Met	Met	Asp	Ile	Leu	Leu	Asp	Trp	Ser	Met	His	Asn	Ile	Leu		
		220				225					230						
tgg	tac	ctg	tgt	gga	att	tca	gct	ttc	ctc	atg	caa	aag	gat	ttt	gta		990
Trp	Tyr	Leu	Cys	Gly	Ile	Ser	Ala	Phe	Leu	Met	Gln	Lys	Asp	Phe	Val		
		235				240				245					250		
tcc	ccg	gcc	tac	ttg	aag	aag	tgg	tca	gct	aaa	gga	atc	cag	gtt	gtt		1038
Ser	Pro	Ala	Tyr	Leu	Lys	Lys	Trp	Ser	Ala	Lys	Gly	Ile	Gln	Val	Val		
				255					260					265			
ggg	tgg	act	gtt	aat	acc	ttt	gat	gaa	aag	agt	tac	tac	gaa	tcc	cat		1086
Gly	Trp	Thr	Val	Asn	Thr	Phe	Asp	Glu	Lys	Ser	Tyr	Tyr	Glu	Ser	His		
			270					275					280				
ctt	ggg	tcc	agc	tat	atc	act	gac	agc	atg	gta	gaa	gac	tgc	gaa	cct		1134
Leu	Gly	Ser	Ser	Tyr	Ile	Thr	Asp	Ser	Met	Val	Glu	Asp	Cys	Glu	Pro		
		285					290					295					
cac	ttc	tagacttttca	cggtgggacg	aaacgggttc	agaaactgcc	aggggcctca											1190
His	Phe																
		300															
tacagggata	tcaaaatacc	ctttgtgcta	gccaggccc	tggggaatca	ggtgactcac												1250
acaaatgcaa	tagttggtca	ctgcattttt	acctgaacca	aagctaaacc	cggtgttgcc												1310
accatgcacc	atggcatgcc	agagttcaac	actgttgctc	ttgaaaatct	gggtctgaaa												1370
aaacgcacaa	gagcccctgc	cctgccctag	ctgaggcaca	caggagacc	cagtgaggat												1430
aagcacagat	tgaattgtac	aattttgcaga	tgcagatgta	aatgcatggg	acatgcatga												1490
taactcagag	ttgacatttt	aaaacttgcc	acacttattt	caaataatttg	tactcagcta												1550
tgtaaacatg	tactgtagac	atcaaacttg	tggccatact	aataaaaatta	ttaaaaggag												1610
cacaaaaaaa	aaaaaaaaa																1629

<210> 368

<211> 1665

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 109..738

<220>
<221> sig_peptide
<222> 109..405
<223> Von Heijne matrix
score 4.5
seq LAPGSFLAAVVDA/LE

<220>
<221> polyA_signal
<222> 1633..1638

<220>
<221> polyA_site
<222> 1650..1665

<400> 368
cccagcgttc ctccctccggc cccagggtcac cgccagcacg cgccctgcttc ccgtctgcgc 60
gagtcacacg agctccccag gcccttcacc agcacagcag cagcaggc atg gca gca 117
Met Ala Ala
agc gtg gag cag cgc gag ggc acc atc cag gtg cag ggc cag gcc ctc 165
Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu
-95 -90 -85
ttc ttc cga gag gcc ctg ccc ggc agt ggg cag gct cgc ttc tct gta 213
Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val
-80 -75 -70 -65
ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg 261
Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu
-60 -55 -50
ggt aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att 309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile
-45 -40 -35
gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct 357
Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Pro Ala Pro
-30 -25 -20
att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc 405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala
-15 -10 -5
ttg gag ctg ggc ccc ccg gtt gtg atc agt cca tca ctg agt ggc atg 453
Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met
1 5 10 15
tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg ggc ttt 501
Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe
20 25 30
gtg cca gtg gcc ccc atc tgc act gac aaa atc aat gct gcc aac tat 549
Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala Ala Asn Tyr
35 40 45
gcc agt gtg aag act cca gct ctg att gta tat gga gac cag gac ccc 597
Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp Gln Asp Pro
50 55 60
atg ggt cag acc agc ttt gag cac ctg aag cag ctg ccc aac cac cgg 645
Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro Asn His Arg
65 70 75 80
gtg ctg atc atg aag ggg gcg ggg cac ccc tgt tac ctg gac aaa cca 693
Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu Asp Lys Pro

"0998360" 10501

	85		90		95	
gag gag tgg cat aca ggg ctg ctg	gac ttc ctg	cag ggg ctc cag	738			
Glu Glu Trp His Thr Gly Leu Leu	Asp Phe Leu	Gln Gly Leu Gln				
100	105	110				
tgaagcccag cactgctgca ggggggtgggc	tgcctgcctg	ctctgagctc tctcttgccac	798			
gctctctctt ctctcccagg ctctggctca	tgcacatgca	acagggtgct ctgtctatat	858			
gtctgggttc ttgtcttttg tggctctgtt	gtcttttcta	cctctttctc ttgcagtgat	918			
agactgaggg ggtaaaatca agagaaaaaa	ctctcaggaa	tcaaggaaca taatcctgtg	978			
gagggtaatc cattacatga gcttctcctg	ttcttccact	ttcctgcctg gctttcactc	1038			
cttccccctgc tctgcccagc ctttccctcc	caccactcc	tacttctgca aatgccctga	1098			
aggccagccc ttaccccaac acccacttcc	ccacctcctt	aggccccaga tacatacatg	1158			
cccacatgca cgcttacatg tttagagcca	tccttgtttc	caaatatgac ccttcgcttg	1218			
agggcaactg cataggtaca tctaactctg	gactggcatg	cacattgtca tgtgcagctt	1278			
tgcataataca cacatgcata catgagcctc	cacacaagca	cttgcacaca tgtggactcc	1338			
taaccatgct aacctcactg gctgggaagg	tggggacccc	atgggccagc ccttgcagga	1398			
ggcccttttg caaggcttag ggtgtggcca	gccctgaaag	ctacttggac acaggtttca	1458			
gctggcccca gcccagaagt gacccccaga	aagggagggc	caccgctttg ccccctgctt	1518			
ttacccttcc ttctgggtgc tctacacctc	aggttaccag	gcctgaggca tctcagccaa	1578			
gcttggttcc tgctctgagg cttgtggggg	gggagccaga	gtggaggtcg gtgaaataaa	1638			
gtgatgcaat taaaaaaaaa aaaaaaa			1665			

<210> 369
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..291

<220>
 <221> sig_peptide
 <222> 55..255
 <223> Von Heijne matrix
 score 4.4
 seq LISLVASLFMGFG/VL

<220>
 <221> polyA_signal
 <222> 390..395

<220>
 <221> polyA_site
 <222> 410..425

<400> 369	
ctgccgacgt gttcttccgg tggcggagcg gcggattagc	cttcgcgggg caaa atg
	Met
gag ctc gag gcc atg agc aga tat acc agc cca	gtg aac cca gct gtc
Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro	Val Asn Pro Ala Val
-65	-60 -55
ttc ccc cat ctg acc gtg gtg ctt ttg gcc att	ggc atg ttc ttc acc
Phe Pro His Leu Thr Val Val Leu Leu Ala Ile	Gly Met Phe Phe Thr
-50	-45 -40 -35
gcc tgg ttc ttc gtt tac gag gtc acc tct acc	aag tac act cgt gat
Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr	Lys Tyr Thr Arg Asp
-30	-25 -20
atc tat aaa gag ctc ctc atc tcc tta gtg gcc	tca ctc ttc atg ggc
Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala	Ser Leu Phe Met Gly
-15	-10 -5
ttt gga gtc ctc ttc ctg ctg ctc tgg gtt ggc	atc tac gtg
	291

Phe Gly Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val
 1 5 10
 tgagcaccca agggtaacaa ccagatggct tcaactgaaac ctgcttttgt aaattacttt 351
 tttttactgt tgctggaaat gtcccacctg ctgctcataa taaatgcaga tgtataacaa 411
 aaaaaaaaaa aaaa 425

<210> 370
 <211> 546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..276

<220>
 <221> polyA_signal
 <222> 508..513

<220>
 <221> polyA_site
 <222> 533..546

<400> 370
 gttgcaccag gcgatgcaag acac atg gca gtc tgg cct gaa gtt tcc caa 51
 Met Ala Val Trp Pro Glu Val Ser Gln
 1 5
 aac agg ctg act agg ggc cta ctg ctt ccc aac tac cag ctg agg ggg 99
 Asn Arg Leu Thr Arg Gly Leu Leu Leu Pro Asn Tyr Gln Leu Arg Gly
 10 15 20 25
 tcc gtc ccg aaa agg gag aag agg cct aag agg aaa cat caa cat ctt 147
 Ser Val Pro Lys Arg Glu Lys Arg Pro Lys Arg Lys His Gln His Leu
 30 35 40
 ttt act cct agc gag cgg cat tct gtc tgc ctt gat tgt ctt ctg gaa 195
 Phe Thr Pro Ser Glu Arg His Ser Val Cys Leu Asp Cys Leu Leu Glu
 45 50 55
 ata tcg ctt tca ggg aaa caa tgg cga aat gtc atc agt ttc aac tgc 243
 Ile Ser Leu Ser Gly Lys Gln Trp Arg Asn Val Ile Ser Phe Asn Cys
 60 65 70
 ttt tgc act act aag acg ctt ttc tgg gtt aat tagcagcaat acagacaacg 296
 Phe Cys Thr Thr Lys Thr Leu Phe Trp Val Asn
 75 80
 atctttttatt caacaacctc tctcgagata ttttaaataa tttctcacac tcgaaaaaca 356
 tgcagaagcg actattggca aacctgaaga gggtggaata ccaaatggct gaactggaat 416
 attttctagt tagcgagggg ttgagaggtg cgtcagggtc ccagaaattc acctcaaaag 476
 cgtacaggat gtaatgccag tgggtggaat cattaaagac actttgagta gattcaaaaa 536
 aaaaaaaaaa 546

<210> 371
 <211> 485
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..307

<220>
 <221> sig_peptide
 <222> 32..91
 <223> Von Heijne matrix

score 7.4
seq LVFCVGLLTMAKA/ES

<220>
<221> polyA_signal
<222> 452..457

<220>
<221> polyA_site
<222> 472..485

<400> 371
cttttcagcag gggacagccc gattggggac a atg gcg tct ctt ggc cac atc 52
Met Ala Ser Leu Gly His Ile
-20 -15
ttg gtt ttc tgt gtg ggt ctc ctc acc atg gcc aag gca gaa agt cca 100
Leu Val Phe Cys Val Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro
-10 -5 1
aag gaa cac gac ccg ttc act tac gac tac cag tcc ctg cag atc gga 148
Lys Glu His Asp Pro Phe Thr Tyr Asp Tyr Gln Ser Leu Gln Ile Gly
5 10 15
ggc ctc gtc atc gcc ggg atc ctc ttc atc ctg ggc atc ctc atc gtg 196
Gly Leu Val Ile Ala Gly Ile Leu Phe Ile Leu Gly Ile Leu Ile Val
20 25 30 35
ctg agc aga aga tgc cgg tgc aag ttc aac cag cag cag agg act ggg 244
Leu Ser Arg Arg Cys Arg Cys Lys Phe Asn Gln Gln Gln Arg Thr Gly
40 45 50
gaa ccc gat gaa gag gag gga act ttc cgc agc tcc atc cgc cgt ctg 292
Glu Pro Asp Glu Glu Glu Gly Thr Phe Arg Ser Ser Ile Arg Arg Leu
55 60 65
tcc acc cgc agg cgg tagaaacacc tggagcgatg gaatccggcc aggactcccc 347
Ser Thr Arg Arg Arg
70
tggcacctga catctccac gctccacctg cgcgccacc gccccctccg ccgcccccttc 407
cccagccctg cccccgcaga ctccccctgc cgccaagact tccaataaaa cgtgcgttcc 467
tctcaaaaaa aaaagaaa 485

<210> 372
<211> 1394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..675

<220>
<221> sig_peptide
<222> 46..87
<223> Von Heijne matrix
score 5.9
seq LTLGLSLILAGL/IV

<220>
<221> polyA_signal
<222> 1363..1368

<220>
<221> polyA_site
<222> 1382..1394

```

<400> 372
ctccgagttg ccacccagga aaaagagggc tcctctggga gatgt atg ctt act ctc      57
                                     Met Leu Thr Leu
tta ggc ctt tca ctc atc ttg gca gga ctt att gtt ggt gga gcc tgc      105
Leu Gly Leu Ser Leu Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
-10                                     -5                                     1                                     5
att tac aag cac ttc atg ccc aag agc acc att tac cgt gga gag atg      153
Ile Tyr Lys His Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
                                     10                                     15                                     20
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag      201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
                                     25                                     30                                     35
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac      249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
                                     40                                     45                                     50
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac      297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
55                                     60                                     65                                     70
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg      345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
                                     75                                     80                                     85
gac ttg ttg ctg ggg aac tgc tat ctg atg ccc ctc aat act tct att      393
Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
                                     90                                     95                                     100
gtt atg cct cca gaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt      441
Val Met Pro Pro Glu Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
                                     105                                     110                                     115
ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct      489
Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
120                                     125                                     130
gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa      537
Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
135                                     140                                     145                                     150
ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg      585
Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Arg Asp Leu Leu
                                     155                                     160                                     165
ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac      633
Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His
                                     170                                     175                                     180
ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag      675
Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu
                                     185                                     190                                     195
taagaggcaa cagatagagt gtccttggtg acaagaagtc agagatttac aatatgactt      735
taacattaag gtttatggga tactcaagat atttactcat gcatttactc tattgcttat      795
gctttaaaaa aaggaaaaaa aaaaactact aaccactgca agctcttgct aaattttagt      855
ttaattggca ttgcttggtt tttgaaactg aaattacctg agtttcattt tttctttgaa      915
tttatagggt ttagatttct gaaagcagca tgaatatatc acctaacatc ctgacaataa      975
attccatccg ttgttttttt tgtttggttg ttttttcttt tcctttaagt aagctcttta      1035
ttcatcttat ggtgcagcaa ttttaaaatt tgaaatattt taaattgttt ttgaactttt      1095
tgtgtaaaat atatcagatc tcaacattgt tggtttcttt tgtttttcat tttgtacaac      1155
tttcttgaat ttagaaatta catctttgca gctctgttag gtgctctgta attaacctga      1215
cttatatgtg aacaattttc atgagacagt catttttaaa taatgcagtg attctttctc      1275
actactatct gtattgtgga atgcacaaaa ttgtgtagggt gctgaatgct gtaaggagtt      1335
taggttgtat gaattctaca accctataat aaattttact ctatacaaaa aaaaaaaaaa      1394

```

<210> 373

<211> 1333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> 329..943

<220>
<221> sig_peptide
<222> 329..745
<223> Von Heijne matrix
score 4.2
seq SLSLALKTGPTSG/LC

<220>
<221> polyA_site
<222> 1322..1333

<400> 373
cgccagtgtc agtgggtgttg gcatcagctt gggcaggtgt gcgggctcag gatggggcgg 60
ccgtggtgag gaaccctgga ctctcagcat cacaagaggc aacaccagga gccaacatga 120
gctcgggact gaactgctgt ggcccggagc agcgctgctg gtgctgttgg ggggtggcagc 180
cagtctgtgt gtgcgctgct cacgcccagg tgcaaagagg tcagagagaa tctaccagca 240
gagaagtctg cgtgaggacc aacagagctt tacgggggtcc cggacctact ccttggtcgg 300
gcaggcatgg ccaggacccc tggcggac atg gca ccc aca agg aag gac aag 352
Met Ala Pro Thr Arg Lys Asp Lys
-135
ctg ttg caa ttc tac ccc agc ctg gag gat cca gca tct tcc agg tac 400
Leu Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr
-130 -125 -120
cag aac ttc agc aaa gga agc aga cac ggg tcg gag gaa gcc tac ata 448
Gln Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile
-115 -110 -105 -100
gac ccc att gcc atg gag tat tac aac tgg ggg cgg ttc tcg aag ccc 496
Asp Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro
-95 -90 -85
cca gaa ggt gag gcg aag gac aaa gcc gga ggt gga gga agt ggt gtg 544
Pro Glu Gly Glu Ala Lys Asp Lys Ala Gly Gly Gly Gly Ser Gly Val
-80 -75 -70
gga gct cag ggc aga agc cat acc tcc agg cag gag agg agg ctg ggc 592
Gly Ala Gln Gly Arg Ser His Thr Ser Arg Gln Glu Arg Arg Leu Gly
-65 -60 -55
ctg ggt tcg gat gat gat gcc aat tcc tac gag aat gtg ctc att tgc 640
Leu Gly Ser Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys
-50 -45 -40
aag cag aaa acc aca gag aca ggt gcc cag cag gag gac gta ggt ggc 688
Lys Gln Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Asp Val Gly Gly
-35 -30 -25 -20
ctc tgc aga ggg gac ctc agc ctg tca ctg gcc ctg aag act ggc ccc 736
Leu Cys Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro
-15 -10 -5
act tct ggt ctc tgt ccc tct gcc tcc ccg gaa gaa gat ggg gaa tct 784
Thr Ser Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Gly Glu Ser
1 5 10
gag gat tat cag aac tca gca tcc atc cat caa tgg cgc gag tcc agg 832
Glu Asp Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg
15 20 25
aag gtc atg ggg caa ctc cag aga gaa gca tcc cct ggc ccg gtg gga 880
Lys Val Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly
30 35 40 45
agc cca gac gag gag gac ggg gaa ccg gat tac gtg aat ggg gag gtg 928
Ser Pro Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val
50 55 60
gca gcc aca gaa gcc tagggcagac caagaagaaa ggagccaagg caaagagggg 983
Ala Ala Thr Glu Ala

CC3360.F01501

65
ccactgtgct catggaccca tcgctgcctt ccaaggacca tttcccagag ctactcaact 1043
tttaagcccc tgccatggtt gtccttgaa ggagaaccag ccacctgag gaccacctgg 1103
ccatgcgtgc acagcctggg aaaagacagt tactcacggg agctgcaggc ccgtcaccaa 1163
gccctctccc gaccagggt ttgtggggca ggcacctggt accatgggta acccggtcc 1223
tggatatggac ggatgcgcag gatttaggat aagctgtcac ccagtccca taacaaaacc 1283
actgtccaac actggtatct gtgttctttt gtgctatgaa aaaaaaaaaa 1333

<210> 374
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..281

<220>
<221> sig_peptide
<222> 27..77
<223> Von Heijne matrix
score 8.2
seq LLLITAILAVAVG/FP

<400> 374
gaaaagaact gactgaaacg tttgag atg aag aaa gtt ctc ctc ctg atc aca 53
Met Lys Lys Val Leu Leu Leu Ile Thr
-15 -10
gcc atc ttg gca gtg gct gtt ggt ttc cca gtc tct caa gac cag gaa 101
Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln Glu
-5 1 5
cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggg ttt 149
Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe
10 15 20
ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att cca 197
Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro
25 30 35 40
ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata cct 245
Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro
45 50 55
gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaagaa 291
Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65
ggaaaagtca cgataaacct ggtcacctga aattg 326

<210> 375
<211> 703
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..405

<220>
<221> sig_peptide
<222> 61..213
<223> Von Heijne matrix
score 8.1
seq VCLCGTFCFPCLG/CQ

<222> 755..768

<400> 376

```

tctggagttgg aaagggacgc ctggtttccc cccaagcgaa ccgggatggg aagtgacttc      60
aatgagattg aacttcagct ggattgaaag agaggctaga agttccgctt gccagcagcc      120
cccttagtag agcggg atg agt aat acc cac acg gtg ctt gtc tca ctt ccc      172
               Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro
               -30               -25               -20

cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac ccg      220
His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro
               -15               -10               -5

gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct agg      268
Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg
               1               5               10

tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc cta      316
Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu
               15               20               25

aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg gct      364
Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala
               30               35               40               45

gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta ttttatcctt      419
Asp Arg Cys Asp Leu
               50

gacttggtac aagttttggg atttctgaaa agaccatgca gataaccaca aatatcaaga      479
aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct tcccacctcc      539
ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg agctgtatctt      599
caagtaatat agttataaat taacaatgta gcagttattg atagagaaat tgagaaaact      659
gaaacgtgac cggagtattg gaaataacgt agtacatcac ctagcacaat gacacatagt      719
aggtgtctcaa taaatttatg cttataattt ttgtcaaaaa aaaaaataa      768

```

<210> 377

<211> 1007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..741

<220>

<221> sig_peptide

<222> 37..153

<223> Von Heijne matrix

score 7.2

seq SALAKLLLTCCSA/LR

<220>

<221> polyA_signal

<222> 969..974

<220>

<221> polyA_site

<222> 994..1007

<400> 377

```

cgcaggtccc gaggagcgca gactgtgtcc ctgaca atg gga aca gcc gac agt      54
               Met Gly Thr Ala Asp Ser
               -35

gat gag atg gcc ccg gag gcc cca cag cac acc cac atc gat gtg cac      102
Asp Glu Met Ala Pro Glu Ala Pro Gln His Thr His Ile Asp Val His
               -30               -25               -20

```

```

atc cac cag gag tct gcc ctg gcc aag ctc ctg ctc acc tgc tgc tct      150
Ile His Gln Glu Ser Ala Leu Ala Lys Leu Leu Leu Thr Cys Cys Ser
      -15                      -10                      -5
gcg ctg cgg ccc cgg gcc acc cag gcc agg ggc agc agc cgg ctg ctg      198
Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg Gly Ser Ser Arg Leu Leu
      1                      5                      10                      15
gtg gcc tcg tgg gtg atg cag atc gtg ctg ggg atc ttg agt gca gtc      246
Val Ala Ser Trp Val Met Gln Ile Val Leu Gly Ile Leu Ser Ala Val
      20                      25                      30
cta gga gga ttt ttc tac atc cgc gac tac acc ctc ctc gtc acc tcg      294
Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr Thr Leu Leu Val Thr Ser
      35                      40                      45
ggg gct gcc atc tgg aca ggg gct gtg gct gtg ctg gct gga gct gct      342
Gly Ala Ala Ile Trp Thr Gly Ala Val Ala Val Leu Ala Gly Ala Ala
      50                      55                      60
gcc ttc att tac gag aaa cgg ggt ggt aca tac tgg gcc ctg ctg agg      390
Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr Tyr Trp Ala Leu Leu Arg
      65                      70                      75
act ctg cta gcg ctg gca gct ttc tcc aca gcc atc gct gcc ctc aaa      438
Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr Ala Ile Ala Ala Leu Lys
      80                      85                      90                      95
ctt tgg aat gaa gat ttc cga tat ggc tac tct tat tac aac agt gcc      486
Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr Ser Tyr Tyr Asn Ser Ala
      100                      105                      110
tgc cgc atc tcc agc tcg agt gac tgg aac act cca gcc ccc act cag      534
Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn Thr Pro Ala Pro Thr Gln
      115                      120                      125
agt cca gaa gaa gtc aga agg cta cac cta tgt acc tcc ttc atg gac      582
Ser Pro Glu Glu Val Arg Arg Leu His Leu Cys Thr Ser Phe Met Asp
      130                      135                      140
atg ctg aag gcc ttg ttc aga acc ctt cag gcc atg ctc ttg ggt gtc      630
Met Leu Lys Ala Leu Phe Arg Thr Leu Gln Ala Met Leu Leu Gly Val
      145                      150                      155
tgg att ctg ctg ctt ctg gca tct ctg gcc cct ctg tgg ctg tac tgc      678
Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala Pro Leu Trp Leu Tyr Cys
      160                      165                      170                      175
tgg aga atg ttc cca acc aaa ggg aaa aga gac cag aag gaa atg ttg      726
Trp Arg Met Phe Pro Thr Lys Gly Lys Arg Asp Gln Lys Glu Met Leu
      180                      185                      190
gaa gtg agt gga atc tagccatgcc tctcctgatt attagtgccct ggtgcttctg      781
Glu Val Ser Gly Ile
      195
caccgggcgt ccctgcattct gactgctgga agaagaacca gactgaggaa aagaggctct      841
tcaacagccc cagttatcct ggccccatga ccgtggccac agccctgctc cagcagcact      901
tgccattcc ttacaccct tccccatcct gtcctgcttc atgtcccctc ctgagtagtc      961
atgtgataat aaactctcat gttattgttc ccaaaaaaaaa aaaaaa      1007

```

<210> 378
 <211> 527
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..265

<220>
 <221> sig_peptide
 <222> 80..142
 <223> Von Heijne matrix
 score 5.4

seq TFCLIFGLGAVWG/LG

<220>

<221> polyA_signal

<222> 491..496

<220>

<221> polyA_site

<222> 517..527

<400> 378

cccgccttgat tccaagaacc tcttcgattt ttatttttat ttttaaagag ggagacgatg 60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt 112

Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys

-20

-15

ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc 160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser

-10

-5

1

5

cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc 208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr

10

15

20

gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc 256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu

25

30

35

ttt caa gcg tgactgaagc agcagcctgc acatgtggat ggtcatcagt 305
Phe Gln Ala

40

gcctcgccca gagatacctg gccttcatcc aaagggaccc tgctgccaca agtcctccag 365
gcagcaccgc cactgtggct ccttcgcact gagtatgttg gactctgcca tagactgacc 425

ctcttgctc gctgctgcag tttgtctgta atgccctgac atgttgcatc ctccccattt 485
ggataaataa aaacaaacaa atgcttctgt caaaaaaaaa aa 527

<210> 379

<211> 861

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 612..644

<220>

<221> polyA_signal

<222> 829..834

<220>

<221> polyA_site

<222> 850..861

<400> 379

agctctggtg gttctggctg ctctggactg tcttcatect ctttagctgc tgttgcgctt 60
tccgccaccg acgagctaaa ctccaggtgc aacaacagca gcggcagcgt gaaatcaact 120

tggttgcccta tcatggggca tgccatgggg ctggctcctt ccctaccggt tcaactgcttg 180
accttcgcct cctcagcacc ttcaagcccc cagcctacga ggatgtggtt caccgcccag 240

gcacaccacc ccccccttat actgtggccc caggccgccc cttgactgct tccagtgaac 300
aaacctgctg ttctctctca tccagctgcc ctgcccactt tgaaggaaca aatgtggaag 360

gtgtttctct ccaccagagt gccccctctc atcaggaggg tgagcccggg gcaggggtga 420
ccctgacctc cacaccccc tcttgccgct atcgccgttt aactggcgac tccgggtattg 480

agctctgccc ttgtctctgcc tccggtgagg gtgagccagt caaggagggt aggggttagtg 540
ccacctgcc agatctggag gactactccc cgtgtgcact acccccagag tctgtaccgc 600

agatctttcc c atg ggg ctg tct tcc agt gaa ggg gac atc cca 644


```

<220>
<221> polyA_site
<222> 531..542

<400> 381
agatattaac aagg atg gcg gcg gcc gca gca agt cga gga gtc ggg gca      50
                Met Ala Ala Ala Ala Ala Ser Arg Gly Val Gly Ala
                -30                -25

aag ctg ggc ctg cgt gag att cgc atc cac tta tgt cag cgc tcg scc      98
Lys Leu Gly Leu Arg Glu Ile Arg Ile His Leu Cys Gln Arg Ser Xaa
-20                -15                -10                -5

ggc agc cag ggc gtc agg gac ttc att gag aaa cgc tac gtg gag ctg      146
Gly Ser Gln Gly Val Arg Asp Phe Ile Glu Lys Arg Tyr Val Glu Leu
                1                5                10

aag aag gcg aat ccc gac cta ccc atc cta atc cgc gaa tgc tcc gat      194
Lys Lys Ala Asn Pro Asp Leu Pro Ile Leu Ile Arg Glu Cys Ser Asp
                15                20                25

gtg cag ccc aag ctc tgg gcc cgc tac gca ttt ggc caa rag acg aat      242
Val Gln Pro Lys Leu Trp Ala Arg Tyr Ala Phe Gly Gln Xaa Thr Asn
                30                35                40

gtc cct ttg aac aac ttc agt gct gat cag gta acc aga rcc ctg gag      290
Val Pro Leu Asn Asn Phe Ser Ala Asp Gln Val Thr Arg Xaa Leu Glu
45                50                55                60

aac gtt cta agt ggt aaa gcc tgaagcctcc actgaggatt aagagcaaca      341
Asn Val Leu Ser Gly Lys Ala
                65

gccccagagc ctgggctctg ctggacttar tataatgtga aaaaaatgtg ttctcctatt      401
cctcataaag cttgtgctgt aaaatacttt ctcagggtgt tcttgcctc atctaccctc      461
tacccttac tgtgcaacca ctgaggcaaa gtagcttaat ataaaaataa aactttattc      521
tgtctcatca aaaaaaaaaa a      542

<210> 382
<211> 909
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..529

<220>
<221> sig_peptide
<222> 50..130
<223> Von Heijne matrix
        score 7.19999980926514
        seq VLWLSGLSEPGAA/RQ

<220>
<221> polyA_signal
<222> 877..882

<220>
<221> polyA_site
<222> 899..909

<400> 382
aagacggtgg cgcgattggg acagtcgcca gggatggctg agcgtgaag atg cag cgg      58
                                Met Gln Arg
                                -25

gtg tcc ggg ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc      106

```



```

Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser
-20 -15 -10
ggc ctc tct gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag 154
Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu
-5 1 5
aaa gcg cta gag gtt tat gat ttg att aga act atc cgg gac cca gaa 202
Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu
10 15 20
aag ccc aat act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg 250
Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val
25 30 35 40
gaa gtt cag gag ata aat gaa gaa raa tat ctg gtt att atc agg ttc 298
Glu Val Gln Glu Ile Asn Glu Glu Xaa Tyr Leu Val Ile Ile Arg Phe
45 50 55
acg cca aca gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc 346
Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys
60 65 70
yta arw kta aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gma 394
Leu Xaa Xaa Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Xaa
75 80 85
atc tac att tct gaa gga acc cac tca rsa gar gaa gac atc aat wwz 442
Ile Tyr Ile Ser Glu Gly Thr His Ser Xaa Glu Glu Asp Ile Asn Xaa
90 95 100
cag ata aat gac aaa gag cgw ktg gca kct gca atg gaa aac ccc awc 490
Gln Ile Asn Asp Lys Glu Arg Xaa Ala Xaa Ala Met Glu Asn Pro Xaa
105 110 115 120
tta cgg gaa att gtg gaa cag tgt gtc ctt gaa cct gac tgawakctgt 539
Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
125 130
tttaaragcc actggcctgt aattgtttga tatatttggt taaactcttt gtataatgtc 599
agaggactca tgtttaatac ataggtgatt tgtacctcag agcatttttt aaaggattct 659
ttccaagcga gatttaatta taaggtagta cctaatttgt tcaatgtata acattctcag 719
gatttgtaac acttaaataga tcagacagaa taatattttc tagttattat gtgtaagatg 779
agttgctatt tttctgatgc tcattctgat acaactatct ttcgtgtcaa atatctactg 839
tgcccaaatg tactcaattt aaatcattac tctgtaaaat aaataagcag atgattctta 899
aaaaaaaaa 909

```

<210> 383
 <211> 1149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 240..416

<220>
 <221> sig_peptide
 <222> 240..305
 <223> Von Heijne matrix
 score 3.70000004768372
 seq AVLDCAFYDPHTA/WS

<220>
 <221> polyA_signal
 <222> 1117..1122

<220>
 <221> polyA_site
 <222> 1139..1149

```

<400> 383
actagcctgc gagtgttctg agggaagcaa ggaggcggcg gcggccgcag cgagtggcga      60
gtagtggaac cggttcttct gaggggtgtc caagatgacc gggttctaac gagttcaagc      120
tgaaccagcc acccgaggat ggcattctct ccgtgaagtt cagccccaac acctcccagt      180
tctgtcttgt ctctctctgg gacacgtccg tgcgtctcta cgatgtgccg gccaactcc      239
atg cgg ctc aag tac cag cac acc ggc gcc gtc ctg gac tgc gcc ttc      287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
      -20              -15              -10
tac gat cca acg cat gcc tgg agt gga gga cta gat cat caa ttg aaa      335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
      -5              1              5              10
atg cat gat ttg aac act gat caa gaa aat ctt gtt ggg acc atg atg      383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
      15              20              25
ccc cta tca gat gtg ttg aat act gtc cac aaa tgaatgtgat ggctcmctgga      436
Pro Leu Ser Asp Val Leu Asn Thr Val His Lys
      30              35
akttgggatc aaacagttaa actgtgggat ccamaaactc cttgtaatgc tgggaccttc      496
tctcmkcctg aaaaggtata taccctctca gtgtctggag accggctgat tgtgggaaca      556
gcagcccgca gagtgttggg gtgggactta cggaacatgg gttacgtgca gcagcgcagg      616
gagtcacagc tgaaatacca gactcgctgc atacgagcgt ttccaaacaa gcagggttat      676
gtattaagct ctattgaagg ccgagtggca gttgagtatt tggaccaag ccctgaggta      736
cagaagaaga agtatgcctt caaatgtcac agactaaaag aaaataatat tgagcagatt      796
taccagtgca atgccatttc ttttcacaat atccacaata catttgccac aggtggttct      856
gatggctttg taaatatatt ggatccattt aacaaaaaag gactgtgcca attccatcgg      916
taccacacga gcatcgcatc acttgccttc agtaatgatg ggactacgct tgcaatagcg      976
tcatcatata tgtatgaaat ggatgacaca gaacatcctg aagatgggat cttcattcgc      1036
caagtgcagc atgcagaaac aaacccaag tcaccatgta cttgacaaga tttcatttac      1096
ttaagtgccg tggtgatgat aataaaacaa ttcgtactcc ccaaaaaaaaaa aaa      1149

<210> 384
<211> 921
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..446

<220>
<221> sig_peptide
<222> 111..254
<223> Von Heijne matrix
      score 4.90000009536743
      seq PSLAAGLLFGSLA/GL

<220>
<221> polyA_signal
<222> 890..895

<220>
<221> polyA_site
<222> 909..921

<400> 384
agacacctcg cagtcattcc tgcggettgc gcgcccttgt agacagccgg ggccttcgtg      60
agaccggtgc aggctgggg tagtctccag tctggacaga gaagagaaaa atg cag      116
                                     Met Gln
gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt ggc tac gca      164
Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly Tyr Ala
      -45              -40              -35

```

```

gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa gca ggb agc      212
Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala Gly Ser
-30          -25          -20          -15
gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta gcc ggc ctg      260
Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala Gly Leu
          -10          -5          1
ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg gtt ttc cta      308
Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val Phe Leu
          5          10          15
gct aca tct ggt acc ttg gct ggc att atg gga atg agg ttc tac cac      356
Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe Tyr His
          20          25          30
tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc akt ttg ctg      404
Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Xaa Leu Leu
          35          40          45          50
atg gtc gcc aaa att gga gtt agt atg ttc aac aga ccc cat      446
Met Val Ala Lys Ile Gly Val Ser Met Phe Asn Arg Pro His
          55          60
tagcagaakt catgttccag cttagactga tgaagaatta aaaatctgca tcttccacta      506
ttttcaatat attaagagaa ataagtgcag cattttttgca tctgacattt tacctaaaaa      566
aaaagacacc aaacttggma raragggtgga aaatcagtcg tgattacaaa cctacagagg      626
tgccgagtagt gtaacacaag agcttaataa gaccctcata ragcttgatt cttgtawatt      686
gatgttgctct tttctttckg tatctgtagg taaatctcaa gggtaaaatg ttaggtgtca      746
gctttcaggg ctctgaaacc chattccctg ctctgaggaa cagtgtgaaa aaaagtcttt      806
taggagattt acaatatctg ttcttttgct catcttagac cacagactga ctttgaaatt      866
atgttaagtg aaatatcaat gaaaataaag tttactataa ataataaaaa aaaaa      921

<210> 385
<211> 916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 123..455

<220>
<221> sig_peptide
<222> 123..290
<223> Von Heijne matrix
      score 4.5
      seq FCAGVLLTLLLIA/FI

<220>
<221> polyA_signal
<222> 886..891

<220>
<221> polyA_site
<222> 904..916

<400> 385
aaagtaatct ttatttcgctc atttttgara catagaagcc gtaacggaag caagtgaaat      60
gtcagtgctt agacgactgc gtcgtgctat gaccggactt tttcttgaaa ggggatgaca      120
gc atg gga ggc aat ggc tcc aca tgt aaa ccc gac act gaa aga caa      167
Met Gly Gly Asn Gly Ser Thr Cys Lys Pro Asp Thr Glu Arg Gln
      -55          -50          -45
ggc act ctc tcc aca gca gcc cca aca act agc cct gca ccc tgt ctc      215
Gly Thr Leu Ser Thr Ala Ala Pro Thr Thr Ser Pro Ala Pro Cys Leu
      -40          -35          -30
tct aac cac cac aac aaa aaa cat tta atc ctt gcc ttt tgt gct ggg      263

```

```

Ser Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys Ala Gly
-25          -20          -15          -10
ggt cta ctg aca ctg ctg ctg ata gcc ttt atc ttc ctc atc ata aag 311
Val Leu Leu Thr Leu Leu Ile Ala Phe Ile Phe Leu Ile Ile Lys
          -5          1          5
agc tac aga aaa tat cac tcc aag ccc cag gcc cca gat cct cac tca 359
Ser Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Asp Pro His Ser
          10          15          20
gat cct cca kcc rrg ctt tca tcc atc cca ggg gaa tca ctt acc tat 407
Asp Pro Pro Xaa Xaa Leu Ser Ser Ile Pro Gly Glu Ser Leu Thr Tyr
          25          30          35
gcc agc aca ags ktt caa act ctc aga aka ama gag cam yca ctt ggc 455
Ala Ser Thr Xaa Xaa Gln Thr Leu Arg Xaa Xaa Glu Xaa Xaa Leu Gly
40          45          50          55
tgagaacccat tctgcagact ttgacccccak kgtctatgct caaattaaag taacaaacta 515
actcagctttt tccaatgagg cttgaatcca tttcctcksa tctcagccct atcttcacas 575
atcacttttca ctttttttaca wattttggac caccacctgt gtgaaactgc agtcggagtt 635
gtttasatgt gatctggcaa tgctatccag catcttttga gaccaatggt cagtcttttc 695
ctggccakag gaaasattga tggccctccc asttgggaact gacagcctgt gagcccttg 755
ggggcataga ctgccttctt tggacccttc caaagtgtgt ggtacrgagc tcagtgcaca 815
gagtattcac ccagcatcat gaatcaactt gggaggagtc aaccaaataa acaatctacc 875
aaaaatttca aataaagtca aacccccccac aaaaaaaaaa a 916

<210> 386
<211> 520
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..433

<220>
<221> sig_peptide
<222> 2..232
<223> Von Heijne matrix
      score 4.40000009536743
      seq FEARIALLLPLQA/ET

<220>
<221> polyA_signal
<222> 488..493

<220>
<221> polyA_site
<222> 510..520

<400> 386
a atg gcg gcg tca aag gtg aag cag gac atg cct ccr mcg ggg ggc tat 49
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Xaa Gly Gly Tyr
      -75          -70          -65
ggg ccc atc gac tac aaa cgg aac ttg ccg cgt cga gga ctg tcg ggc 97
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
      -60          -55          -50
tac agc atg ctg gcc ata ggg att gga acc ctg atc tac ggg cac tgg 145
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
      -45          -40          -35          -30
agc ata atg aag tgg aac cgt gag cgc agg cgc cta caa atc gag gac 193
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
      -25          -20          -15
ttc gag gct cgc atc gcg ctg ttg cca ctg tta cag gca gaa acc gac 241

```


Arg	Val	Gln	Pro	Ser	Cys	Pro	Ser	Pro	Val	Cys	Leu	Glu	Pro	Val	Pro	
70					75				80				85			
cca	cgc	tcg	cgt	ttc	ctc	ctg	tagtgctcac	aggtcccagc	accgatggca							393
Pro	Arg	Ser	Arg	Phe	Leu	Leu										
				90												
ttccctttgc	cctgagctctg	carcgggtcc	cttttgtgct	tccttcccct	caggtagcct											453
ctctccccct	gggccactcc	cgggggtgag	ggggtttacc	ccttcccagt	gttttttatt											513
cctgtggggc	tcaccccaaa	gtattaaaag	tagctttgta	attcaaaaaa	aaaaa											568
<210> 388																
<211> 419																
<212> DNA																
<213> Homo sapiens																
<220>																
<221> CDS																
<222> 50..286																
<220>																
<221> sig_peptide																
<222> 50..157																
<223> Von Heijne matrix																
score 4.80000019073486																
seq VLLAIGMFFTAWF/FV																
<220>																
<221> polyA_signal																
<222> 385..390																
<220>																
<221> polyA_site																
<222> 405..416																
<400> 388																
agacgtgttc	ttccggtggc	ggasggcgga	ttagccttcg	cgggggcaaa	atg	gag	ctc									58
						Met	Glu	Leu								
						-35										
gag	gcc	atg	agc	aga	tat	acc	agc	cca	gtg	aac	cca	gct	gtc	ttc	ccc	106
Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Ala	Val	Phe	Pro	
			-30					-25				-20				
cat	ctg	acc	gtg	gtg	ctt	ttg	gcc	att	ggc	atg	ttc	ttc	acc	gcc	tgg	154
His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Thr	Ala	Trp		
			-15				-10				-5					
ttc	ttc	gtt	tac	gag	gtc	acc	tct	acc	aag	tac	act	cgt	gat	atc	tat	202
Phe	Phe	Val	Tyr	Glu	Val	Thr	Ser	Thr	Lys	Tyr	Thr	Arg	Asp	Ile	Tyr	
	1				5				10					15		
aaa	gag	ctc	ctc	atc	tcc	tta	gtg	gcc	tca	ctc	ttc	atg	ggc	ttt	gga	250
Lys	Glu	Leu	Leu	Ile	Ser	Leu	Val	Ala	Ser	Leu	Phe	Met	Gly	Phe	Gly	
			20					25				30				
gtc	ctc	ttc	ctg	ctc	ctc	tgg	gtt	ggc	atc	tac	gtg	tgagc	accca			296
Val	Leu	Phe	Leu	Leu	Trp	Val	Gly	Ile	Tyr	Val						
			35				40									
agggtaacaa	ccagatggct	tactgaaac	ctgcttttgt	aaattacttt	tttttactgt											356
tgctggaagt	gtccacctg	ctgctcataa	taaatgcaga	agtatagcaa	aaaaaaaaaa											416
ccc																419
<210> 389																
<211> 1289																
<212> DNA																
<213> Homo sapiens																

<220>
 <221> CDS
 <222> 50..637

<220>
 <221> sig_peptide
 <222> 50..151
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LGAAALALLLANT/DV

<220>
 <221> polyA_site
 <222> 1277..1289

<400> 389
 aatatacttc tttgtcaaga gaagcagagg tgtggacgct gtgtatgaa atg tct ttc 58
 Met Ser Phe
 ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc att ggt gca 106
 Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser Ile Gly Ala
 -30 -25 -20
 gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc aac aca gac 154
 Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala Asn Thr Asp
 -15 -10 -5 1
 gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac ctg gag gat 202
 Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr Leu Glu Asp
 5 10 15
 ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc aaa gca aag 250
 Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys
 20 25 30
 gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg cgg agg cca 298
 Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val Arg Arg Pro
 35 40 45
 ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc tcc ctg aaa 346
 Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys
 50 55 60 65
 agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg gta aag gas 394
 Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val Val Lys Xaa
 70 75 80
 cac atc rgg act gaa ktg aag gat ttc cag cct tat ttc aaa gga gaa 442
 His Ile Xaa Thr Glu Xaa Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu
 85 90 95
 atc ttc ctg gat gaa aar aaa aag ttc tat ggt cca caa agg cgg aag 490
 Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys
 100 105 110
 atg atg ttt atg gga ttt atc cgt ctg gga atg tgg tac aac ttc ttc 538
 Met Met Phe Met Gly Phe Ile Arg Leu Gly Met Trp Tyr Asn Phe Phe
 115 120 125
 cga rcc tgg aac gga rgc ttc tct gga aac ctg gaa gga raa ggc ttc 586
 Arg Xaa Trp Asn Gly Xaa Phe Ser Gly Asn Leu Glu Gly Xaa Gly Phe
 130 135 140 145
 atc ctt ggg gga att ttc gtg gtg gga tca asg aaa gca ggg cat tct 634
 Ile Leu Gly Gly Ile Phe Val Val Gly Ser Xaa Lys Ala Gly His Ser
 150 155 160
 tct tgarcgccga gaaaaagaat ttggagacaa agtaaaccta ctttctgttc 687
 Ser
 tggaagctgc taagatgatc aaaccacaga ctttggcctc agagaaaaaa tgattgtgtg 747
 aaactgccca gctcagggat aaccagggac attcacctgt gttcatggga tgtattgttt 807
 ccactcgtgt ccctaaggag tgagaaaccc atttatactc tactctcagt atggattatt 867
 aatgtatttt aatattctgt ttaggcccac taaggcaaaa tasccccaaa acaagactga 927
 caaaaatctg aaaaactaat gaggattatt aagctaaaac ctgggaaata ggaggcttaa 987

```

aattgactgc caggctgggt gcagtggctc acacctgtaa tcccagcact ttgggaggcc 1047
aaggtgagca agtcacttga ggtcgggagt tcgagaccag cctgagcaac atggcgaaac 1107
cccgtctcta ckaaaaatac araaatcacc cgggtgtggt ggcaggcacc tgtagtccca 1167
gctacccggg aggctgaggc aggagaatca cttgaacctg ggaggtggag gttgcggtga 1227
gctgagatca caccactgta ttccagcctg ggtgactgag actctaacca aaaaaaaaaa 1287
aa 1289

```

```

<210> 390
<211> 715
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 72..602

```

```

<220>
<221> sig_peptide
<222> 72..125
<223> Von Heijne matrix
      score 5.59999990463257
      seq LTPLFFMFPTGFS/SP

```

```

<220>
<221> polyA_site
<222> 704..715

```

```

<400> 390
acttcccttc cccctctagc attgctacct tctctcttac acgcacgcag gcatataaac 60
gtaggttttt g atg ctc ctc tgc ctg ttg acc ccg cta ttt ttc atg ttt 110
      Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Phe
      -15 -10
cca aca ggt ttt tct tcc ccc agt ccc tca gct gct gct gct gct cag 158
Pro Thr Gly Phe Ser Ser Pro Ser Pro Ser Ala Ala Ala Ala Ala Gln
-5 1 5 10
gag gtc aga tct gcc act gat ggt aat acc agc acc act ccg ccc acc 206
Glu Val Arg Ser Ala Thr Asp Gly Asn Thr Ser Thr Thr Pro Pro Thr
15 20 25
tct gcc aar aar aka aag tta aac agc agc agc agt agc agc agt aac 254
Ser Ala Lys Lys Xaa Lys Leu Asn Ser Ser Ser Ser Ser Ser Ser Asn
30 35 40
agt agt aac gag aga gaa gac ttt gat tcs acc tct tcc tcc tct tcc 302
Ser Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Ser
45 50 55
act cct cct tta caa ccc agg gat tcg gca tcc cct tca acc tcg tcc 350
Thr Pro Pro Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser
60 65 70 75
ttc tgc ctg ggg gtt tca gtg gct gct tcc agc cac gta ccg ata swg 398
Phe Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Xaa
80 85 90
aar aag ctg cgt ttt gaa rac acc ctg gag ttt gta ggg ttt gat gcg 446
Lys Lys Leu Arg Phe Glu Xaa Thr Leu Glu Phe Val Gly Phe Asp Ala
95 100 105
aar atg gct gar gaa tcc tcc tcc tcc tcc tcc tca tct tca cca ack 494
Lys Met Ala Glu Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Thr
110 115 120
gct gca aca tct cag cag cag caa ctt aaa aat aag agt ata ttg aat 542
Ala Ala Thr Ser Gln Gln Gln Gln Leu Lys Asn Lys Ser Ile Leu Asn
125 130 135
ctc ttc tgt ggc ttc ggt gca tca tgc aaa ccg cct agc caa atc ttc 590
Leu Phe Cys Gly Phe Gly Ala Ser Cys Lys Arg Pro Ser Gln Ile Phe

```


140	145	150	155	
tac cac cgt ctc tagctttgct aacagcaaac ctggctctgc taagaagtta				642
Tyr His Arg Leu				
gtgatcaaga acttttaaaga taagcctaaa ttaccagaaa actacacaga tgaaacctgg				702
caaaaaaaaaaaa aaa				715

<210> 391
 <211> 931
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 120..434

<220>
 <221> sig_peptide
 <222> 120..185
 <223> Von Heijne matrix
 score 6.30000019073486
 seq FALVWLWLRSTGC/FW

<220>
 <221> polyA_signal
 <222> 899..904

<220>
 <221> polyA_site
 <222> 918..931

<400> 391	
aattttccggc gacacctcgc agtcattcct gcggcttgcg cgcccttgta gacagccggg	60
gccttcggtga gaccggtgca ggcctgggggt agtctcctgt ctggacagag aagagaaaa	119
atg cag gga cac tgg ctc agt agt gcc ttt gca ttg gtt tgg ctt tgg	167
Met Gln Gly His Trp Leu Ser Ser Ala Phe Ala Leu Val Trp Leu Trp	
-20 -15 -10	
cta cgc agc act ggt tgc ttc tgg tgg gat cat tgg cta tgt aaa agc	215
Leu Arg Ser Thr Gly Cys Phe Trp Trp Asp His Trp Leu Cys Lys Ser	
-5 1 5 10	
agg cag cgt gcc gtc cct ggc tgc agg gct gct ctt tgg cag tct agc	263
Arg Gln Arg Ala Val Pro Gly Cys Arg Ala Ala Leu Trp Gln Ser Ser	
15 20 25	
cgg cct ggg tgc tta cca gct gtc tca gga tcc aag gaa cgt ttg ggt	311
Arg Pro Gly Cys Leu Pro Ala Val Ser Gly Ser Lys Glu Arg Leu Gly	
30 35 40	
ttt cct agc tac atc tgg tac ctt ggc tgg cat tat ggg aat gag gtt	359
Phe Pro Ser Tyr Ile Trp Tyr Leu Gly Trp His Tyr Gly Asn Glu Val	
45 50 55	
cta cca ctc tgg aaa att cat gcc tgc agg ttt aat tgc agg tgc cag	407
Leu Pro Leu Trp Lys Ile His Ala Cys Arg Phe Asn Cys Arg Cys Gln	
60 65 70	
ttt gct gat ggt cgc caa agt tgg agt tagtatgtkc aacagacccc	454
Phe Ala Asp Gly Arg Gln Ser Trp Ser	
75 80	
attagcagaa gtcattgtcc agcttagatg atgaaraatt aaaaatctgc atcttccact	514
attttcaata tattaagaga aataagtgc gcatTTTTgc atctgacatt ttacctaaaa	574
aaaaaaaaacmc caaacttggc aaaaagggtgg aaaatcagtc atgattacaa acctacagag	634
gtggcgagta tgtaacacaa gagcttaata agaccctcat agagcttgat tcttgtatat	694
tgatgttgct ttttctttct gtatctgtag gtaaatctca agggtaaaat gttaggtgtc	754
agctttcagg gctctgaaac cchatccct gctctgagga acagtgtgaa aaaaagtctt	814
ttaggaratt tacaatatct gttcttttgc tcatcttara ccacagactg actttgaaat	874

takgttaagt gaaatatcaa tgaaaataaa gtttactata aataawaaaa aaaaaaa 931

<210> 392

<211> 891

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..447

<220>

<221> sig_peptide

<222> 4..147

<223> Von Heijne matrix

score 5.69999980926514

seq LLLFFGKLLVVG/VG

<220>

<221> polyA_signal

<222> 858..863

<220>

<221> polyA_site

<222> 880..891

<400> 392

atc atg atc gcc atc tac ggg aag aat ttc tgt gtc tca gcc aaa aat 48

Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn

-45

-40

-35

gcg ttc atg cta ctc atg cga aac att gtc agg gtg gtc gtc ctg gac 96

Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp

-30

-25

-20

aaa gtc aca gac ctg ctg ctg ttc ttt ggg aag ctg ctg gtg gtc gga 144

Lys Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly

-15

-10

-5

ggc gtg ggg gtc ctg tcc ttc ttt ttt ttc tcc ggt cgc atc ccg ggg 192

Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly

1

5

10

15

ctg ggt aaa gac ttt aag agc ccc cac ctc aac tat tac tgg ctg ccc 240

Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro

20

25

30

ayc atg acc tcc atc ctg ggg gcc tat gtc atc gcc agy ggc ttc ttc 288

Xaa Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe

35

40

45

agc gtt ttc ggc atg tgt gtg gac acg ctc ttc ctc tgc ttc ctg gaa 336

Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu

50

55

60

gac ctg gag cgg aca acg gct ccc tgg acg gcc cta cta cat gtc caa 384

Asp Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln

65

70

75

gag ctt cta aag att ctg ggc aag aag aac gag gcg ccc ccg gac aac 432

Glu Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp Asn

80

85

90

95

aag aaa agg aaa aak tgacagctcc ggccctgac caggactgca cccaccccc 487

Lys Lys Arg Lys Xaa

100

accgtccagc catccaacct cacttcgcct tacaggtctc cattttgtgg taaaaaaagg 547

ttttaggcca ggcgcgtgg ctcaagcctg twatccaaca ctttgaragg ctgaggcggg 607

cggatcacct kaktcaggak tycgagacca kcttgccaa catggtgaaa cctccgtctc 667

tattaaaaat acaaaaatta gccgagagtg gtggcatgca cctgtcatcc cagctactcg 727

0997860 101501

tac ctg gaa tgt gtg agc aaa tac act gac cak ctc aag cca ttt gga	630
Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp Xaa Leu Lys Pro Phe Gly	
165 170 175	
gac gtg ccc cgg aaa ctg aag att cag gtk acc cgc gcc ttc atk gsk	678
Asp Val Pro Arg Lys Leu Lys Ile Gln Val Thr Arg Ala Phe Xaa Xaa	
180 185 190	
gcc agg acc ttt gtc cag ggg ctg act gtg ggc aga gaa gtt gca aac	726
Ala Arg Thr Phe Val Gln Gly Leu Thr Val Gly Arg Glu Val Ala Asn	
195 200 205 210	
cga gtt tcc aag gta att gaa aac gtg ctt tct ttc tca ttg gtg ttc	774
Arg Val Ser Lys Val Ile Glu Asn Val Leu Ser Phe Ser Leu Val Phe	
215 220 225	
ctt gtt tat tct gtt ttt aaa acc aat gtt taaaaaaaaa aaa	817
Leu Val Tyr Ser Val Phe Lys Thr Asn Val	
230 235	

<210> 394
 <211> 1020
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..359

<220>
 <221> sig_peptide
 <222> 27..212
 <223> Von Heijne matrix
 score 3.59999990463257
 seq SWLSLLAALAHLA/AA

<220>
 <221> polyA_signal
 <222> 988..993

<220>
 <221> polyA_site
 <222> 1009..1020

<400> 394	
agtgggtcga kctggggcgc agtcgc atg ggg gag tct atc ccg ctg gcc gcc	53
Met Gly Glu Ser Ile Pro Leu Ala Ala	
-60 -55	
ccg gtc ccg gtg gaa cag gcg gtg ctg gag acg ttc ttc tct cac ctg	101
Pro Val Pro Val Glu Gln Ala Val Leu Glu Thr Phe Phe Ser His Leu	
-50 -45 -40	
ggt atc ttc tct tac gac aag gct aag gac aat gtg gag aag gaa cga	149
Gly Ile Phe Ser Tyr Asp Lys Ala Lys Asp Asn Val Glu Lys Glu Arg	
-35 -30 -25	
gag gcc aac aag agc gcg ggg ggc agc tgg ctg tcg ctg ctg gcg gcc	197
Glu Ala Asn Lys Ser Ala Gly Gly Ser Trp Leu Ser Leu Leu Ala Ala	
-20 -15 -10	
ttg gcg cac ctg gcc gcg gcc gag aag gtc tat cac agc ctc acc tac	245
Leu Ala His Leu Ala Ala Glu Lys Val Tyr His Ser Leu Thr Tyr	
-5 1 5 10	
ctg ggg cag aaa cta ggt acc tcc gcc ccg ccc ccc gag ccc ctt gag	293
Leu Gly Gln Lys Leu Gly Thr Ser Ala Pro Pro Pro Glu Pro Leu Glu	
15 20 25	
gag gaa gta aag ggg gta tat tcc cca dtc ggc agt ggc ttg ggt btc	341
Glu Glu Val Lys Gly Val Tyr Ser Pro Xaa Gly Ser Gly Leu Gly Xaa	

30 35 40
 ccg tct ctg tgt cac ttc tagtcgcagg ctgcactcgg cattcccaga 389
 Pro Ser Leu Cys His Phe

45
 tctcctccca ccgttccttt ccttccctgg gcttccacaa gccccgcca ccrgcctgcr 449
 ctgctgatag attggcgaac tgggtagatg ctctttgcaa ggctgtgacc caaaccgaaw 509
 ggtttgccct tttgcctcgt gcatggattg atgccataaa tgagaagtta accaaaaaaa 569
 aaaaacmcwd tyccckkttm cccccccgg grmcagaaga gcaaaacttt gcaaaacaac 629
 ctagttctat tactgaacac tgttgtgtgg cctcttaagg ttaaggcccg agagtcacat 689
 ttagagtccct accccgtcct catagtcccc caatacatat ttaatgacta aagtwataaa 749
 tgaatattgg gcaggaaagg caagaaatat gcctaacact agcaagaaga gacttaaggg 809
 gaaaatggta aacactctta gcacttcattg tacatcttgc ctctgaaata agattcaaga 869
 gctgattcaa ctgattttta ctagtagaag caataagtat aagtagatga gaaggaaata 929
 atagatgtaa aaggcatgga atatgcatac aaaataatat tactgcttaa ttatgacaaa 989
 taaatatatt ttgaatccta aaaaaaaaaa a 1020

<210> 395
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..957

<220>
 <221> sig_peptide
 <222> 25..93
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LEAFSQAISAIQA/LR

<220>
 <221> polyA_signal
 <222> 1368..1373

<220>
 <221> polyA_site
 <222> 1388..1399

<400> 395
 aakagctgct gtggcggcgg caac atg gcg gac gtg ata aat gtc agt gtg 51
 Met Ala Asp Val Ile Asn Val Ser Val
 -20 -15
 aac ctg gag gcc ttt tcc cag gcc att agt gcc atc cag gcg ctg cga 99
 Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
 -10 -5 1
 tcc agc gtg agc agg gtg ttc gac tgc ctg aag gat ggg atg cgg aac 147
 Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
 5 10 15
 aag gag acg ctg gag ggc cgg gag aag gcc ttt att gcg cac ttc cag 195
 Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
 20 25 30
 gac aac tta cat tcg gtc aac cgg gac ctc aat gag ctg gaa cgt ctg 243
 Asp Asn Leu His Ser Val Asn Arg Asp Leu Asn Glu Leu Glu Arg Leu
 35 40 45 50
 agc aat ctg gta ggc arg cca tct gar aac cat cct ctt cat aac agt 291
 Ser Asn Leu Val Gly Xaa Pro Ser Glu Asn His Pro Leu His Asn Ser
 55 60 65
 ggg ctg tta asc ctg gat cct gtg car gac aaa act cct ctc tat agt 339
 Gly Leu Leu Xaa Leu Asp Pro Val Gln Asp Lys Thr Pro Leu Tyr Ser

09978360.101501

70	75	80	
caa ctc ctt caa gca tat aag tgg tca aac aag ttg cag tac cat gca			387
Gln Leu Leu Gln Ala Tyr Lys Trp Ser Asn Lys Leu Gln Tyr His Ala			
85	90	95	
gga cta gca tct ggc ctt tta aat cas car tca ktg aag cgt ycc gct			435
Gly Leu Ala Ser Gly Leu Leu Asn Xaa Gln Ser Xaa Lys Arg Xaa Ala			
100	105	110	
aat cag atg gga gta tct gcc aaa cgt aga cca aag gct cag ccc aca			483
Asn Gln Met Gly Val Ser Ala Lys Arg Arg Pro Lys Ala Gln Pro Thr			
115	120	125	130
act ctt gtc cta cca cct caa tat gtt gat gat gtg atc agc cgc att			531
Thr Leu Val Leu Pro Pro Gln Tyr Val Asp Asp Val Ile Ser Arg Ile			
135	140	145	
gac agg atg ttt cct gaa atg tcc atc cac tta tcc aga ccc aat gga			579
Asp Arg Met Phe Pro Glu Met Ser Ile His Leu Ser Arg Pro Asn Gly			
150	155	160	
aca tca gca atg ctt ctg gtg acc ttg gga aar gtg ttg aaa gtg awc			627
Thr Ser Ala Met Leu Leu Val Thr Leu Gly Lys Val Leu Lys Val Xaa			
165	170	175	
gtc gtc rtr cgg arm ctg ttc att gat cga aca ata gtw aag gga tat			675
Val Val Xaa Arg Xaa Leu Phe Ile Asp Arg Thr Ile Val Lys Gly Tyr			
180	185	190	
wac gag aat gtc tac rca gaa kat ggc mag ctt gat ata tgg tcc aaa			723
Xaa Glu Asn Val Tyr Xaa Glu Xaa Gly Xaa Leu Asp Ile Trp Ser Lys			
195	200	205	210
tcc aac tat caa gta ttc cag aag gtg aca gac cat gcc acc act gcc			771
Ser Asn Tyr Gln Val Phe Gln Lys Val Thr Asp His Ala Thr Thr Ala			
215	220	225	
ctg ctc cac taw mag ctg ccc cag atg ccg gat gtc gtg gtc cga tcc			819
Leu Leu His Xaa Xaa Leu Pro Gln Met Pro Asp Val Val Val Arg Ser			
230	235	240	
ttc awg acc tgg tta aga agt tac ata aag ctg ttc cag gcc ccg tgc			867
Phe Xaa Thr Trp Leu Arg Ser Tyr Ile Lys Leu Phe Gln Ala Pro Cys			
245	250	255	
cag cgc tgc ggg aag ttt ctg cag gac ggc ctt ccc ccg aca tgg agg			915
Gln Arg Cys Gly Lys Phe Leu Gln Asp Gly Leu Pro Pro Thr Trp Arg			
260	265	270	
gat ttc cga acc ctc gaa gcc ttc cat gac acc tgc cgg cag			957
Asp Phe Arg Thr Leu Glu Ala Phe His Asp Thr Cys Arg Gln			
275	280	285	
tagccccac gctggccca gcctcagacc ccaccagca ccttcccaga cacgcaggaa			1017
gcccacagaa ggctcagctg gttectcact gccagatgt gtacagctgc tcctcccttt			1077
cataaagcag cgccatgtgt gcagaggcca ctcttgaaga gcagactccc tctgtggctg			1137
atgggactaa ttattccac tagccagcgg actgaaggca aagaagacct ttctagaacc			1197
tggtagaagg aagctgtgca gcatgctcct cgtccatgtg tgtcggcagt gctggtgtct			1257
gtcgtctccg cgagctgtta ctggaatgag cccttgtgtt catgggtatc gtcatgcggg			1317
gttcttgtgt tttgtggggc ttgggttttg gttaacttat ttttataagc aataaacctt			1377
ttgtatcctg aaaaaaaaaa aa			1399

<210> 396
 <211> 666
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..319
 <220>
 <221> sig_peptide
 <222> 47..226


```

<400> 397
agttggtggg gctgggggat gagagctgca ccgcgcgga yaagtcgccg gcggcgcccg      60
amggagcaga acagagagc atg gag ctg gag agg atc gtc agt gca gcc ctc      112
                Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu
                -15                -10
ctt gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg      160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
      -5                1                5                10
gat gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc      208
Asp Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly
                15                20                25
ccc tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag      256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
                30                35                40
atg atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca      304
Met Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
                45                50                55
ata ggg gac atg atg cag aar ctc tca ggg cag ctg agc gat gcc vgg      352
Ile Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Xaa
                60                65                70
aac aaa gag aac ctg caa ccg cag aac tct ggt gtc caa ggt cag gtg      400
Asn Lys Glu Asn Leu Gln Pro Gln Asn Ser Gly Val Gln Gly Gln Val
                75                80                85                90
ccc atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag      448
Pro Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu
                95                100                105
act agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act      496
Thr Arg Ser Ser Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr
                110                115                120
ggc gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg      544
Gly Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val
                125                130                135
ttc cct acc tgt tcg gtg gag cag gcc cag tgg gtg ctg gcc aaa gct      592
Phe Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala
                140                145                150
cgg ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa      640
Arg Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu
                155                160                165                170
gag ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc      688
Glu Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg
                175                180                185
ctc aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag      736
Leu Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys
                190                195                200
tac atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg      784
Tyr Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met
                205                210                215
gct ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag      832
Ala Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln
                220                225                230
gta gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag      880
Val Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu
                235                240                245                250
gcc gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag      928
Ala Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys
                255                260                265
tac cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca      980
Tyr Arg Phe His
                270
gatcccagag ggatgcagga gccctatacc cctacacagg ggccccctaa ctctgtccc      1040
ccttctctac tcctttgctc catagtgtta acctactctc ggagctgcct ccatgggcac      1100

```


agtaaagggtg gcccaaggaa aaaaaaaaaaw t

1131

<210> 398
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..457

<220>
<221> sig_peptide
<222> 146..292
<223> Von Heijne matrix
score 5.19999980926514
seq CFLCLYPIPLCTS/HP

<220>
<221> polyA_signal
<222> 442..447

<220>
<221> polyA_site
<222> 465..475

<400> 398
attgtaacaa acagtaccaa tttatttttg ccgtggggtt ttgctttttt tccagttgat 60
gactttgtga acattcccag gtattggagc ctctgtggcc ttaaagtgtg ctcagtggag 120
ggagacccag catagccagg ccagt atg gag cac ctc acg cac agc tct cag 172
Met Glu His Leu Thr His Ser Ser Gln
-45
aag ctg cag gcg gac gaa cat ctg acc aaa gag gtg tgg tcg agg ctc 220
Lys Leu Gln Ala Asp Glu His Leu Thr Lys Glu Val Trp Ser Arg Leu
-40 -35 -30 -25
ctg aaa gag aaa ggg cct gct ggt ctc atc ctc tgc ttc ctt tgc ctt 268
Leu Lys Glu Lys Gly Pro Ala Gly Leu Ile Leu Cys Phe Leu Cys Leu
-20 -15 -10
tac cct ata cct ctc tgc acg tcc cac ccc gtt tkg ctg tgt gcy cac 316
Tyr Pro Ile Pro Leu Cys Thr Ser His Pro Val Xaa Leu Cys Ala His
-5 1 5
ccc cag gat gtg tac ccg gtt gta gta aga gct gaa atc cat gct gag 364
Pro Gln Asp Val Tyr Pro Val Val Val Arg Ala Glu Ile His Ala Glu
10 15 20
ctg tac cag gaa ctt gca tat cta aaa aca gaa act gag tca ctg gcc 412
Leu Tyr Gln Glu Leu Ala Tyr Leu Lys Thr Glu Thr Glu Ser Leu Ala
25 30 35 40
cat ctc ttt gct ctt gtg ccc cag gcc aaa ata aag aat aga gtg 457
His Leu Phe Ala Leu Val Pro Gln Ala Lys Ile Lys Asn Arg Val
45 50 55
taragtgtgaaa aaaaaaaaaa 475

<210> 399
<211> 949
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..351

0997360 10501

Demographic Data		Health Status		Healthcare Utilization		Healthcare Costs		Healthcare Access		Healthcare Quality		Healthcare Equity		Healthcare Innovation			
Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value		
Age	65.2	Gender	Male	Prevalence	12.5%	Incidence	8.3%	Prevalence	15.2%	Incidence	9.1%	Prevalence	18.7%	Incidence	10.4%	Prevalence	21.3%
Gender	Female	Prevalence	10.1%	Incidence	6.7%	Prevalence	12.8%	Incidence	7.5%	Prevalence	14.5%	Incidence	8.9%	Prevalence	16.2%	Incidence	9.8%
Ethnicity	White	Prevalence	11.3%	Incidence	7.2%	Prevalence	13.5%	Incidence	8.1%	Prevalence	15.7%	Incidence	9.3%	Prevalence	17.9%	Incidence	10.6%
Ethnicity	Black	Prevalence	9.8%	Incidence	6.5%	Prevalence	11.9%	Incidence	7.0%	Prevalence	13.2%	Incidence	8.0%	Prevalence	15.4%	Incidence	9.5%
Ethnicity	Hispanic	Prevalence	10.5%	Incidence	6.9%	Prevalence	12.6%	Incidence	7.4%	Prevalence	14.8%	Incidence	9.0%	Prevalence	17.1%	Incidence	10.3%
Ethnicity	Asian	Prevalence	11.7%	Incidence	7.3%	Prevalence	13.8%	Incidence	8.2%	Prevalence	16.0%	Incidence	9.4%	Prevalence	18.2%	Incidence	10.7%
Ethnicity	Other	Prevalence	10.2%	Incidence	6.8%	Prevalence	12.4%	Incidence	7.3%	Prevalence	14.6%	Incidence	8.8%	Prevalence	16.8%	Incidence	9.9%
Education	High School	Prevalence	10.8%	Incidence	7.0%	Prevalence	12.9%	Incidence	7.6%	Prevalence	15.1%	Incidence	9.1%	Prevalence	17.3%	Incidence	10.4%
Education	College	Prevalence	11.5%	Incidence	7.4%	Prevalence	13.6%	Incidence	8.3%	Prevalence	15.8%	Incidence	9.5%	Prevalence	18.0%	Incidence	10.8%
Education	Postgraduate	Prevalence	12.1%	Incidence	7.8%	Prevalence	14.2%	Incidence	8.7%	Prevalence	16.4%	Incidence	9.7%	Prevalence	18.6%	Incidence	11.0%
Income	Low	Prevalence	10.3%	Incidence	6.9%	Prevalence	12.5%	Incidence	7.2%	Prevalence	14.7%	Incidence	8.9%	Prevalence	16.9%	Incidence	10.1%
Income	Medium	Prevalence	11.0%	Incidence	7.1%	Prevalence	13.1%	Incidence	7.7%	Prevalence	15.3%	Incidence	9.2%	Prevalence	17.5%	Incidence	10.5%
Income	High	Prevalence	11.8%	Incidence	7.5%	Prevalence	13.9%	Incidence	8.1%	Prevalence	16.1%	Incidence	9.6%	Prevalence	18.3%	Incidence	10.9%
Insurance	Medicaid	Prevalence	10.6%	Incidence	7.0%	Prevalence	12.7%	Incidence	7.5%	Prevalence	14.9%	Incidence	9.0%	Prevalence	17.1%	Incidence	10.3%
Insurance	Medicare	Prevalence	11.2%	Incidence	7.3%	Prevalence	13.3%	Incidence	7.9%	Prevalence	15.5%	Incidence	9.4%	Prevalence	17.7%	Incidence	10.6%
Insurance	Private	Prevalence	11.9%	Incidence	7.6%	Prevalence	14.0%	Incidence	8.2%	Prevalence	16.2%	Incidence	9.7%	Prevalence	18.4%	Incidence	11.0%
Insurance	Uninsured	Prevalence	10.4%	Incidence	6.8%	Prevalence	12.6%	Incidence	7.3%	Prevalence	14.8%	Incidence	8.8%	Prevalence	17.0%	Incidence	10.2%
Access	Urban	Prevalence	11.4%	Incidence	7.2%	Prevalence	13.5%	Incidence	8.0%	Prevalence	15.7%	Incidence	9.3%	Prevalence	17.9%	Incidence	10.7%
Access	Suburban	Prevalence	10.9%	Incidence	6.9%	Prevalence	13.0%	Incidence	7.6%	Prevalence	15.2%	Incidence	9.1%	Prevalence	17.4%	Incidence	10.5%
Access	Rural	Prevalence	10.1%	Incidence	6.7%	Prevalence	12.2%	Incidence	7.0%	Prevalence	14.4%	Incidence	8.6%	Prevalence	16.6%	Incidence	9.9%
Quality	High	Prevalence	11.6%	Incidence	7.4%	Prevalence	13.7%	Incidence	8.3%	Prevalence	15.9%	Incidence	9.6%	Prevalence	18.1%	Incidence	10.9%
Quality	Medium	Prevalence	11.1%	Incidence	7.1%	Prevalence	13.2%	Incidence	7.8%	Prevalence	15.4%	Incidence	9.2%	Prevalence	17.6%	Incidence	10.6%
Quality	Low	Prevalence	10.7%	Incidence	6.8%	Prevalence	12.8%	Incidence	7.4%	Prevalence	15.0%	Incidence	8.7%	Prevalence	17.2%	Incidence	10.3%
Equity	High	Prevalence															

```
<220>  
<221> misc_feature  
<222> 745  
<223> n=a, g, c or t
```

```
<210> 400
<211> 940
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> sig_peptide
<222> 177..236
<223> Von Heijne matrix
      score 11.1999998092651
```

seq AFLLLVALSYTLA/RD

<220>

<221> polyA_site

<222> 931..939

<220>

<221> misc_feature

<222> 482

<223> n=a, g, c or t

<400> 400

```
agaagataat cacttgggga aaggaaggtt cgtttctgag ttagcaacaa gtaaattgcag      60
cactagtggg tgggattgag gtatgccctg gtgcataaat agagactcag ctgtgctggc      120
acactcagaa gcttggaccg catcctagcc gccgactcac acaaggcaga gttgcc atg      179
Met
-20
gaa aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac      227
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr
-15 -10 -5
act ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca      275
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
1 5 10
aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt      323
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
15 20 25
gac caa ctc atc tgg aca car aca tat gaa raa rct cta twt aaa tcc      371
Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Xaa Xaa Leu Xaa Lys Ser
30 35 40 45
aar aca agc aac aaa ccc ttg atg att att cat cac ttg gat gad tgc      419
Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Xaa Cys
50 55 60
cca cac agt caa gct tta aaa aaa ktg ttt gct gaa aat aaa raa atc      467
Pro His Ser Gln Ala Leu Lys Lys Xaa Phe Ala Glu Asn Lys Xaa Ile
65 70 75
cag aaa ttg gca ran cag ttt gtc cyc ctc aat ctg gtt tat gaa aca      515
Gln Lys Leu Ala Xaa Gln Phe Val Xaa Leu Asn Leu Val Tyr Glu Thr
80 85 90
act gac aaa cac ctt tct cct gat ggc caa tat ktc ccc cmg gat tat      563
Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Xaa Pro Xaa Asp Tyr
95 100 105
gtt tgt tgacccatct ctgacagtta gagccgatat cactggaaga tattcaaayc      619
Val Cys
110
gtctctatgc ttacgaacct gcagatacag ctctgttgct tgacaacatg aagaaagctc      679
tcaagttgct gaagactgaa ttgtaaagaa aaaaaatctc caagcccttc tgtctgtcag      739
gccttgagac ttgaaaccag aagaagtgtg agaagactgg ctagtgtgga agcatagtga      799
acacactgat taggttatgg tttaatgtta caacaactat tttttaagaa aaacaagttt      859
tagaaatttg gtttcaagtg tacatgtgtg aaaacaatat tgtatactac catagtgagc      919
catgattttc taaaaaaaaa a      940
```

<210> 401

<211> 887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..459

<220>

09978360.101501

<221> sig_peptide
 <222> 67..135
 <223> Von Heijne matrix
 score 5.19999980926514
 seq IGVGLYLLASAAA/FY

<220>
 <221> polyA_signal
 <222> 856..861

<220>
 <221> polyA_site
 <222> 875..887

<400> 401
 agcggcggca tccgggacgg cgggcgggct ggccaccacg ggacaggaag gcacagagca 60
 tggaga atg atg aac ttc cgt cag cgg atg gga tgg att gga gtg gga 108
 Met Met Asn Phe Arg Gln Arg Met Gly Trp Ile Gly Val Gly
 -20 -15 -10
 ttg tat ctg tta gcc agt gca gca gca ttt tac tat gtt ttt gaa atc 156
 Leu Tyr Leu Leu Ala Ser Ala Ala Ala Phe Tyr Tyr Val Phe Glu Ile
 -5 1 5
 agt gag act tac aac agg ctg gcc ttg gaa cac att caa cag cac cct 204
 Ser Glu Thr Tyr Asn Arg Leu Ala Leu Glu His Ile Gln Gln His Pro
 10 15 20
 ggg gag ccc ctt gaa gga acc aca tgg aca cac tcc ttg aaa gct caa 252
 Gly Glu Pro Leu Glu Gly Thr Thr Trp Thr His Ser Leu Lys Ala Gln
 25 30 35
 tta ctc tcc ttg cct ttt tgg gtg tgg aca gtt att ttt ctg gta cct 300
 Leu Leu Ser Leu Pro Phe Trp Val Trp Thr Val Ile Phe Leu Val Pro
 40 45 50 55
 tac tta car atk ttt ttg ttc cta tac tct tgt aca aaa vct gat ccc 348
 Tyr Leu Gln Xaa Phe Leu Phe Leu Tyr Ser Cys Thr Lys Xaa Asp Pro
 60 65 70
 aaa aca gtg ggc tac tgt wtc atc cct ata tgc ttg gca rtt att tsc 396
 Lys Thr Val Gly Tyr Cys Xaa Ile Pro Ile Cys Leu Ala Xaa Ile Xaa
 75 80 85
 aat cgc cac cag gat ttt gtc aag gct tct aat caa atc agc aaa cta 444
 Asn Arg His Gln Asp Phe Val Lys Ala Ser Asn Gln Ile Ser Lys Leu
 90 95 100
 caa ctg att gac acg taaaatcagt caccgttttt tccctacgat tacaaaactg 499
 Gln Leu Ile Asp Thr
 105
 ccagtccat atggagtctg atcacaagac tgcagtttct tcacagatct caggaagttg 559
 tcgtggggca gaggcttttt aaaaacatgt gattagggag ctatctttat ctgaataata 619
 acgaattttt aggtaaaacc tgagatagag tactacaaaa tcatgttgat gacttcagat 679
 tttggaagtt aaatcatgtc tggtatttgc attctttaga aacttgacta agtacctgaa 739
 ttcataatttc tattctactg tgcaacatag tgatgattca gaaatttttc ctttggggaa 799
 aaaaatgaat atgaacattt ccattgtgtt aagtgtaaaa aggtccagka catgatcata 859
 aaattttaat ttatatacaa aaaaaaaaa 887

<210> 402
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..1069

<220>

<221> sig_peptide
 <222> 65..112
 <223> Von Heijne matrix
 score 12.5
 seq FVVLALVAGVLG/NE

<220>
 <221> polyA_signal
 <222> 1978..1983

<220>
 <221> polyA_site
 <222> 1999..2010

<400> 402
 atgtcgcccg tgtcccgccg gcccggttccg tgtcgccccg cagtgytgcg gccgccgckk 60
 cacc atg gct gtg ttt gtc gtg ctc ctg gcg ttg gtg gcg ggt gtt ttg 109
 Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu
 -15 -10 -5
 ggg aac gag ttt agt ata tta aaa tca cca ggg tct gtt gtt ttc cga 157
 Gly Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg
 1 5 10 15
 aat gga aat tgg cct ata cca gga gag cgg atc cca gac gtg gct gca 205
 Asn Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala
 20 25 30
 ttg tcc atg ggc ttc tct gtg aaa gaa gac ctt tct tgg cca gga ctc 253
 Leu Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu
 35 40 45
 gca gtg ggt aac ctg ttt cat cgt cct cgg gct agc gtc atg gtg atg 301
 Ala Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met
 50 55 60
 gtg aag gga gtt aac aac tmc cct cta ccc cca ggc tgt gtc att tcg 349
 Val Lys Gly Val Asn Asn Xaa Pro Leu Pro Pro Gly Cys Val Ile Ser
 65 70 75
 tac cct ttg gag aat gca gtt cct ttt agt ctt gac agt gtt gca aat 397
 Tyr Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn
 80 85 90 95
 tcc att cac tcc tta ttt tct gag gaa act cct gtt gtt ttg cag ttg 445
 Ser Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu
 100 105 110
 gct ccc agt gag gaa aga gtg tat atg gta ggg aag gcm aac tca gtg 493
 Ala Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val
 115 120 125
 tgg aar acc ttt cag tca ctt gcg cca gct ccg kta atc rcc tgt ttc 541
 Trp Lys Thr Phe Gln Ser Leu Ala Pro Ala Pro Xaa Ile Xaa Cys Phe
 130 135 140
 aag aaa act ctg ttc tca gtt cac tcc ccc ycc att cma ctg agt agg 589
 Lys Lys Thr Leu Phe Ser Val His Ser Pro Xaa Ile Xaa Leu Ser Arg
 145 150 155
 aac aat gaa gtt gac cyg ctc ttt ctt tct gaa ctg caa gtg cta cat 637
 Asn Asn Glu Val Asp Xaa Leu Phe Leu Ser Glu Leu Gln Val Leu His
 160 165 170 175
 gat att tca agc ttg ctg tct cgt cat aag cat cta gcc aag gat cat 685
 Asp Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His
 180 185 190
 tct cct gat tta tat tca ctg gag ctg gca ggt ttg gat gaa att ggg 733
 Ser Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly
 195 200 205
 aag cgt tat ggg gaa gac tct gaa caa ttc aga gat gct tct aag atc 781
 Lys Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile
 210 215 220

```

ctt gtt gac gct ctg caa aag ttt gca gat gac atg tac agt ctt tat      829
Leu Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr
    225                230                235
ggg ggg aat gca gtg gta gag tta gtc act gtc aag tca ttt gac acc      877
Gly Gly Asn Ala Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr
240                245                250                255
tcc ctc att agg aag aca agg act atc ctt gag gca aaa caa gcg aag      925
Ser Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys
    260                265                270
aac cca gca agt ccc tat aac ctt gca tat aag tat aat ttt gaa tat      973
Asn Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr
    275                280                285
tcc gtg gtt ttc aac atg gta ctt tgg ata atg atc gcc ttg gcc ttg     1021
Ser Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu
    290                295                300
gct gtg att atc acc tct tac aat att tgg aac atg gaa tcc tgg ata     1069
Ala Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Glu Ser Trp Ile
    305                310                315
tgatagcatc atttatagga tgacaaacca gaagattcgg aatggattga atgttacctg     1129
tgccagaatt akaaaagggg gttggaaatt ggctgttttg ttaaaatata tcttttagtg     1189
tgctttaaag tagatagtat actttacatt tataaaaaaa aatcaaattt tgttctttat     1249
tttgtgtgtg cctgtgatgt ttttctagag tgaattatag tattgacgtg aatcccactg     1309
tggtatagat tccataatat gcttgaatat tatgatatag ccatttaata acattgattt     1369
cattctgttt aatgaatttg gaaatatgca ctgaaagaaa tgtaaaacat ttagaatagc     1429
tcgtgtttatg gaaaaaagtg cactgaattt attagacaaa cttacgaatg cttaacttct     1489
ttacacagca taggtgaaaa tcatatttgg gctattgtat actatgaaca atttgtaaat     1549
gtcttaattt gatgtaaata actctgaaac aagagaaaag gtttttaact tagagtagcc     1609
ctaaaatatg gatgtgctta tataatcgct tagttttgga actgtatctg agtaacagag     1669
gacagctgtt ttttaaccct cttctgcaag tttgttgacc tacatgggct aatatggata     1729
ctaaaaatac tacattgatc taagaagaaa ctagccttgt ggagtatata gatgcttttc     1789
attatacaca caaaaatccc tgagggacat tttgaggcat gaatataaaa catttttatt     1849
tcagtaactt ttccccctgt gtaagttact atggtttgtg gtacaacttc attctataga     1909
atattaagtg gaagtgggtg aattctactt tttatgttgg agtggaccaa tgtctatcaa     1969
gagtgcacaaa taaagttaat gatgattcca aaaaaaaaaa a                               2010

```

<210> 403
 <211> 387
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..321

<220> .
 <221> sig_peptide
 <222> 70..234
 <223> Von Heijne matrix
 score 4.09999990463257
 seq AVCAALLASHPTA/EV

<220>
 <221> polyA_signal
 <222> 364..369

<220>
 <221> polyA_site
 <222> 375..387

<400> 403
 agaaatcgta ggacttccga aagcagcggc ggcgtttgct tctactgcttg gaagtgtgag 60

```

tgcgcggaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att 111
      Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
      -55          -50          -45
ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat 159
Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
      -40          -35          -30
ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct 207
Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
      -25          -20          -15          -10
gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg 255
Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
      -5          1          5
gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag 303
Asp Val Ser Asn Leu Gln Ser Phe Arg Ala Ser Lys Glu Leu Lys
      10          15          20
caa agg atg atc tct tgc tgatggattt tttttctcat gtgattgtgc 351
Gln Arg Met Ile Ser Cys
      25
ascataacac ttaataaaaat aagaaaaaaaa aaaaaa 387

<210> 404
<211> 983
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..877

<220>
<221> sig_peptide
<222> 38..91
<223> Von Heijne matrix
      score 7.40000009536743
      seq GWLVLCVLAISLA/SM

<220>
<221> polyA_signal
<222> 947..952

<220>
<221> polyA_site
<222> 974..983

<400> 404
aatccagtyg gasttgacaa caggaggcag aggcatac atg gag ggt ccc cgg gga 55
      Met Glu Gly Pro Arg Gly
      -15
tgg ctg gtg ctc tgt gtg ctg gcc ata tcg ctg gcc tct atg gtg acc 103
Trp Leu Val Leu Cys Val Leu Ala Ile Ser Leu Ala Ser Met Val Thr
      -10          -5          1
gag gac ttg tgc cga gca cca gac ggg aag aaa ggg gag gca gga aga 151
Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys Lys Gly Glu Ala Gly Arg
      5          10          15          20
cct ggc aga cgg ggg cgg cca ggc ctc aag ggg gag caa ggg gag ccg 199
Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys Gly Glu Gln Gly Glu Pro
      25          30          35
ggg gcc cct ggc atc cgg aca ggc atc caa ggc ctt aaa gga gac cag 247
Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln Gly Leu Lys Gly Asp Gln
      40          45          50
ggg gaa cct ggg ccc tct gga aac ccc ggc aag gtg ggc tac cca ggg 295

```

Gly	Glu	Pro	Gly	Pro	Ser	Gly	Asn	Pro	Gly	Lys	Val	Gly	Tyr	Pro	Gly		
		55					60					65					
ccc	agc	ggc	ccc	ctc	gga	gcc	cgt	ggc	atc	ccg	gga	att	aaa	ggc	acc		343
Pro	Ser	Gly	Pro	Leu	Gly	Ala	Arg	Gly	Ile	Pro	Gly	Ile	Lys	Gly	Thr		
	70					75				80							
aag	ggc	agc	cca	gga	aac	atc	aag	gac	cag	ccg	agg	cca	gcc	ttc	tcc		391
Lys	Gly	Ser	Pro	Gly	Asn	Ile	Lys	Asp	Gln	Pro	Arg	Pro	Ala	Phe	Ser		
85					90					95					100		
gcc	att	cgg	cgg	aac	ccc	cca	atg	ggg	ggc	aac	gtg	gtc	atc	ttc	gac		439
Ala	Ile	Arg	Arg	Asn	Pro	Pro	Met	Gly	Gly	Asn	Val	Val	Ile	Phe	Asp		
				105					110					115			
acg	gtc	atc	acc	aac	cag	gaa	gaa	ccg	tac	cag	aac	cac	tcc	ggc	cga		487
Thr	Val	Ile	Thr	Asn	Gln	Glu	Glu	Pro	Tyr	Gln	Asn	His	Ser	Gly	Arg		
			120					125					130				
ttc	gtc	tgc	act	gta	ccc	gct	act	act	act	tca	cct	tcc	agg	tgc	tgt		535
Phe	Val	Cys	Thr	Val	Pro	Ala	Thr	Thr	Thr	Ser	Pro	Ser	Arg	Cys	Cys		
		135				140						145					
ccc	agt	ggg	aaa	tct	gcc	tgt	cca	tcg	tct	cct	cct	caa	ggg	gcc	agg		583
Pro	Ser	Gly	Lys	Ser	Ala	Cys	Pro	Ser	Ser	Pro	Pro	Gln	Gly	Ala	Arg		
	150				155					160							
tcc	gac	gct	ccc	tgg	gct	tct	gtg	aca	cca	cca	aca	agg	ggc	tct	tcc		631
Ser	Asp	Ala	Pro	Trp	Ala	Ser	Val	Thr	Pro	Pro	Thr	Arg	Gly	Ser	Ser		
	165			170					175					180			
agg	tgg	tgt	cag	ggg	gca	tgg	tgc	ttc	agc	tgc	agc	agg	gtg	acc	agg		679
Arg	Trp	Cys	Gln	Gly	Ala	Trp	Cys	Phe	Ser	Cys	Ser	Arg	Val	Thr	Arg		
			185					190					195				
tct	ggg	ttg	aaa	aag	acc	cca	aaa	agg	gtc	aca	ttt	acc	agg	gct	ctg		727
Ser	Gly	Leu	Lys	Lys	Thr	Pro	Lys	Arg	Val	Thr	Phe	Thr	Arg	Ala	Leu		
		200				205						210					
agg	ccg	aca	gcg	tct	tca	gcg	gct	tcc	tca	tct	tcc	cat	ctg	cct	gag		775
Arg	Pro	Thr	Ala	Ser	Ser	Ala	Ala	Ser	Ser	Ser	Ser	His	Leu	Pro	Glu		
	215				220							225					
cca	ggg	aag	gac	ccc	ctc	ccc	cac	cca	cct	ctc	tgg	ctt	cca	tgc	tcc		823
Pro	Gly	Lys	Asp	Pro	Leu	Pro	His	Pro	Pro	Leu	Trp	Leu	Pro	Cys	Ser		
	230				235					240							
gcc	tgt	aaa	atg	ggg	gcg	cta	ttg	ctt	cag	ctg	ctg	aag	gga	ggg	ggc		871
Ala	Cys	Lys	Met	Gly	Ala	Leu	Leu	Leu	Gln	Leu	Leu	Lys	Gly	Gly	Gly		
	245				250				255				260				
tgg	ctc	tgagagcccc	aggactggct	gccccgtgac	acatgctcta	agaagctcgt											927
Trp	Leu																
ttcttagacc	tcttctctgga	ataaacatct	gtgtctgtgt	ctgctgaaaa	aaaaaa												983

<210> 405
 <211> 1614
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..470

<220>
 <221> sig_peptide
 <222> 51..203
 <223> Von Heijne matrix
 score 5.80000019073486
 seq AVGLFPAPTECFR/RV

<220>
 <221> polyA_signal
 <222> 1585..1590

<220>
 <221> polyA_site
 <222> 1604..1614

<400> 405

ataagcctgt ggttgatgga aattcacaaa gtgaggcatt atcactggaa atg aga	56
Met Arg	
-50	
aag gat ccg agc ggg gct ggc ctc tgg ctt cac agt ggc ggc cca gtg	104
Lys Asp Pro Ser Gly Ala Gly Leu Trp Leu His Ser Gly Gly Pro Val	
-45 -40 -35	
ctt cca tat gtg aga gaa tca gta aga aga aat cca gcc tca gca gcc	152
Leu Pro Tyr Val Arg Glu Ser Val Arg Asn Pro Ala Ser Ala Ala	
-30 -25 -20	
act ccg agc aca gcc gtg ggt ttg ttc cct gct cca aca gag tgt ttt	200
Thr Pro Ser Thr Ala Val Gly Leu Phe Pro Ala Pro Thr Glu Cys Phe	
-15 -10 -5	
gct cgg gtg tcc tgc agt ggt gtt gaa gct ctg ggg cgg cga gac tgg	248
Ala Arg Val Ser Cys Ser Gly Val Glu Ala Leu Gly Arg Arg Asp Trp	
1 5 10 15	
ctg gga gga ggg ccc agg gcc cac tgr msg gcv aca gag gmc agt gcc	296
Leu Gly Gly Gly Pro Arg Ala His Xaa Xaa Ala Thr Glu Xaa Ser Ala	
20 25 30	
cca aag gag agc ctc ggg tgt cac gac tgc cac gcc atc aaa aag tgc	344
Pro Lys Glu Ser Leu Gly Cys His Asp Cys His Ala Ile Lys Lys Cys	
35 40 45	
cgg aaa tgg gaa gtt ttc agg atg acc cac caa gtg ctt ttc cca agg	392
Arg Lys Trp Glu Val Phe Arg Met Thr His Gln Val Leu Phe Pro Arg	
50 55 60	
gtc tgg gct ctg agt tgg aac ccg ctt gcc tgc act cca tcc tgt ctg	440
Val Trp Ala Leu Ser Trp Asn Pro Leu Ala Cys Thr Pro Ser Cys Leu	
65 70 75	
caa cgc tgc aca tgt atc ccg aak tgc tcc tgagtgagga racaaaacgc	490
Gln Arg Cys Thr Cys Ile Pro Xaa Cys Ser	
80 85	
atktyccttg accgtytaaa gcccatggtt ycaaagcaaa caatavaatt caaraarrtg	550
cttaaaagca cctcaratgg tckgcaaata acactgggggt tactggctct gcaacctttt	610
gaattavcaa atacattatg ccatagttaa ggtacaagca gaacaatacc aatagattaa	670
ttttaagagt tgtcttagaa tgatttcttt cgcataaagt ctggatgcaa actgtgcagc	730
ccttaggtmc ctgctgtagt tttgtacgac ctggcagact taaagtaaat tgagttaaaa	790
ttcaaaagcca gttgatgcgg aaggaacttt tttggcatgt gttaaattgt gctttaaaag	850
acataataaag aattgggaaa catttcagga gacgatcata gcctgtataa ataccagatt	910
agaacatacg gatattccat gaagttctgt cttcaacatc cattctaaag ggctactgtc	970
ccaaatcctg tgtgtccttt tgacttgtct gatcacccaa tggaagtgga tacttgtaaa	1030
gtctacacca ctgtacttgg cgttaaatct tgctgaattc gtggttaagct gttaccatgt	1090
ctacattttg tagaatgatt ttggtctgca gcaaaattcg atttcacttc tcataccctt	1150
ttccttccac ttgaaatgca atttagacag akgccctgtg gtgaaagttg caatattaag	1210
tttaccttta gaagatccct tctcaaactc agaaccctag cagtgttacc ttaaacaaaa	1270
atgaktctga gaaaaaagta gctcagttac agagaagcaa atcgagttat ttcccacata	1330
aaaagtcttc cagattctaa gaattgcagt atcctgtacc ctaaaatttt tcaaggtgac	1390
tctgtgtgac gtctgttgat aactttaata aagggtcattt aaggacataa gtttttaaa	1450
actcccaaag tgaaacttaa acattttcgg gattatcgat tgcataatc agtttatgct	1510
gtgtgctgaa ttactatgcc atgtgctatt ttagtggttg gggaaaatga aaaataaaat	1570
ttgttcttta gcttaataaa tawgtcttat tttaaaaaaa aaaa	1614

<210> 406
 <211> 325
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 406
 Met Ala Thr Pro Leu Pro Pro Pro Ser Pro Arg His Leu Arg Leu Leu
 -25 -20 -15
 Arg Leu Leu Leu Ser Gly Leu Val Leu Gly Ala Ala Leu Arg Gly Ala
 -10 -5 1 5
 Ala Ala Gly His Pro Asp Val Ala Ala Cys Pro Gly Ser Leu Asp Cys
 10 15 20
 Ala Leu Lys Arg Arg Ala Arg Cys Pro Pro Gly Ala His Ala Cys Gly
 25 30 35
 Pro Cys Leu Gln Pro Phe Gln Glu Asp Gln Gln Gly Leu Cys Val Pro
 40 45 50
 Arg Met Arg Arg Pro Pro Gly Gly Gly Arg Pro Gln Pro Arg Leu Glu
 55 60 65 70
 Asp Glu Ile Asp Phe Leu Ala Gln Glu Leu Ala Arg Lys Glu Ser Gly
 75 80 85
 His Ser Thr Pro Pro Leu Pro Lys Asp Arg Gln Arg Leu Pro Glu Pro
 90 95 100
 Ala Thr Leu Gly Phe Ser Ala Arg Gly Gln Gly Leu Glu Leu Gly Leu
 105 110 115
 Pro Ser Thr Pro Gly Thr Pro Thr Pro Thr Pro His Thr Ser Leu Gly
 120 125 130
 Ser Pro Val Ser Ser Asp Pro Val His Met Ser Pro Leu Glu Pro Arg
 135 140 145 150
 Gly Gly Gln Gly Asp Gly Leu Ala Leu Val Leu Ile Leu Ala Phe Cys
 155 160 165
 Val Ala Gly Ala Ala Ala Leu Ser Val Ala Ser Leu Cys Trp Cys Arg
 170 175 180
 Leu Gln Arg Glu Ile Arg Leu Thr Gln Lys Ala Asp Tyr Ala Thr Ala
 185 190 195
 Lys Ala Pro Gly Ser Pro Ala Ala Pro Arg Ile Ser Pro Gly Asp Gln
 200 205 210
 Arg Leu Ala Gln Ser Ala Glu Met Tyr His Tyr Gln His Gln Arg Gln
 215 220 225 230
 Gln Met Leu Cys Leu Glu Arg His Lys Glu Pro Pro Lys Glu Leu Asp
 235 240 245
 Thr Ala Ser Ser Asp Glu Glu Asn Glu Asp Gly Asp Phe Thr Val Tyr
 250 255 260
 Glu Cys Pro Gly Leu Ala Pro Thr Gly Glu Met Glu Val Arg Asn Pro
 265 270 275
 Leu Phe Asp His Ala Ala Leu Ser Ala Pro Leu Pro Ala Pro Ser Ser
 280 285 290
 Pro Pro Ala Leu Pro
 295

<210> 407
 <211> 302
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 407
 Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
 -15 -10 -5
 Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu

09978350 "101501
 TOSTOT" 09E6660

	1					5					10					
Cys 15	Leu	Ala	Thr	Cys	Leu 20	Asp	His	His	Phe	Pro 25	Thr	Gly	Ser	Arg	Pro 30	
Thr	Val	Pro	Gly	Pro 35	Leu	His	Phe	Ser	Gly 40	Tyr	Ser	Ser	Val	Pro 45	Asp	
Gly	Lys	Pro	Leu 50	Val	Arg	Glu	Pro	Cys 55	Arg	Ser	Cys	Ala	Val 60	Val	Ser	
Ser	Ser	Gly 65	Gln	Met	Leu	Gly	Ser 70	Gly	Leu	Gly	Ala	Glu	Ile 75	Asp	Ser	
Ala	Glu	Cys	Val	Phe	Arg	Met 85	Asn	Gln	Ala	Pro	Thr 90	Val	Gly	Phe	Glu	
Ala 95	Asp	Val	Gly	Gln	Arg	Ser 100	Thr	Leu	Arg	Val 105	Val	Ser	His	Thr	Ser 110	
Val	Pro	Leu	Leu 115	Leu	Arg	Asn	Tyr	Ser	His 120	Tyr	Phe	Gln	Lys	Ala 125	Arg	
Asp	Thr	Leu	Tyr 130	Met	Val	Trp	Gly	Gln 135	Gly	Arg	His	Met	Asp 140	Arg	Val	
Leu	Gly	Gly 145	Arg	Thr	Tyr	Arg	Thr 150	Leu	Leu	Gln	Leu	Thr 155	Arg	Met	Tyr	
Pro	Gly	Leu 160	Gln	Val	Tyr	Thr 165	Phe	Thr	Glu	Arg 170	Met	Met	Ala	Tyr	Cys	
Asp 175	Gln	Ile	Phe	Gln 180	Asp	Glu	Thr	Gly	Lys 185	Asn	Arg	Arg	Gln	Ser	Gly 190	
Ser	Phe	Leu	Ser 195	Thr	Gly	Trp	Phe	Thr	Met 200	Ile	Leu	Ala	Leu	Glu 205	Leu	
Cys	Glu	Glu 210	Ile	Val	Val	Tyr	Gly 215	Met	Val	Ser	Asp	Ser	Tyr 220	Cys	Arg	
Glu	Lys	Ser 225	His	Pro	Ser	Val	Pro 230	Tyr	His	Tyr	Phe	Glu 235	Lys	Gly	Arg	
Leu	Asp	Glu 240	Cys	Gln	Met	Tyr 245	Leu	Ala	His	Glu	Gln	Ala	Pro	Arg	Ser	
Ala 255	His	Arg	Phe	Ile 260	Thr	Glu	Lys	Ala	Val	Phe 265	Ser	Arg	Trp	Ala	Lys 270	
Lys	Arg	Pro	Ile 275	Val	Phe	Ala	His	Pro	Ser 280	Trp	Arg	Thr	Glu			

```
<220>
<221> SIGNAL
<222> -15..-1
```

<400> 408															
Met	Leu	Gln	Leu	Trp	Lys	Leu	Val	Leu	Leu	Cys	Gly	Val	Leu	Thr	Gly
-15					-10					-5					1
Thr	Ser	Glu	Ser	Leu	Leu	Asp	Asn	Leu	Gly	Asn	Asp	Leu	Ser	Asn	Val
			5					10					15		
Val	Asp	Lys	Leu	Glu	Pro	Val	Leu	His	Glu	Gly	Leu	Glu	Thr	Val	Asp
		20					25					30			
Asn	Thr	Leu	Lys	Gly	Ile	Leu	Glu	Lys	Leu	Lys	Val	Asp	Leu	Gly	Val
	35				40					45					
Leu	Gln	Lys	Ser	Ser	Ala	Trp	Gln	Leu	Ala	Lys	Gln	Lys	Ala	Gln	Glu
50					55					60					65
Ala	Glu	Lys	Leu	Leu	Asn	Asn	Val	Ile	Ser	Lys	Leu	Leu	Pro	Thr	Asn
				70					75					80	
Thr	Asp	Ile	Phe	Gly	Leu	Lys	Ile	Ser	Asn	Ser	Leu	Ile	Leu	Asp	Val
			85					90					95		
Lys	Ala	Glu	Pro	Ile	Asp	Asp	Gly	Lys	Gly	Leu	Asn	Leu	Ser	Phe	Pro

100	105	110
Val Thr Ala Asn Val Thr	Val Ala Gly Pro Ile	Ile Gly Gln Ile Ile
115	120	125
Asn Leu Lys Ala Ser Leu	Asp Leu Leu Thr Ala	Val Thr Ile Glu Thr
130	135	140
Asp Pro Gln Thr His Gln	Pro Val Ala Val Leu	Gly Glu Cys Ala Ser
150	155	160
Asp Pro Thr Ser Ile Ser	Leu Ser Leu Leu Asp	Lys His Ser Gln Ile
165	170	175
Ile Asn Lys Phe Val Asn	Ser Val Ile Asn Thr	Leu Lys Ser Thr Val
180	185	190
Ser Ser Leu Leu Gln Lys	Glu Ile Cys Pro Leu	Ile Arg Ile Phe Ile
195	200	205
His Ser Leu Asp Val Asn	Val Ile Gln Gln Val	Val Asp Asn Pro Gln
210	215	220
His Lys Thr Gln Leu Gln	Thr Leu Ile	
230		

<210> 409
 <211> 84
 <212> PRT
 <213> Homo Sapiens

<400> 409
Met Lys Val Lys Ile Lys Cys Trp Asn Gly Val Ala Thr Trp Leu Trp
1 5 10 15
Val Ala Asn Asp Glu Asn Cys Gly Ile Cys Arg Met Ala Phe Asn Gly
20 25 30
Cys Cys Pro Asp Cys Lys Val Pro Gly Asp Asp Cys Pro Leu Val Trp
35 40 45
Gly Gln Cys Ser His Cys Phe His Met His Cys Ile Leu Lys Trp Leu
50 55 60
His Ala Gln Gln Val Gln Gln His Cys Pro Met Cys Arg Gln Glu Trp
65 70 75 80
Lys Phe Lys Glu

<210> 410
 <211> 554
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<220>
 <221> UNSURE
 <222> 259
 <223> Xaa = Asp,His,Asn,Tyr

<400> 410
Met Leu Tyr Leu Gln Gly Trp Ser Met Pro Ala Val Ala Glu Val Lys
-10 -5 1
Leu Arg Asp Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met
5 10 15
Tyr Asn Tyr Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr
20 25 30 35
Ile Asp Thr Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr
40 45 50
Ala Leu Gly Lys Pro Arg Glu Val Phe Arg Leu Pro Thr Asp Leu Thr
55 60 65

09978360.101501

Ala	Cys	Asp	Asn	Arg	Leu	Cys	Ala	Ser	Ile	His	Phe	Ser	Ser	Ser	Thr
	70						75					80			
Trp	Val	Thr	Leu	Ser	Asp	Gly	Thr	Gly	Arg	Leu	Tyr	Val	Ile	Gly	Thr
	85					90					95				
Gly	Glu	Arg	Gly	Asn	Ser	Ala	Ser	Glu	Lys	Trp	Glu	Ile	Met	Phe	Asn
100					105					110					115
Glu	Glu	Leu	Gly	Asp	Pro	Phe	Ile	Ile	Ile	His	Ser	Ile	Ser	Leu	Leu
				120						125				130	
Asn	Ala	Glu	Glu	His	Ser	Ile	Ala	Thr	Leu	Leu	Leu	Arg	Ile	Glu	Lys
				135				140					145		
Glu	Glu	Leu	Asp	Met	Lys	Gly	Ser	Gly	Phe	Tyr	Val	Ser	Leu	Glu	Trp
		150					155					160			
Val	Thr	Ile	Ser	Lys	Lys	Asn	Gln	Asp	Asn	Lys	Lys	Tyr	Glu	Ile	Ile
	165					170					175				
Lys	Arg	Asp	Ile	Leu	Arg	Gly	Lys	Ser	Val	Pro	His	Tyr	Ala	Ala	Ile
180					185					190					195
Lys	Pro	Asp	Gly	Asn	Gly	Leu	Met	Ile	Val	Ser	Tyr	Lys	Ser	Leu	Thr
				200					205					210	
Phe	Val	Gln	Ala	Gly	Gln	Asp	Leu	Glu	Glu	Asn	Met	Asp	Glu	Asp	Ile
			215					220					225		
Ser	Glu	Lys	Ile	Lys	Glu	Pro	Leu	Tyr	Tyr	Trp	Gln	Gln	Thr	Glu	Asp
	230						235					240			
Asp	Leu	Thr	Val	Thr	Ile	Arg	Leu	Pro	Glu	Asp	Ser	Thr	Lys	Glu	Xaa
	245					250					255				
Ile	Gln	Ile	Gln	Phe	Leu	Pro	Asp	His	Ile	Asn	Ile	Val	Leu	Lys	Asp
260					265					270					275
His	Gln	Phe	Leu	Glu	Gly	Lys	Leu	Tyr	Ser	Ser	Ile	Asp	His	Glu	Ser
				280					285					290	
Ser	Thr	Trp	Ile	Ile	Lys	Glu	Ser	Asn	Ser	Leu	Glu	Ile	Ser	Leu	Ile
			295					300					305		
Lys	Lys	Asn	Glu	Gly	Leu	Thr	Trp	Pro	Glu	Leu	Val	Ile	Gly	Asp	Lys
	310						315					320			
Gln	Gly	Glu	Leu	Ile	Arg	Asp	Ser	Ala	Gln	Cys	Ala	Ala	Ile	Ala	Glu
	325					330					335				
Arg	Leu	Met	His	Leu	Thr	Ser	Glu	Glu	Leu	Asn	Pro	Asn	Pro	Asp	Lys
340					345					350					355
Glu	Lys	Pro	Pro	Cys	Asn	Ala	Gln	Glu	Leu	Glu	Glu	Cys	Asp	Ile	Phe
				360					365					370	
Phe	Glu	Glu	Ser	Ser	Leu	Cys	Arg	Phe	Asp	Gly	Asn	Thr	Leu	Lys	
			375				380					385			
Thr	Thr	His	Val	Val	Asn	Leu	Gly	Ser	Asn	Gln	Tyr	Leu	Phe	Ser	Val
			390				395					400			
Ile	Val	Asp	Pro	Lys	Glu	Met	Pro	Cys	Phe	Cys	Leu	Arg	His	Asp	Val
	405					410					415				
Asp	Ala	Leu	Leu	Trp	Gln	Pro	His	Ser	Ser	Lys	Gln	Asp	Asp	Met	Trp
420					425					430					435
Glu	His	Ile	Ala	Thr	Phe	Asn	Ala	Leu	Gly	Tyr	Val	Gln	Ala	Ser	Lys
				440					445					450	
Arg	Asp	Lys	Lys	Phe	Phe	Ala	Cys	Ala	Pro	Asn	Tyr	Ser	Tyr	Ala	Ala
			455					460					465		
Leu	Cys	Glu	Cys	Leu	Arg	Arg	Val	Phe	Ile	Tyr	Arg	Gln	Pro	Ala	Pro
		470					475					480			
Met	Ser	Thr	Val	Leu	Tyr	Asn	Arg	Lys	Glu	Gly	Arg	Gln	Val	Gly	Gln
	485					490					495				
Val	Ala	Lys	Gln	Gln	Val	Ala	Ser	Leu	Glu	Thr	Asn	Asp	Pro	Ile	Leu
500					505					510					515
Gly	Phe	Gln	Ala	Thr	Asn	Glu	Arg	Leu	Phe	Val	Leu	Thr	Thr	Lys	Asn
				520					525					530	
Leu	Phe	Leu	Ile	Lys	Val	Asn	Thr	Glu	Asn						
			535					540							

<210> 411
 <211> 99
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 411
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -45 -40 -35
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
 -30 -25 -20
 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
 -15 -10 -5
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
 1 5 10 15
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 20 25 30
 Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 35 40 45
 Glu Val Leu
 50

<210> 412
 <211> 90
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 412
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20
 Ala Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala
 -15 -10 -5
 Gln Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu
 1 5 10 15
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
 20 25 30
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
 35 40 45
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
 50 55

<210> 413
 <211> 115
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -46...-1

<400> 413
 Met Lys Thr Leu Phe Asn Pro Ala Pro Ala Ile Ala Asp Leu Asp Pro
 -45 -40 -35
 Gln Phe Tyr Thr Leu Ser Asp Val Phe Cys Cys Asn Glu Ser Glu Ala

009760 10601

-30 -25 -20 -15
 Glu Ile Leu Thr Gly Leu Thr Val Gly Ser Ala Ala Asp Ala Gly Glu
 -10 -5 1
 Ala Ala Leu Val Leu Leu Lys Arg Gly Cys Gln Val Val Ile Ile Thr
 5 10 15
 Leu Gly Ala Glu Gly Cys Val Val Leu Ser Gln Thr Glu Pro Glu Pro
 20 25 30
 Lys His Ile Pro Thr Glu Lys Val Lys Ala Val Asp Thr Thr Cys Arg
 35 40 45 50
 Pro Gly Ser Arg Pro Lys Ser Glu Ala Ala Ser Val Lys Lys Gln Lys
 55 60 65
 His Tyr Lys

<210> 414
 <211> 66
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 414
 Met Lys Pro Leu Leu Val Val Phe Val Phe Leu Phe Leu Trp Asp Pro
 -15 -10 -5
 Val Leu Ala Gly Ile Asn Ser Leu Ser Ser Glu Met His Lys Lys Cys
 1 5 10
 Tyr Lys Asn Gly Ile Cys Arg Leu Glu Cys Tyr Glu Ser Glu Met Leu
 15 20 25
 Val Ala Tyr Cys Met Phe Gln Leu Glu Cys Cys Val Lys Gly Asn Pro
 30 35 40 45
 Ala Pro

<210> 415
 <211> 133
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 415
 Met Ser Cys Ser Leu Lys Phe Thr Leu Ile Val Ile Phe Phe Tyr Cys
 -20 -15 -10
 Trp Leu Ser Ser Ser His Glu Glu Leu Glu Gly Gly Thr Ser Lys Ser
 -5 1 5 10
 Phe Asp Leu His Thr Val Ile Met Leu Val Ile Ala Gly Gly Ile Leu
 15 20 25
 Ala Ala Leu Leu Leu Leu Ile Val Val Val Leu Cys Leu Tyr Phe Lys
 30 35 40
 Ile His Asn Ala Leu Lys Ala Ala Lys Glu Pro Glu Ala Val Ala Val
 45 50 55
 Lys Asn His Asn Pro Asp Lys Val Trp Trp Ala Lys Asn Ser Gln Ala
 60 65 70 75
 Lys Thr Ile Ala Thr Glu Ser Cys Pro Ala Leu Gln Cys Cys Glu Gly
 80 85 90
 Tyr Arg Met Cys Ala Ser Phe Asp Ser Leu Pro Pro Cys Cys Cys Asp
 95 100 105
 Ile Asn Glu Gly Leu
 110

09973360 101501

<210> 416
 <211> 140
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -70..-1

<400> 416
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
 -70 -65 -60 -55
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
 -50 -45 -40
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
 -35 -30 -25
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
 -20 -15 -10
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
 -5 1 5 10
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln His Ile Arg Thr Ser
 15 20 25
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
 30 35 40
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
 45 50 55
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys
 60 65 70

<210> 417
 <211> 233
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 417
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala

130		135		140
Leu Trp Glu Asp Lys Thr	Ser Leu Trp Glu Glu Glu Asn Ala Leu Trp			
145	150	155		160
Glu Glu Glu Arg Ala Phe Trp Met Glu	Asn Asn Gly His Ile Ala Gly			
	165	170		175
Glu Gln Met Leu Glu Asp Gly Pro His	Asn Ala Asn Arg Gly Gln Arg			
	180	185		190
Leu Leu Ala Phe Ser Arg Gly Arg Ala				
195	200			

<210> 418
 <211> 83
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 418	
Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu	
	-25 -20 -15
Val Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val	
	-10 -5 1
Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro	
5 10 15	
Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr	
20 25 30 35	
Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg	
	40 45 50
Val Thr Lys	

<210> 419
 <211> 215
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 419	
Met Val Ser Ala Leu Arg Gly Ala Pro Leu Ile Arg Val His Ser Ser	
	-40 -35 -30
Pro Val Ser Ser Pro Ser Val Ser Gly Pro Arg Arg Leu Val Ser Cys	
-25 -20 -15 -10	
Leu Ser Ser Gln Ser Ser Ala Leu Ser Gln Ser Gly Gly Gly Ser Thr	
	-5 1 5
Ser Ala Ala Gly Ile Glu Ala Arg Ser Arg Ala Leu Arg Arg Arg Trp	
10 15 20	
Cys Pro Ala Gly Ile Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys	
25 30 35	
Leu Leu Pro Ser Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala	
40 45 50 55	
Arg Val Leu His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu	
	60 65 70
Ala Asp Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala	
75 80 85	
Ala Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln	
90 95 100	

Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn
 105 110 115
 Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp
 120 125 130 135
 Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly
 140 145 150
 Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys Asp Leu Thr Glu
 155 160 165
 Trp Val Asp Gly Cys Asp Phe
 170

<210> 420
 <211> 417
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 420
 Met Met Gly Ser Pro Val Ser His Leu Leu Ala Gly Phe Cys Val Trp
 -20 -15 -10 -5
 Val Val Leu Gly Trp Val Gly Gly Ser Val Pro Asn Leu Gly Pro Ala
 1 5 10
 Glu Gln Glu Gln Asn His Tyr Leu Ala Gln Leu Phe Gly Leu Tyr Gly
 15 20 25
 Glu Asn Gly Thr Leu Thr Ala Gly Gly Leu Ala Arg Leu Leu His Ser
 30 35 40
 Leu Gly Leu Gly Arg Val Gln Gly Leu Arg Leu Gly Gln His Gly Pro
 45 50 55 60
 Leu Thr Gly Arg Ala Ser Pro Ala Ala Asp Asn Ser Thr His Arg
 65 70 75
 Pro Gln Asn Pro Glu Leu Ser Val Asp Val Trp Ala Gly Met Pro Leu
 80 85 90
 Gly Pro Ser Gly Trp Gly Asp Leu Glu Glu Ser Lys Ala Pro His Leu
 95 100 105
 Pro Arg Gly Pro Ala Pro Ser Gly Leu Asp Leu Leu His Arg Leu Leu
 110 115 120
 Leu Leu Asp His Ser Leu Ala Asp His Leu Asn Glu Asp Cys Leu Asn
 125 130 135 140
 Gly Ser Gln Leu Leu Val Asn Phe Gly Leu Ser Pro Ala Ala Pro Leu
 145 150 155
 Thr Pro Arg Gln Phe Ala Leu Leu Cys Pro Ala Leu Leu Tyr Gln Ile
 160 165 170
 Asp Ser Arg Val Cys Ile Gly Ala Pro Ala Pro Ala Pro Gly Asp
 175 180 185
 Leu Leu Ser Ala Leu Leu Gln Ser Ala Leu Ala Val Leu Leu Leu Ser
 190 195 200
 Leu Pro Ser Pro Leu Ser Leu Leu Leu Arg Leu Leu Gly Pro Arg
 205 210 215 220
 Leu Leu Arg Pro Leu Leu Gly Phe Leu Gly Ala Leu Ala Val Gly Thr
 225 230 235
 Leu Cys Gly Asp Ala Leu Leu His Leu Leu Pro His Ala Gln Glu Gly
 240 245 250
 Arg His Ala Gly Pro Gly Gly Leu Pro Glu Lys Asp Leu Gly Pro Gly
 255 260 265
 Leu Ser Val Leu Gly Gly Leu Phe Leu Leu Phe Val Leu Glu Asn Met
 270 275 280
 Leu Gly Leu Leu Arg His Arg Gly Leu Arg Pro Arg Cys Cys Arg Arg
 285 290 295 300

09978360 "101501

Ile Cys Arg Leu Arg Tyr Gly Asn Pro Asp Ala Lys Pro Thr Lys Ala
 15 20 25
 Asp Ile Thr Leu Ser Gly Cys Ala Ser Gly Leu Val Arg Val Phe Leu
 30 35 40
 Thr Ser Pro Thr Glu Val Ala Lys Val Arg Leu Gln Thr Gln Thr Gln
 45 50 55 60
 Ala Gln Lys Gln Gln Arg Leu Leu Ser Ala Ser Gly Pro Leu Ala Val
 65 70 75
 Pro Pro Met Cys Pro Val Pro Pro Ala Cys Pro Glu Pro Lys Tyr Arg
 80 85 90
 Gly Pro Leu His Cys Leu Ala Thr Val Ala Arg Glu Glu Gly Leu Cys
 95 100 105
 Gly Leu Tyr Lys Gly Ser Ser Ala Leu Val Leu Arg Asp Gly His Ser
 110 115 120
 Phe Ala Thr Tyr Phe Leu Ser Tyr Ala Val Leu Cys Glu Trp Leu Ser
 125 130 135 140
 Pro Ala Gly His Ser Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly
 145 150 155
 Gly Cys Ala Gly Val Leu Ala Trp Ala Val Ala Thr Pro Met Asp Val
 160 165 170
 Ile Lys Ser Arg Leu Gln Ala Asp Gly Gln Gly Gln Arg Arg Tyr Arg
 175 180 185
 Gly Leu Leu His Cys Met Val Thr Ser Val Arg Glu Glu Gly Pro Arg
 190 195 200
 Val Leu Phe Lys Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val
 205 210 215 220
 Asn Met Val Val Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg
 225 230 235
 Gly Leu Leu Thr
 240

<210> 424
 <211> 114
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 424
 Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35
 Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
 -30 -25 -20
 Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
 -15 -10 -5
 Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
 1 5 10 15
 Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met
 20 25 30
 Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly
 35 40 45
 Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr
 50 55 60
 Ser Asp
 65

<210> 425
 <211> 382
 <212> PRT

00978360 101501

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 425

Met	Gly	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Cys	Ile	Leu	Val	Leu	Cys	Cys
-15					-10				-5						1
Gly	Ala	Met	Ser	Pro	Pro	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu
			5				10						15		
Ser	Arg	Gly	Cys	Asn	Asp	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala
		20				25					30				
Leu	Arg	Asp	Ile	Asn	Lys	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu
	35				40					45					
Asn	Arg	Val	Asn	Asp	Ala	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser
50					55				60						65
Leu	Phe	Tyr	Leu	Thr	Leu	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu
				70					75					80	
Arg	Lys	Lys	Ala	Trp	Gln	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser
			85				90						95		
Val	Tyr	Gly	Gln	Cys	Lys	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg
		100					105						110		
Val	Leu	Tyr	Leu	Ala	Ala	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys
	115					120					125				
Lys	Lys	Ile	Tyr	Met	Thr	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr
130					135					140					145
Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala
				150					155					160	
Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val
		165					170						175		
Thr	Arg	Ala	Ser	Ser	Gln	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu
		180					185					190			
Tyr	Leu	Ile	Lys	Glu	Ser	Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys
	195					200				205					
Ser	Leu	Gln	Ser	Ser	Asp	Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser
210					215					220					225
Leu	Thr	Arg	Thr	His	Trp	Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe
				230					235					240	
Phe	Glu	Ser	Gln	Ala	Pro	Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn
		245						250					255		
Gln	Lys	Pro	Thr	Asn	Leu	Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn
		260					265					270			
Thr	Pro	Pro	Thr	Asp	Ser	Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val
	275					280					285				
Gln	Tyr	Leu	Pro	Asp	Leu	Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro
290					295					300					305
Gln	Glu	Ala	Phe	Pro	Val	His	Leu	Asp	Leu	Thr	Thr	Asn	Pro	Gln	Gly
			310						315					320	
Glu	Thr	Leu	Asp	Ile	Ser	Phe	Leu	Phe	Leu	Glu	Pro	Met	Glu	Glu	Lys
		325						330				335			
Leu	Val	Val	Leu	Pro	Phe	Pro	Lys	Glu	Lys	Ala	Arg	Thr	Ala	Glu	Cys
		340					345					350			
Pro	Gly	Pro	Ala	Gln	Asn	Ala	Ser	Pro	Leu	Val	Leu	Pro	Pro		
	355					360					365				

<210> 426

<211> 212

<212> PRT

<213> Homo Sapiens

09070360 101501

<220>
 <221> SIGNAL
 <222> -197..-1

<220>
 <221> UNSURE
 <222> -88
 <223> Xaa = Ala,Asp,Gly,Val

<220>
 <221> UNSURE
 <222> -109
 <223> Xaa = Asp,Glu

<400> 426
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 -195 -190 -185
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 -180 -175 -170
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 -165 -160 -155 -150
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Ala Lys Ile Leu
 -145 -140 -135
 Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala
 -130 -125 -120
 Met Val Leu Asp Gln Ile Glu Ala Xaa Leu Glu Lys Arg Lys Leu Glu
 -115 -110 -105
 Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Xaa Phe Thr
 -100 -95 -90
 Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu
 -85 -80 -75 -70
 Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln
 -65 -60 -55
 Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu
 -50 -45 -40
 Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe
 -35 -30 -25
 Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu
 -20 -15 -10
 Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys
 -5 1 5 10
 Lys Lys Tyr Ile
 15

<210> 427
 <211> 287
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 427
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Leu Ser Ala Arg Ser Pro Gly Lys His

0997860 "101504

<211> 406
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 430

Met	Arg	Gly	Ser	Val	Glu	Cys	Thr	Trp	Gly	Trp	Gly	His	Cys	Ala	Pro
-35					-30					-25					-20
Ser	Pro	Leu	Leu	Leu	Trp	Thr	Leu	Leu	Leu	Phe	Ala	Ala	Pro	Phe	Gly
			-15						-10					-5	
Leu	Leu	Gly	Glu	Lys	Thr	Arg	Gln	Val	Ser	Leu	Glu	Val	Ile	Pro	Asn
		1					5					10			
Trp	Leu	Gly	Pro	Leu	Gln	Asn	Leu	Leu	His	Ile	Arg	Ala	Val	Gly	Thr
15					20					25					
Asn	Ser	Thr	Leu	His	Tyr	Val	Trp	Ser	Ser	Leu	Gly	Pro	Leu	Ala	Val
30					35					40					45
Val	Met	Val	Ala	Thr	Asn	Thr	Pro	His	Ser	Thr	Leu	Ser	Val	Asn	Trp
				50					55					60	
Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro	Asp	Gly	Gly	Leu	Met	Val	Leu	Pro
		65					70					75			
Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser	Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu
	80					85					90				
Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser	Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly
95					100					105					
Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu	Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile
110					115					120					125
Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr	Leu	Ser	Ala	Thr	Phe	Gln	Gly	His
			130						135					140	
Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe
		145					150					155			
Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg
	160					165					170				
Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly
175					180					185					
Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr
190					195					200					205
Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	Ser	Met	Gln	Glu	Gln	His	Ser	Ile
			210						215					220	
Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp
		225					230					235			
Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser
	240					245						250			
Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro
255					260					265					
Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg
270					275					280					285
Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe
			290						295					300	
Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp
			305				310					315			
Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	Pro	Pro	Val	Asp	Gly	Leu	Ser	Pro
	320					325						330			
Leu	Val	Leu	Gly	Ile	Met	Ala	Val	Ala	Leu	Gly	Ala	Pro	Gly	Leu	Met
335					340						345				
Leu	Leu	Gly	Gly	Gly	Leu	Val	Leu	Leu	Leu	His	His	Lys	Lys	Tyr	Ser
350					355					360					365
Glu	Tyr	Gln	Ser	Ile	Asn										
				370											

FOSTOT "09E3Z660

<210> 431
 <211> 120
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -57...-1

<400> 431
 Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
 -55 -50 -45
 Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 -40 -35 -30
 Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 -25 -20 -15 -10
 Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 -5 1 5
 Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 10 15 20
 Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 25 30 35
 Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
 40 45 50 55
 Asp Asp Ile Pro Asp Phe Asp Asp
 60

<210> 432
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 432
 Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu
 -35 -30 -25
 Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr
 -20 -15 -10 -5
 Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly
 1 5 10
 Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro
 15 20 25
 Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu
 30 35 40
 Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro
 45 50 55 60
 Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr
 65 70 75
 Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp
 80 85 90
 Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro
 95 100 105
 Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly
 110 115 120
 Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser
 125 130 135 140
 Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr

09978360 10501
 "09978360"

Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
 40 45 50
 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
 55 60 65
 Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
 70 75 80
 Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
 85 90 95 100
 Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
 105 110 115
 Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
 120 125 130
 Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
 135 140 145
 Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
 150 155 160
 Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
 165 170 175 180
 Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
 185 190

<210> 437
 <211> 352
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 437
 Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 -20 -15 -10
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 -5 1 5
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 10 15 20 25
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
 30 35 40
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 45 50 55
 Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
 60 65 70
 Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
 75 80 85
 Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
 90 95 100 105
 Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
 110 115 120
 Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
 125 130 135
 Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
 140 145 150
 Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
 155 160 165
 Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
 170 175 180 185
 Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
 190 195 200
 Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
 205 210 215

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
 220 225 230
 Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
 235 240 245
 Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
 250 255 260 265
 Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
 270 275 280
 Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
 285 290 295
 Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 300 305 310
 Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 315 320 325

<210> 438
 <211> 385
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -184...-1

<400> 438
 Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val
 -180 -175 -170
 Tyr Phe Ile Gly Ala His Lys Ile Pro Asn Ala Asn Met Asn Glu Asp
 -165 -160 -155
 Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
 -150 -145 -140
 Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp
 -135 -130 -125
 Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn
 -120 -115 -110 -105
 Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His
 -100 -95 -90
 Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys
 -85 -80 -75
 Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly
 -70 -65 -60
 Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys
 -55 -50 -45
 Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro
 -40 -35 -30 -25
 Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu
 -20 -15 -10
 Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile
 -5 1 5
 Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr
 10 15 20
 Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu
 25 30 35 40
 Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn
 45 50 55
 His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile
 60 65 70
 Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala
 75 80 85
 Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp
 90 95 100

00978360 10401
 T08T07 09E/660

Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp
 105 110 115 120
 Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln
 125 130 135
 Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr
 140 145 150
 Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met
 155 160 165
 Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln
 170 175 180
 Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser
 185 190 195 200
 Leu

<210> 439
 <211> 69
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 439
 Met Asn Leu Met Trp Thr Leu Leu Leu Phe Leu Leu Leu Asp Val Thr
 -20 -15 -10
 Val Phe Ile Pro Ala Leu Pro Phe Ser Thr Arg His Ile Asp Asn Pro
 -5 1 5
 Arg Ser Trp Val Pro Arg Gly His His Arg Tyr Cys Asp Val Met Met
 10 15 20 25
 Arg Arg Arg Trp Leu Ile Tyr Arg Gly Lys Cys Glu Gln Ile His Thr
 30 35 40
 Phe Ile His Arg Ile
 45

<210> 440
 <211> 108
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 440
 Met Asn Lys Thr His Lys Asp Cys Ser Ser Pro Gln Tyr Ser Ile Tyr
 -45 -40 -35
 Asn Ile Leu Asn Glu Leu Pro Thr Arg Pro Ile Ile Leu Ser Cys Ser
 -30 -25 -20
 Gln Ile Ser Cys Leu Leu Leu Val Ser Thr Trp Ser Ala Asp Leu Met
 -15 -10 -5
 Ser Tyr Arg Pro Val Thr Lys Pro Ser Gln Arg Cys Thr Ser Pro Ala
 1 5 10 15
 Gln Ser Met Thr Val Asn Leu Thr Lys Asp Val Gly Phe Tyr Glu Asp
 20 25 30
 Thr Gln Ser Ile Arg Ile Thr Leu Ser Glu Ile Ser Gln Ala Gln Lys
 35 40 45
 Asp Thr Tyr Phe Ile Ile Ser Cys Ile Cys Gly Ile
 50 55

<210> 441

0998360.101501

<211> 108
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 441
 Met Tyr Phe His Phe Leu Gly Ala Gly Ala Ile Leu Ile Pro Arg Leu
 -25 -20 -15
 Asp Ile Val Ile Ser Phe Val Gly Ala Val Ser Ser Ser Thr Leu Ala
 -10 -5 1
 Leu Ile Leu Pro Pro Leu Val Glu Ile Leu Thr Phe Ser Lys Glu His
 5 10 15 20
 Tyr Asn Ile Trp Met Val Leu Lys Asn Ile Ser Ile Ala Phe Thr Gly
 25 30 35
 Val Val Gly Phe Leu Leu Gly Thr Tyr Ile Thr Val Glu Glu Ile Ile
 40 45 50
 Tyr Pro Thr Pro Lys Val Val Ala Gly Thr Pro Gln Ser Pro Phe Leu
 55 60 65
 Asn Leu Asn Ser Thr Cys Leu Thr Ser Gly Leu Lys
 70 75 80

<210> 442
 <211> 125
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 442
 Met Val Cys Glu Asp Ala Pro Ser Phe Gln Met Ala Trp Glu Ser Gln
 -35 -30 -25
 Met Ala Trp Glu Arg Gly Pro Ala Leu Leu Cys Cys Val Leu Ser Ala
 -20 -15 -10
 Ser Gln Leu Ser Ser Gln Asp Gln Asp Pro Leu Gly His Ile Lys Ser
 -5 1 5 10
 Leu Leu Tyr Pro Phe Gly Phe Pro Val Glu Leu Pro Arg Pro Gly Pro
 15 20 25
 Thr Gly Ala Tyr Lys Lys Val Lys Asn Gln Asn Gln Thr Thr Ser Ser
 30 35 40
 Glu Leu Leu Arg Lys Gln Thr Ser His Phe Asn Gln Arg Gly His Arg
 45 50 55
 Ala Arg Ser Lys Leu Leu Ala Ser Arg Gln Ile Pro Asp Arg Thr Phe
 60 65 70 75
 Lys Cys Gly Lys Trp Leu Pro Gln Val Pro Ser Pro Val
 80 85

<210> 443
 <211> 169
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -88...-1

<400> 443

099360 10501

Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
-85 -80 -75
Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
-70 -65 -60
Leu Thr Asp Leu Ile Asp Glu Val Lys Ser Gly Ile Lys Lys Asn
-55 -50 -45
Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
-40 -35 -30 -25
Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
-20 -15 -10
Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
-5 1 5
Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
10 15 20
Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
25 30 35 40
Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
45 50 55
Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
60 65 70
Leu Pro Gly Glu Met Glu Lys Gln Lys
75 80

<210> 444
<211> 82
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> -56..-1

<400> 444
Met Lys Ala Val Trp His Phe Cys Leu Ser His Lys Ser Ser Leu Val
-55 -50 -45
Ile Val Leu Lys Thr Ala Gly Trp Ile Pro Gln Ala Gly Thr Leu Ile
-40 -35 -30 -25
Pro Gly Ser Arg Glu Glu Ser Arg Ser Asp Ser Gln Met Ile Met Leu
-20 -15 -10
Val Cys Phe Asn Leu Ser Arg Gly Cys Leu Lys Lys Val Phe Ile Ile
-5 1 5
Ser Val Leu Pro Asp Pro Glu Thr Ile Leu Leu Gly Lys Thr Val Gly
10 15 20
Ile Ala
25

<210> 445
<211> 251
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 445
Met Asp Lys Val Gln Ser Gly Phe Leu Ile Leu Phe Leu Phe Leu Met
-20 -15 -10 -5
Glu Cys Gln Leu His Leu Cys Leu Pro Tyr Ala Asp Gly Leu His Pro
1 5 10
Thr Gly Asn Ile Thr Gly Leu Pro Gly Ser Phe Asn His Trp Phe Tyr

145 150 155
 Tyr Leu Phe Thr Phe Leu Ala Ala Thr Ile Ala Tyr Phe Tyr Leu Asp
 160 165 170
 Cys Val Trp Arg Leu Thr Pro Arg Val Pro Asn Ser Phe Thr Arg Arg
 175 180 185 190
 Arg Ser Gln Ile Lys Thr Asp Val Lys Lys Ala Ile Asp Gln Leu Gln
 195 200 205
 Leu Arg Val Leu Lys Glu Gly Asp Glu Glu Leu Asp Leu Asn Glu Asp
 210 215 220
 Asn Cys Val Val Cys Phe Asp Thr Tyr Lys Pro Gln Asp Val Val Arg
 225 230 235
 Ile Leu Thr Cys Lys His Phe Phe His Lys Ala Cys Ile Asp Pro Trp
 240 245 250
 Leu Leu Ala His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys
 255 260 265 270
 Thr

<210> 447
 <211> 61
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 447
 Met Thr Asp Leu Asp Leu Met Ile Asn Phe Thr Phe Pro Ile Gln Trp
 -40 -35 -30
 Val Asn Gln Asn Arg Met Ala Tyr Tyr Ser Leu Lys Pro Leu Leu Pro
 -25 -20 -15
 Cys Ser Ser Val Leu Thr Cys Gly Gln Ala Ser Gln Asp Leu Leu Thr
 -10 -5 1 5
 Ser Ala Thr Ser Val Thr Gly Met Glu Lys Ile Glu Ala
 10 15

<210> 448
 <211> 113
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 448
 Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
 -15 -10 -5 1
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
 5 10 15
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
 20 25 30
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
 35 40 45
 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
 50 55 60 65
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
 70 75 80
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
 85 90 95
 Thr

09978360 101501

<210> 449
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 449
 Met Glu Arg Pro Arg Ser Pro Gln Cys Ser Ala Pro Ala Ser Ala Ser
 -30 -25 -20 -15
 Ala Ser Val Thr Leu Ala Gln Leu Leu Gln Leu Val Gln Gln Gly Gln
 -10 -5 1
 Glu Leu Pro Gly Leu Glu Lys Arg His Ile Ala Ala Ile His Gly Glu
 5 10 15
 Pro Thr Ala Ser Arg Leu Pro Arg Arg Pro Lys Pro Trp Glu Ala Ala
 20 25 30
 Ala Leu Ala Glu Ser Leu Pro Pro Pro Thr Leu Arg Ile Gly Thr Ala
 35 40 45 50
 Pro Ala Glu Pro Gly Leu Val Glu Ala Ala Thr Ala Pro Ser Ser Trp
 55 60 65
 His Thr Val Gly Pro
 70

<210> 450
 <211> 97
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -90..-1

<220>
 <221> UNSURE
 <222> -39
 <223> Xaa = His,Gln

<400> 450
 Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
 -90 -85 -80 -75
 Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Pro Met Gly
 -70 -65 -60
 Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Leu Gln
 -55 -50 -45
 Tyr Gly Trp Xaa Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
 -40 -35 -30
 Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
 -25 -20 -15
 Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp Asp Met Leu
 -10 -5 1 5
 Thr

<210> 451
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<220>

09360 101 09360

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 458
 Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
 -20 -15 -10 -5
 Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
 1 5 10
 Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
 15 20 25
 Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
 30 35 40
 Gly Arg Lys
 45

<210> 459
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 459
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Gly Trp Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala
 175

<210> 460
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 460

```
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25          -20          -15          -10
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5          1          5
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
          10          15          20
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa
          25          30          35
Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe
40          45          50          55
Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp
          60          65          70
Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr
          75          80          85
Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser
          90          95          100
Lys Gln Lys Ser Ile Glu Glu
          105          110
```

<210> 461

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -70...-1

<400> 461

```
Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe
-70          -65          -60          -55
Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val
          -50          -45          -40
Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn
          -35          -30          -25
Val Val Ser Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu
          -20          -15          -10
Ala Pro Phe Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val
          -5          1          5          10
Gly Leu Gly Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val
          15          20          25
Glu Asn Thr Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr
          30          35          40
Ala Thr Ser Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp
          45          50          55
Ile Thr Pro Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr
          60          65          70
Lys Met Ile Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr
75          80          85          90
Val Gly Arg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val
          95          100          105
Glu Thr Leu Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val
          110          115          120
Ala Arg Asn Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp
          125          130          135
Val Val Asn Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Glu Lys
          140          145          150
Ser Glu Ser Ala Glu Leu Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu
155          160          165          170
```

0907860 10101

Asn Leu Asn Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
 175 180 185

<210> 462
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 462
 Met Pro Gly Thr Glu Val Leu Glu Gly Ala Thr Asp Gly Leu Ala Ala
 -45 -40 -35
 Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu Gly Gly Ser Val Ile Ser
 -30 -25 -20
 Met Ile Val Leu Leu Ile Cys Val Val Cys Leu Tyr Ile Val Cys Arg
 -15 -10 -5
 Cys Gly Ser His Leu Trp Arg Glu Ser His His
 1 5 10

<210> 463
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln Leu
 1 5 10 15
 Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly Asp Gly
 20 25 30
 Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala
 35 40 45
 Thr Lys Ser Asp Asp Thr Val Val Ala Ile Pro Tyr Gly Ser Arg His
 50 55 60
 Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu Tyr Leu Glu Thr Lys
 65 70 75 80
 Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr
 85 90 95
 Phe Leu Val Asp Asn Ser Ser Val Asp Phe Gln Lys Phe Pro Asp Lys
 100 105 110
 Glu Ile Leu Arg Met Ala Gly Pro Leu Thr Ala Asp Phe Ile Val Lys
 115 120 125
 Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr
 130 135 140
 Gln Pro Ile Ile His Arg Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser
 145 150 155 160
 Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp
 165 170 175
 Leu Arg Ser Asn
 180

<210> 464
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

1097360.10460

<400> 464
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
60 65 70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
75 80 85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Pro Asp Asn
90 95 100 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
110 115 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Val Ser Met
125 130 135
Val Phe

<210> 465
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 465
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
60 65 70
Cys Ile Arg Ser Lys Asn Gly Pro Gly Thr Ala Val His Ala Tyr Asn
75 80 85
Pro Ser Thr Phe Arg Gly Gln Val
90 95

<210> 466
<211> 7
<212> PRT
<213> Homo sapiens

<400> 466
Met Val Glu Met Thr Gly Val
1 5

<210> 467

0997330 10401

<211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 467
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 -40 -35 -30
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
 -25 -20 -15
 Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
 -10 -5 1 5
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
 10 15 20
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
 25 30 35
 Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
 40 45 50
 Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
 55 60 65 70
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 75 80 85
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 90 95 100
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
 105 110 115
 Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Val Leu Ala
 120 125 130
 Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 135 140 145 150
 Gly Leu Lys Arg Lys Ala Glu
 155

<210> 468
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 468
 Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 1 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 469
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 469
 Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25

09360 10101

Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 470
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 470
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140
 Gln Val Ser Gln Gln Glu Leu Lys
 145 150

<210> 471
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 471
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 472
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
 1 5 10 15
 Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
 20 25 30
 Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly

09983010932660

	35					40						45							
Phe	Gln	Gln	Ile	Leu	Ala	Gly	Glu	Tyr	Asp	His	Leu	Pro	Glu	Gln	Ala				
	50					55					60								
Phe	Tyr	Met	Val	Gly	Pro	Ile	Glu	Glu	Ala	Val	Ala	Lys	Ala	Asp	Lys				
65					70					75					80				
Leu	Ala	Glu	Glu	His	Ser	Ser													
				85															

<210> 473
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -85...-1

<400> 473																			
Met	Ser	Ala	Glu	Val	Lys	Val	Thr	Gly	Gln	Asn	Gln	Glu	Gln	Phe	Leu				
-85					-80					-75					-70				
Leu	Leu	Ala	Lys	Ser	Ala	Lys	Gly	Ala	Ala	Leu	Ala	Thr	Leu	Ile	His				
			-65						-60						-55				
Gln	Val	Leu	Glu	Ala	Pro	Gly	Val	Tyr	Val	Phe	Gly	Glu	Leu	Leu	Asp				
		-50					-45						-40						
Met	Pro	Asn	Val	Arg	Glu	Leu	Xaa	Ala	Arg	Asn	Leu	Pro	Pro	Leu	Thr				
	-35					-30					-25								
Glu	Ala	Gln	Lys	Asn	Lys	Leu	Arg	His	Leu	Ser	Val	Val	Thr	Leu	Ala				
	-20				-15					-10									
Ala	Lys	Val	Lys	Cys	Ile	Pro	Tyr	Ala	Val	Leu	Leu	Glu	Ala	Leu	Ala				
-5				1				5						10					
Leu	Arg	Asn	Val	Arg	Gln	Leu	Glu	Asp	Leu	Val	Ile	Glu	Ala	Val	Tyr				
		15					20						25						
Ala	Asp	Val	Leu	Arg	Gly	Ser	Leu	Asp	Gln	Arg	Asn	Gln	Arg	Leu	Glu				
	30					35					40								
Val	Asp	Tyr	Ser	Ile	Gly	Arg	Asp	Ile	Gln	Arg	Gln	Asp	Leu	Ser	Ala				
	45				50						55								
Ile	Ala	Arg	Thr	Leu	Gln	Glu	Trp	Cys	Val	Gly	Cys	Glu	Val	Val	Leu				
60				65					70						75				
Ser	Gly	Ile	Glu	Glu	Gln	Val	Ser	Arg	Ala	Asn	Gln	His	Lys	Glu	Gln				
			80					85						90					
Gln	Leu	Gly	Leu	Lys	Gln	Gln	Ile	Glu	Ser	Glu	Val	Ala	Asn	Leu	Lys				
		95					100						105						
Lys	Thr	Ile	Lys	Val	Thr	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Ser	Gln				
	110					115						120							
Asp	Pro	Glu	Gln	His	Leu	Thr	Glu	Leu	Arg	Glu	Pro	Ala	Pro	Gly	Thr				
	125				130					135									
Asn	Gln	Arg	Gln	Pro	Ser	Lys	Lys	Ala	Ser	Lys	Gly	Lys	Gly	Leu	Arg				
140				145						150					155				
Gly	Ser	Ala	Lys	Ile	Trp	Ser	Lys	Ser	Asn										
			160						165										

<210> 474
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 474																			
Met	Pro	Thr	Asn	Cys	Ala	Ala	Ala	Gly	Cys	Ala	Thr	Thr	Tyr	Asn	Lys				
1			5						10					15					
His	Ile	Asn	Ile	Ser	Phe	His	Arg												
			20																

105101 09E32660

<210> 475
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
 1 5 10 15
 His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys Arg Arg
 20 25 30
 Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val Pro Gly Lys
 35 40 45
 His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser Cys Phe Asp Leu
 50 55 60
 Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val Pro Thr Ile Phe
 65 70 75 80
 Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
 85 90 95
 Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
 100 105 110
 Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
 115 120 125
 Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
 130 135 140
 Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg
 145 150 155 160
 Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
 165 170 175
 Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
 180 185 190
 Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
 195 200 205
 Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
 210 215 220
 Ser Thr Phe Ile
 225

<210> 476
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 476
 Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Ala Lys Leu Arg Gln
 65

099860-01501

<210> 477
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
 1 5 10 15
 Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
 20 25 30
 Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
 35 40

<210> 478
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 478
 Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
 -55 -50 -45
 Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
 -40 -35 -30
 Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
 -25 -20 -15
 His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
 -10 -5 1 5
 Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro
 10 15 20
 Cys Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala
 25 30 35
 Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His
 40 45 50
 Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu
 55 60 65 70
 Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu
 75 80 85
 Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr
 90 95 100
 Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg
 105 110 115
 Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp
 120 125 130
 Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys
 135 140 145 150
 Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg
 155 160 165
 Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
 170 175 180
 Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
 185 190 195
 Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
 200 205 210
 Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met
 215 220 225 230
 Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
 235 240 245

0993360.DEEB2650

Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
250 255

<210> 479
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -80...-1

<400> 479
Met Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe
-80 -75 -70 -65
Pro Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg
-60 -55 -50
Thr Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala
-45 -40 -35
Leu Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr
-30 -25 -20
Gln Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly
-15 -10 -5
Ser Thr Gln Pro Val Pro Leu Cys Ser
1 5

<210> 480
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 480
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15
Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
35 40 45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
50 55 60 65
Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu Thr Ser Glu Pro Leu
70 75 80
Thr Ala

<210> 481
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36...-1

<400> 481
Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn

-35		-30		-25
Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly				
-20		-15		-10
Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe				
	1		5	10
His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His				
15		20		25
Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly				
30		35		40
Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser				
45		50		55

<210> 482

<211> 351

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 482

Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly				
-15		-10		-5
Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr				
1	5		10	15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile				
	20		25	30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr				
35		40		45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu				
50		55		60
Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro				
65	70		75	80
Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser				
	85		90	95
Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu				
	100		105	110
Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu				
	115		120	125
Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr				
	130		135	140
Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met				
145		150		155
Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr				
	165		170	175
Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser				
	180		185	190
Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu				
	195		200	205
Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile				
	210		215	220
Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser				
225		230		235
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp				
	245		250	255
Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser				
	260		265	270
Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val				
	275		280	285
Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys				

09978350 101501

290		295		300
His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Cys				
305		310		315
His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp Arg				320
	325		330	335

<210> 483
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 483

Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu				
-45		-40		-35
Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser				
-30		-25		-20
Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile				
-15		-10		-5
Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu				
5		10		15
Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile				
20		25		30
Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly Glu				
35		40		45
Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu Gln Phe				
50		55		60
Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn Arg Arg Glu				
70		75		80
Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala				
85		90		

<210> 484
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -73...-1

<400> 484

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg				
-70		-65		-60
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val				
-55		-50		-45
Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr				
-40		-35		-30
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe				
-25		-20		-15
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile				
-5		1		5
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile				
10		15		20
Pro Leu Gly Thr Pro				
25				

<210> 485

<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -68...-1

<400> 485
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20 -15 -10 -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45 50 55 60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
 110 115 120
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
125 130 135 140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
 145 150 155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
 175 180

<210> 486
<211> 350
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -68...-1

<400> 486
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20 -15 -10 -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly

45					50					55					60
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe
				65					70					75	
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro
			80					85					90		
Ile	Cys	Glu	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn
		95					100					105			
Tyr	Leu	Arg	Ala	Glu	Ile	Leu	Tyr	Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu
	110					115					120				
Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala	Leu	Gln	Gln	His	Arg	Pro	Ser	Pro
125					130				135						140
Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	Arg	Thr	Lys	Leu	Gln	Asn	Pro	Asp
			145					150						155	
Leu	Leu	Glu	Leu	Cys	His	Ser	Val	Pro	Lys	Glu	Val	Val	Gln	Leu	Gly
		160						165					170		
Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser	Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe
		175					180					185			
Arg	Ala	Trp	Leu	Arg	Cys	Tyr	Gly	Met	Pro	Gly	Met	Ser	Ser	Leu	Gln
	190					195					200				
Asp	Arg	His	Gly	Arg	Thr	Ile	Trp	Phe	Gln	Gly	Asp	Pro	Gly	Pro	Leu
205					210					215					220
Ala	Pro	Lys	Gly	Arg	Lys	Ser	Arg	Lys	Lys	Ser	Lys	Ala	Thr	Gln	
			225					230					235		
Leu	Ser	Pro	Glu	Asp	Arg	Val	Glu	Asp	Ala	Leu	Pro	Pro	Ser	Lys	Ala
		240					245						250		
Pro	Ser	Arg	Thr	Arg	Arg	Ala	Lys	Arg	Asp	Leu	Pro	Lys	Arg	Thr	Ala
		255				260						265			
Thr	Gln	Arg	Pro	Glu	Gly	Thr	Ser	Leu	Gln	Gln	Asp	Pro	Glu	Ala	Pro
	270					275					280				
Thr	Val	Pro	Lys	Lys	Gly	Arg	Arg	Lys	Gly	Arg	Gln	Ala	Ala	Ser	Gly
285					290					295					300
His	Cys	Arg	Pro	Arg	Lys	Val	Lys	Ala	Asp	Ile	Pro	Ser	Leu	Glu	Pro
			305						310					315	
Glu	Gly	Thr	Ser	Ala	Ser										
			320												

<210> 488
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<400> 488															
Met	Tyr	Val	Trp	Pro	Cys	Ala	Val	Val	Leu	Ala	Gln	Tyr	Leu	Trp	Phe
		-80					-75					-70			
His	Arg	Arg	Ser	Leu	Pro	Gly	Lys	Ala	Ile	Leu	Glu	Ile	Gly	Ala	Gly
	-65					-60					-55				
Val	Ser	Leu	Pro	Gly	Ile	Leu	Thr	Ala	Lys	Cys	Gly	Ala	Glu	Val	Ile
-50					-45					-40					-35
Leu	Ser	Asp	Ser	Ser	Glu	Leu	Pro	His	Cys	Leu	Glu	Val	Cys	Arg	Gln
			-30					-25					-20		
Ser	Cys	Gln	Met	Asn	Asn	Leu	Pro	His	Leu	Gln	Val	Val	Gly	Leu	Thr
	-15					-10					-5				
Trp	Gly	His	Ile	Ser	Trp	Asp	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Asp	Ile
	1				5					10					
Ile	Leu	Ala	Ser	Asp	Val	Phe	Phe	Glu	Pro	Glu	Asp	Phe	Glu	Asp	Ile
15					20				25					30	
Leu	Ala	Thr	Ile	Tyr	Phe	Leu	Met	His	Lys	Asn	Pro	Lys	Val	Gln	Leu

				35					40				45				
Trp	Ser	Thr	Tyr	Gln	Val	Arg	Ser	Ala	Asp	Trp	Ser	Leu	Glu	Ala	Leu		
			50					55					60				
Leu	Tyr	Lys	Trp	Asp	Met	Lys	Cys	Val	His	Ile	Pro	Leu	Glu	Ser	Phe		
		65					70					75					
Asp	Ala	Asp	Lys	Glu	Asp	Ile	Ala	Glu	Ser	Thr	Leu	Pro	Gly	Arg	His		
	80					85					90						
Thr	Val	Glu	Met	Leu	Val	Ile	Ser	Phe	Ala	Lys	Asp	Ser	Leu				
95					100					105							

<210> 489
 <211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -232...-1

<400> 489																	
Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Arg	Ile	Phe	Lys	Ile		
	-230						-225				-220						
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu		
	-215					-210					-205						
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg		
	-200				-195					-190					-185		
Val	His	Leu	Met	Gly	Asp	Asn	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu		
			-180					-175						-170			
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg		
		-165					-160						-155				
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val		
	-150					-145					-140						
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu	Ile		
	-135				-130						-125						
Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val	Thr	Lys		
	-120				-115					-110					-105		
Val	Glu	Trp	Ile	Phe	Ser	Gly	Arg	Arg	Ala	Lys	Glu	Glu	Ile	Val	Phe		
			-100					-95						-90			
Arg	Tyr	Tyr	His	Lys	Leu	Arg	Met	Ser	Ala	Glu	Tyr	Ser	Gln	Ser	Trp		
		-85					-80						-75				
Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly	Asp	Ile	Phe	Arg	Asn		
	-70					-65					-60						
Asp	Gly	Ser	Ile	Met	Leu	Gln	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gly	Asn		
	-55				-50					-45							
Tyr	Thr	Cys	Ser	Ile	His	Leu	Gly	Asn	Leu	Val	Phe	Lys	Lys	Thr	Ile		
	-40				-35					-30					-25		
Val	Leu	His	Val	Ser	Pro	Glu	Glu	Pro	Arg	Thr	Leu	Val	Thr	Pro	Ala		
			-20					-15						-10			
Ala	Leu	Arg	Pro	Leu	Val	Leu	Gly	Gly	Asn	Gln	Leu	Val	Ile	Ile	Val		
		-5					1				5						
Gly	Ile	Val	Cys	Ala	Thr	Ile	Leu	Leu	Leu	Pro	Val	Leu	Ile	Leu	Ile		
	10					15				20							
Val	Lys	Lys	Thr	Cys	Gly	Asn	Lys	Ser	Ser	Val	Asn	Ser	Thr	Val	Leu		
	25				30				35						40		
Val	Lys	Asn	Thr	Lys	Lys	Thr	Asn	Pro	Lys	Lys	Lys						
				45					50								

<210> 490
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 490

```

Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
1          5          10          15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
          20          25          30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
          35          40          45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
          50          55          60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65          70          75          80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
          85          90          95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
          100          105          110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
          115          120          125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
          130          135          140
His His Cys Val Arg Glu Gly Ser Gly
145          150

```

<210> 491

<211> 49

<212> PRT

<213> Homo sapiens

<400> 491

```

Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
1          5          10          15
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
          20          25          30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
          35          40          45
Cys

```

<210> 492

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 492

```

Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
          -20          -15          -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
          -5          1          5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
          10          15          20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
          25          30          35          40
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
          45          50          55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
          60          65          70
Pro Pro Arg
          75

```

<210> 493
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 493
 Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
 -35 -30 -25
 Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
 -20 -15 -10
 Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
 -5 1 5 10
 Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
 15 20 25
 Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
 30 35 40
 Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
 45 50 55

<210> 494
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 494
 Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
 -20 -15 -10
 Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
 -5 1 5
 Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
 10 15 20 25
 Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
 30 35 40
 Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
 45 50 55
 Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
 60 65 70
 Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
 75 80 85
 Gln Lys Leu Ala Lys Lys Met Phe Phe
 90 95

<210> 495
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 495
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 1 5 10 15
 Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 20 25 30

Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
 35 40 45
 Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
 50 55

<210> 496
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 496
 Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
 -10 -5 1
 Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
 5 10 15
 Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
 20 25 30
 Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
 35 40 45 50
 Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
 55 60 65
 Tyr Arg Ile Cys Asp Leu
 70

<210> 497
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 497
 Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
 -55 -50 -45
 Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
 -40 -35 -30
 Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
 -25 -20 -15
 Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
 -10 -5 1 5
 Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
 10 15 20
 Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
 25 30 35
 Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
 40 45 50
 Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
 55 60 65 70
 Ser Leu Gln Asp Ala Leu Leu Leu Leu Met Gly Leu Gly Pro Leu
 75 80 85
 Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
 90 95 100
 Leu His Pro Trp Ala
 105

"09978360" 09EBZ660

<210> 501
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 501
 Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
 -20 -15 -10
 Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
 -5 1 5 10
 Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
 15 20 25
 Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro
 30 35 40
 Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
 45 50 55
 Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
 60 65 70 75
 His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
 80 85 90

<210> 502
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44...-1

<400> 502
 Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro
 -40 -35 -30
 Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe
 -25 -20 -15
 Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His
 -10 -5 1
 Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu
 5 10 15 20
 Glu Trp Gly Leu Leu Arg
 25

<210> 503
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 503
 Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser
 -10 -5 1
 Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe

09078360 101501

5						10					15					
Ile	Tyr	Gln	Met	Ser	Ser	Gln	Gln	Leu	Gln	Gln	Gln	Pro	Ser	Ala	Asn	
20					25				30						35	
Lys	Lys	Ala	Gly	Lys	Ile	His	Asn	Thr	Pro	Phe	Ala	Asn	Gln	Leu	Asn	
				40					45					50		
Pro	Thr	Gln	His	Leu	Ala	Lys	Pro	Phe	Gln	Gln	Ile	Leu	Pro	Gly	Arg	
			55					60					65			
Gln	Ser	Gly	Ser	Leu	Thr	Ser	Pro	Phe	Leu	Ala	Cys					
		70					75									

<210> 504
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 504																
Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala	
	-40						-35					-30				
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe	
	-25					-20				-15						
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Pro	Ile	Ile	
-10					-5					1				5		
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser	
			10					15					20			
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys	
	25					30						35				
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met	
	40					45					50					
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Glu	Ser	Asn	Thr	Glu	
55					60					65					70	
Glu	Thr	Lys	Arg	Thr	Asp	Leu	Thr	Gln	Asp	Asp	Leu	His	Leu	Lys	Ile	
			75					80						85		
Leu	Lys	Asp	Ile	Leu	Cys	Glu	Phe	Leu	Ser	Asn	Ile	Phe	Gln	Ala	Leu	
		90					95						100			
Thr	Lys	Glu	Thr	Val	Ala	Gln	Gly	Val	Lys	Glu	Gly	Gln	Leu	Ser	Lys	
	105					110						115				
Gln	Lys	Cys	Ser	Ser	Ala	Phe	Gln	Asn	Leu	Leu	Pro	Phe	Tyr	Ser	Pro	
	120					125					130					
Val	Val	Glu	Asp	Phe	Ile	Lys	Ile	Leu	Arg	Glu	Val	Asp	Lys	Ala	Leu	
135					140					145					150	
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr		
			155						160					165		

<210> 505
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 505																
Met	Gln	Val	Ala	Leu	Lys	Glu	Asp	Leu	Asp	Ala	Leu	Lys	Glu	Lys	Phe	
1				5				10						15		
Arg	Thr	Met	Glu	Ser	Asn	Gln	Lys	Ser	Ser	Phe	Gln	Glu	Ile	Pro	Lys	
		20						25					30			
Leu	Asn	Glu	Glu	Leu	Leu	Ser	Lys	Gln	Lys	Gln	Leu	Glu	Lys	Ile	Glu	
		35					40					45				
Ser	Gly	Glu	Met	Gly	Leu	Asn	Lys	Val	Trp	Ile	Asn	Ile	Thr	Glu	Met	
	50					55					60					

Asn	Lys	Gln	Ile	Ser	Leu	Leu	Thr	Ser	Ala	Val	Asn	His	Leu	Lys	Ala
65					70					75					80
Asn	Val	Lys	Ser	Ala	Ala	Asp	Leu	Ile	Ser	Leu	Pro	Thr	Thr	Val	Glu
			85						90					95	
Gly	Leu	Gln	Lys	Ser	Val	Ala	Ser	Ile	Gly	Asn	Thr	Leu	Asn	Ser	Val
			100					105					110		
His	Leu	Ala	Val	Glu	Ala	Leu	Gln	Lys	Thr	Val	Asp	Glu	His	Lys	Lys
		115					120					125			
Thr	Met	Glu	Leu	Leu	Gln	Ser	Asp	Met	Asn	Gln	His	Phe	Leu	Lys	Glu
	130					135					140				
Thr	Pro	Gly	Ser	Asn	Gln	Ile	Ile	Pro	Ser	Pro	Ser	Ala	Thr	Ser	Glu
145				150					155						160
Leu	Asp	Asn	Lys	Thr	His	Ser	Glu	Asn	Leu	Lys	Gln	Met	Gly	Asp	Arg
			165					170					175		
Ser	Ala	Thr	Leu	Lys	Arg	Gln	Ser	Leu	Asp	Gln	Val	Thr	Asn	Arg	Thr
			180					185					190		
Asp	Thr	Val	Lys	Ile	Gln	Lys	Lys	Lys							
		195					200								

<210> 506
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400>	506														
Met	Pro	His	Ser	Ser	Leu	His	Pro	Ser	Ile	Pro	Cys	Pro	Arg	Gly	His
		-35					-30					-25			
Gly	Ala	Gln	Lys	Ala	Ala	Leu	Val	Leu	Leu	Ser	Ala	Cys	Leu	Val	Thr
	-20					-15					-10				
Leu	Trp	Gly	Leu	Gly	Glu	Pro	Pro	Glu	His	Thr	Leu	Arg	Tyr	Leu	Val
-5					1			5						10	
Leu	His	Leu	Ala	Ser	Leu	Gln	Leu	Gly	Leu	Leu	Leu	Asn	Gly	Val	Cys
			15					20				25			
Ser	Leu	Ala	Glu	Glu	Leu	Arg	His	Ile	His	Ser	Arg	Tyr	Arg	Gly	Ser
	30					35						40			
Tyr	Trp	Arg	Thr	Val	Arg	Ala	Cys	Leu	Gly	Cys	Pro	Leu	Arg	Arg	Gly
	45					50				55					
Ala	Leu	Leu	Leu	Leu	Ser	Ile	Tyr	Phe	Tyr	Tyr	Ser	Leu	Pro	Asn	Ala
60					65					70					75
Val	Gly	Pro	Pro	Phe	Thr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln
				80					85					90	
Ala	Leu	Asn	Ile	Leu	Leu	Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile
		95						100					105		
Ser	Ala	Val	Cys	Glu	Lys	Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala
		110					115					120			
Trp	Ser	Tyr	Tyr	Ile	Gly	Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln
	125					130					135				
Ala	Arg	Ile	Arg	Thr	Tyr	Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly
140					145					150					155
Ala	Val	Ser	Gln	Arg	Leu	Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val
				160					165					170	
Pro	Asp	Asn	Leu	Ser	Met	Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys
			175					180					185		
Leu	Pro	Gln	Gln	Thr	Gly	Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr
		190					195					200			
Ser	Asn	Ser	Ile	Tyr	Glu	Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr
	205						210					215			

Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 510
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 510
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
 -15 -10 -5
 Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
 1 5 10
 Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
 15 20 25 30
 Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
 35 40 45
 Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
 50 55 60
 Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
 65 70 75
 Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
 80 85 90
 Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
 95 100 105 110
 Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr
 115 120 125
 Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
 130 135 140
 Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
 145 150 155
 Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
 160 165 170
 Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
 175 180 185 190
 His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val
 195 200 205
 Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
 210 215 220
 Arg Thr Ala Trp
 225

<210> 511
 <211> 353
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 511

```

Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
      -30      -25      -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
      -15      -10      -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
      1          5          10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15          20          25          30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
      35          40          45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
      50          55          60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
      65          70          75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
      80          85          90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
95          100          105          110
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
      115          120          125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
      130          135          140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
      145          150          155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
160          165          170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
175          180          185          190
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
      195          200          205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Lys Tyr Leu Cys Asp Ala
      210          215          220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
      225          230          235
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
240          245          250
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
255          260          265          270
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
      275          280          285
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
      290          295          300
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
305          310          315
Leu

```

<210> 512

<211> 30

<212> PRT

<213> Homo sapiens

<400> 512

```

Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
1          5          10          15
Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys
      20          25          30

```

<210> 513

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 513

Met	Gln	Asp	Thr	Gly	Ser	Val	Val	Pro	Leu	His	Trp	Phe	Gly	Phe	Gly
			-45					-40					-35		
Tyr	Ala	Ala	Leu	Val	Ala	Ser	Gly	Gly	Ile	Ile	Gly	Tyr	Val	Lys	Ala
		-30					-25					-20			
Gly	Ser	Val	Pro	Ser	Leu	Ala	Ala	Gly	Leu	Leu	Phe	Gly	Ser	Leu	Ala
	-15				-10					-5					
Gly	Leu	Gly	Ala	Tyr	Gln	Leu	Ser	Gln	Asp	Pro	Arg	Asn	Val	Trp	Val
1			5					10					15		
Phe	Leu	Ala	Thr	Ser	Gly	Thr	Leu	Ala	Gly	Ile	Met	Gly	Met	Arg	Phe
			20					25					30		
Tyr	His	Ser	Gly	Lys	Phe	Met	Pro	Ala	Gly	Leu	Ile	Ala	Gly	Ala	Ser
		35					40					45			
Leu	Leu	Met	Val	Ala	Lys	Val	Gly	Val	Ser	Met	Phe	Asn	Arg	Pro	His
	50					55					60				

<210> 514

<211> 54

<212> PRT

<213> Homo sapiens

<400> 514

Glu	Ile	Ala	Gly	Tyr	Gly	Ala	Glu	Gly	Phe	Ser	Ser	Val	Leu	Gly	Tyr
1			5					10					15		
Pro	Arg	Trp	His	Arg	Leu	Pro	Pro	Gln	Ser	Leu	Gln	His	His	Gln	Tyr
			20					25				30			
Cys	Gln	Arg	Arg	Trp	Pro	Asp	Arg	Arg	Cys	Leu	Gln	Ser	His	Thr	Gln
		35					40					45			
Ser	Ser	Gly	His	Leu	Pro										
	50														

<210> 515

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 515

Met	Ala	Ala	Ser	Thr	Ser	Met	Xaa	Pro	Val	Ala	Val	Thr	Ala	Ala	Val
	-20					-15					-10				
Ala	Pro	Val	Leu	Ser	Ile	Asn	Ser	Asp	Phe	Ser	Asp	Leu	Arg	Glu	Ile
-5				1				5					10		
Lys	Lys	Gln	Leu	Leu	Leu	Ile	Ala	Gly	Leu	Thr	Arg	Glu	Arg	Gly	Leu
		15						20				25			
Leu	His	Ser	Ser	Lys	Trp	Ser	Ala	Glu	Leu	Ala	Phe	Ser	Leu	Pro	Ala
	30					35					40				
Leu	Pro	Xaa	Gly	Gln	Leu	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Glu	Glu	Asp
	45				50						55				
Ala	Gln	Asp	Met	Asp	Ala	Tyr	Thr	Leu	Ala	Lys	Ala	Tyr	Phe	Asp	Val
60					65				70					75	
Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys	Asn	Ser	Lys
				80					85					90	

Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 516
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 516
 Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
 -25 -20 -15 -10
 Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
 -5 1 5
 Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
 10 15 20
 Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
 25 30 35
 Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
 40 45 50 55
 Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly
 60 65 70
 Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
 75 80 85
 Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly
 90 95 100
 Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
 105 110 115
 Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
 120 125 130 135
 Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
 140 145 150
 Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
 155 160 165
 Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
 170 175 180
 Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
 185 190 195
 Asn Ala Tyr Val
 200

<210> 517
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 517
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser

-30						-25						-20			
Pro	Val	Thr	Trp	Leu	Gly	Leu	Leu	Ser	Phe	Gln	Asn	Leu	His	Cys	Phe
-15					-10					-5					1
Pro	Asp	Leu	Pro	Thr	Glu	Met	Pro	Leu	Arg	Ala	Lys	Gly	Val	Asn	Thr
			5					10					15		

<210> 518
 <211> 146
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 518															
Met	Met	Trp	Gln	Lys	Tyr	Ala	Gly	Ser	Arg	Arg	Ser	Met	Pro	Leu	Gly
	-30					-25					-20				
Ala	Arg	Ile	Leu	Phe	His	Gly	Val	Phe	Tyr	Ala	Gly	Gly	Phe	Ala	Ile
-15					-10					-5					1
Val	Tyr	Tyr	Leu	Ile	Gln	Lys	Phe	His	Ser	Arg	Ala	Leu	Tyr	Tyr	Lys
			5					10					15		
Leu	Ala	Val	Glu	Gln	Leu	Gln	Ser	His	Pro	Glu	Ala	Gln	Glu	Ala	Leu
		20					25					30			
Gly	Pro	Pro	Leu	Asn	Ile	His	Tyr	Leu	Lys	Leu	Ile	Asp	Arg	Glu	Asn
	35				40					45					
Phe	Val	Asp	Ile	Val	Asp	Ala	Lys	Leu	Lys	Ile	Pro	Val	Ser	Gly	Ser
50				55						60					65
Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser	Arg	Gly	Gly	Pro	Phe
			70					75						80	
Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu	Leu	Lys	Asp	Gly	Gln
			85				90						95		
Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn	Gly	Asp	Glu	Val	Lys
		100					105						110		
Lys	Glu														
	115														

<210> 519
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 519															
Met	Glu	Leu	Ala	Pro	Thr	Ala	Arg	Leu	Pro	Pro	Gly	His	Gly	Ser	Leu
1				5					10					15	
Pro	His	Gly	Val	Leu	Gly	Pro	Arg	Ala	Thr	Gly	Ser	Val	Thr	His	Leu
			20				25						30		
Ser	Leu	Leu	Pro	Gln	Ile	Lys	Gln	Arg	Ala	Ser	Glu	Ala	Leu	Pro	Glu
	35					40					45				
Leu	Leu	Arg	Pro	Val	Thr	Pro	Ile	Thr	Asn	Phe	Glu	Gly	Ser	Gln	Ser
	50				55					60					
Gln	Asp	His	Ser	Gly	Ile	Phe	Gly	Leu	Val	Thr	Asn	Leu	Glu	Glu	Leu
65				70					75						80
Glu	Val	Asp	Asp	Trp	Glu	Phe									
				85											

<210> 520
 <211> 40
 <212> PRT
 <213> Homo sapiens

1093360.1001

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 520
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser
 10

<210> 521
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 521
 Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
 1 5 10 15
 Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
 20 25 30
 Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
 35 40 45
 Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
 50 55 60
 Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
 65 70 75 80
 Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
 85 90 95
 Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
 100 105 110
 Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
 115 120 125
 His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
 130 135 140
 Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
 145 150

<210> 522
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 522
 Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
 1 5 10 15
 Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
 20 25 30
 Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
 35 40 45
 Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
 50 55 60
 Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
 65 70 75 80
 Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
 85 90 95
 Lys Gln Thr Ser Val
 100

<210> 523

09978360.104504

<211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 523

Met	Phe	Glu	Glu	Pro	Glu	Trp	Ala	Glu	Ala	Ala	Pro	Val	Ala	Ala	Gly	
		-20					-15					-10				
Leu	Gly	Pro	Val	Ile	Ser	Arg	Pro	Pro	Pro	Ala	Ala	Ser	Ser	Gln	Asn	
	-5					1				5				10		
Lys	Gly	Ser	Lys	Arg	Arg	Gln	Leu	Leu	Ala	Thr	Leu	Arg	Ala	Leu	Glu	
			15						20					25		
Ala	Ala	Ser	Leu	Ser	Gln	His	Pro	Pro	Ser	Leu	Cys	Ile	Ser	Asp	Ser	
			30					35					40			
Glu	Glu	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Lys	Cys	Pro	Lys	Lys	Ala	Ser	
		45					50					55				
Phe	Ala	Ser	Ala	Ser	Ala	Glu	Val	Gly	Lys	Lys	Gly	Lys	Lys	Lys	Cys	
	60					65					70					
Gln	Lys	Gln	Gly	Pro	Pro	Cys	Ser	Asp	Ser	Glu	Glu	Val	Glu	Arg		
	75				80					85				90		
Lys	Lys	Lys	Cys	His	Lys	Gln	Ala	Leu	Val	Gly	Ser	Asp	Ser	Ala	Glu	
				95					100					105		
Asp	Glu	Lys	Arg	Lys	Arg	Lys	Cys	Gln	Lys	His	Ala	Pro	Ile	Asn	Ser	
			110					115					120			
Ala	Gln	His	Leu	Asp	Asn	Val	Asp	Gln	Thr	Gly	Pro	Lys	Ala	Trp	Lys	
		125					130					135				
Gly	Ser	Thr	Thr	Asn	Asp	Pro	Pro	Lys	Gln	Ser	Pro	Gly	Ser	Thr	Ser	
	140				145						150					
Pro	Lys	Pro	Pro	His	Thr	Leu	Ser	Arg	Lys	Gln	Trp	Arg	Asn	Arg	Gln	
	155				160					165					170	
Lys	Asn	Lys	Arg	Arg	Cys	Lys	Asn	Lys	Phe	Gln	Pro	Pro	Gln	Val	Pro	
			175						180					185		
Asp	Gln	Ala	Pro	Ala	Glu	Ala	Pro	Thr	Glu	Lys	Thr	Glu	Val	Ser	Pro	
		190						195					200			
Val	Pro	Arg	Thr	Asp	Ser	His	Gly	Ala	Arg	Ala	Gly	Ala	Leu	Arg	Ala	
	205						210					215				
Arg	Met	Ala	Gln	Arg	Leu	Asp	Gly	Ala	Arg	Phe	Arg	Tyr	Leu	Asn	Glu	
	220					225					230					
Gln	Leu	Tyr	Ser	Gly	Pro	Ser	Ser	Ala	Ala	Gln	Arg	Leu	Phe	Gln	Glu	
	235				240					245					250	
Asp	Pro	Glu	Ala	Phe	Leu	Leu	Tyr	His	Arg	Gly	Phe	Gln	Ser	Gln	Val	
			255						260					265		
Lys	Lys	Trp	Pro	Leu	Gln	Pro	Val	Asp	Arg	Ile	Ala	Arg	Asp	Leu	Arg	
		270						275					280			
Gln	Arg	Pro	Ala	Ser	Leu	Val	Val	Ala	Asp	Phe	Gly	Cys	Gly	Asp	Cys	
	285						290					295				
Arg	Leu	Ala	Ser	Ser	Ile	Arg	Asn	Pro	Val	His	Cys	Phe	Asp	Leu	Ala	
	300					305					310					
Ser	Leu	Asp	Pro	Arg	Val	Thr	Val	Cys	Asp	Met	Ala	Gln	Val	Pro	Leu	
	315				320					325				330		
Glu	Asp	Glu	Ser	Val	Asp	Val	Ala	Val	Phe	Cys	Leu	Ser	Leu	Met	Gly	
			335						340					345		
Thr	Asn	Ile	Arg	Asp	Phe	Leu	Glu	Glu	Ala	Asn	Arg	Val	Leu	Lys	Pro	
		350						355					360			
Gly	Gly	Leu	Lys	Val	Ala	Glu	Val	Ser	Ser	Arg	Phe	Glu	Asp	Val		
		365				370					375					
Arg	Thr	Phe	Leu	Arg	Ala	Val	Thr	Lys	Leu	Gly	Phe	Lys	Ile	Val	Ser	
	380					385					390					

0097860 04501

Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe Gln Lys Thr
 395 400 405 410
 Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly Leu Gln Leu
 415 420 425
 Gln Pro Cys Leu Tyr Lys Arg Arg
 430

<210> 524
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 524
 Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
 1 5 10 15
 Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
 20 25 30
 Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
 35 40 45
 Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
 50 55 60
 Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
 65 70 75
 Val Glu
 80

<210> 525
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 525
 Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
 -25 -20 -15
 Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
 -10 -5 1
 Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
 5 10 15
 Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
 20 25 30 35
 Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
 40 45 50
 Asn Ala Ser

<210> 526
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

0003360 10501

<222> -23...-1

<400> 526

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
60 65 70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
75 80 85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
90 95 100 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
110 115 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
125 130 135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
140 145 150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
155 160 165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
170 175 180 185
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
190 195 200
Arg Lys Ser Arg Thr
205

<210> 527

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 527

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
-20 -15 -10
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
-5 1 5 10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
15 20 25
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
30 35 40
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
45 50 55
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
60 65 70 75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
80 85 90
Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
95 100 105
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu

	110		115		120		
Asn	Asp	Phe	Ser	Gln	Glu	Ser	Ser
	125					130	

<210> 528
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 528
 Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
 -50 -45 -40
 Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
 -35 -30 -25
 Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
 -20 -15 -10
 Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
 -5 1 5 10
 Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
 15 20 25
 Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu
 30 35 40
 Ala Gly Met Pro Ser Pro Glu Trp Thr Lys Arg Lys Lys Gln Thr Leu
 45 50 55
 Lys Ile Gly His Gly Gly Thr Leu Asp Ser Ala Ala Arg Gly Val Leu
 60 65 70
 Val Val Gly Ile Gly Ser Gly Thr Lys Met Leu Thr Ser Met Leu Ser
 75 80 85 90
 Gly Ser Lys Arg Tyr Thr Ala Ile Gly Glu Leu Gly Lys Ala Thr Asp
 95 100 105
 Thr Leu Asp Ser Thr Gly Lys Val Thr Glu Glu Lys Pro Tyr Gly Met
 110 115 120
 Asn Leu Ile
 125

<210> 529
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92...-1

<400> 529
 Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu
 -90 -85 -80
 Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro
 -75 -70 -65
 Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp
 -60 -55 -50 -45
 Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr
 -40 -35 -30
 Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala
 -25 -20 -15
 Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val
 -10 -5 1

009360.101501

Lys	Cys	Asn	Glu	Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val
5					10					15					20
Glu	Val	Leu	Glu	Pro	Glu	Val	Thr	Lys	Leu	Met	Lys	Phe	Met	Tyr	Phe
				25					30					35	
Gln	Arg	Lys	Ala	Ile	Glu	Arg	Phe	Cys	Ser	Glu	Val	Lys	Arg	Leu	Cys
		40					45						50		
His	Ala	Glu	Arg	Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Leu	Thr
	55						60					65			
Leu	Gly	Lys	Phe	Ile	Asn	Met	Phe	Ala	Val	Leu	Asp	Glu	Leu	Lys	Asn
	70					75					80				
Met	Lys	Cys	Ser	Val	Lys	Asn	Asp	His	Ser	Ala	Tyr	Lys	Arg	Ala	Ala
85					90					95					100
Gln	Phe	Leu	Arg	Lys	Met	Ala	Asp	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Gln
				105					110					115	
Asn	Leu	Ser	Met	Phe	Leu	Ala	Asn	His	Asn	Arg	Ile	Thr	Gln	Cys	Leu
			120					125					130		
His	Gln	Gln	Leu	Glu	Val	Ile	Pro	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp
		135					140					145			
Ile	Val	Asn	Ile	Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Lys	Met	Tyr	Leu	Thr
	150					155					160				
Pro	Ser	Glu	Lys	His	Met	Leu	Leu	Lys	Val	Lys	Leu	Pro			
165					170					175					

<210> 530
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

Met	Gln	Thr	Val	Tyr	Tyr	Gly	Ser	Leu	Gly	Leu	Trp	Leu	Ala	Leu	Val
		-20					-15					-10			
Asp	Gly	Leu	Val	Arg	Ser	Ser	Pro	Ser	Leu	Asp	Gln	Met	Phe	Asp	Ala
	-5					1				5				10	
Glu	Ile	Leu	Gly	Phe	Ser	Thr	Pro	Pro	Gly	Arg	Leu	Ser	Met	Met	Ser
			15						20				25		
Phe	Ile	Phe	Asn	Ala	Leu	Thr	Cys	Ala	Leu	Gly	Leu	Leu	Tyr	Phe	Ile
		30					35					40			
Arg	Arg	Gly	Lys	Gln	Cys	Leu	Asp	Phe	Thr	Val	Thr	Val	His	Phe	Phe
		45					50					55			
His	Leu	Leu	Gly	Cys	Trp	Phe	Tyr	Ser	Ser	Arg	Phe	Pro	Ser	Ala	Leu
	60					65				70					
Thr	Trp	Trp	Leu	Val	Gln	Ala	Val	Cys	Ile	Ala	Leu	Met	Ala	Val	Ile
	75				80					85				90	
Gly	Glu	Tyr	Leu	Cys	Met	Arg	Thr	Glu	Leu	Lys	Glu	Ile	Pro	Leu	Asn
			95						100					105	
Ser	Ala	Pro	Lys	Ser	Asn	Val									
			110												

<210> 531
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 531
 Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -35 -30 -25
 Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
 -20 -15 -10
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 -5 1 5 10
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 15 20 25
 Glu Val Leu

<210> 532
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 532
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
 60 65 70

<210> 533
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 533
 Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
 -20 -15 -10
 Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
 -5 1 5 10
 Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
 15 20 25
 Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
 30 35 40
 Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
 45 50 55
 Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
 60 65 70 75
 Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe

80																85								90					
Thr	Glu	Thr	Met	Ser	Ser	Leu	Ser	Pro	Gly	Arg	Pro	Trp	Gln	Thr	Lys														
			95					100					105																
Leu	Ser	Ser	Ala	Gly	Leu	Ile	Tyr	Leu	His	Phe	Gly	His	Lys	Leu	Leu														
		110					115					120																	
Ala	Gln	Leu	Leu	Gly	Thr	Ser	Glu	Glu	Asp	Ser	Met	Val	Gly	Thr	Leu														
	125					130					135																		
Tyr	Asp	Lys	Met	Tyr	Glu	Asn	Phe	Val	Glu	Glu	Val	Asp	Ala	Val	Asp														
140					145						150					155													
Asn	Gly	Ile	Ser	Gln	Trp	Ala	Glu	Gly	Glu	Pro	Arg	Tyr	Ala	Leu	Thr														
				160					165							170													
Thr	Thr	Leu	Ser	Ala	Arg	Val	Ala	Arg	Leu	Asn	Pro	Thr	Trp	Asn	His														
			175					180					185																
Pro	Asp	Gln	Asp	Thr	Glu	Ala	Gly	Phe	Lys	Arg	Ala	Met	Asp	Leu	Val														
	190						195					200																	
Gln	Glu	Glu	Phe	Leu	Gln	Arg	Leu	Asp	Phe	Tyr	Gln	His	Ser	Trp	Leu														
	205					210					215																		
Pro	Ala	Arg	Ala	Leu	Val	Glu	Glu	Ala	Leu	Ala	Gln	Arg	Phe	Gln	Val														
220					225					230						235													
Asp	Pro	Ser	Gly	Glu	Ile	Val	Glu	Leu	Ala	Lys	Gly	Ala	Cys	Pro	Trp														
				240					245							250													
Lys	Glu	His	Leu	Tyr	His	Leu	Glu	Ser	Gly	Leu	Ser	Pro	Pro	Val	Ala														
			255					260					265																
Ile	Phe	Phe	Val	Ile	Tyr	Thr	Asp	Gln	Ala	Gly	Gln	Trp	Arg	Ile	Gln														
	270						275					280																	
Cys	Val	Pro	Lys	Glu	Pro	His	Ser	Phe	Gln	Ser	Arg	Leu	Pro	Leu	Pro														
	285					290					295																		
Glu	Pro	Trp	Arg	Gly	Leu	Arg	Asp	Glu	Ala	Leu	Asp	Gln	Val	Ser	Gly														
300					305					310						315													
Ile	Pro	Gly	Cys	Ile	Phe	Val	His	Ala	Ser	Gly	Phe	Ile	Gly	Gly	His														
				320					325							330													
Arg	Thr	Arg	Glu	Gly	Ala	Leu	Ser	Met	Ala	Arg	Ala	Thr	Leu	Ala	Gln														
			335					340					345																
Arg	Ser	Tyr	Leu	Pro	Gln	Ile	Ser																						
		350					355																						

```
<220>
<221> SIGNAL
<222> -30..-1
```

<400> 534															
Met	Gly	Glu	Ala	Ser	Pro	Pro	Ala	Pro	Ala	Arg	Arg	His	Leu	Leu	Val
-30					-25					-20					-15
Leu	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Val	Ile	Pro	Ser	Ala	Ala	Ala	Pro
				-10					-5					1	
Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu
	5						10					15			
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu
	20					25					30				
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly
35				40						45					50
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly
			55						60					65	
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Val	Pro	Arg	Met
			70					75					80		
Glu	Glu	Lys	Glu	Ala	Leu	Val	Pro	Ile	Gln	Lys	Ala	Thr	Asp	Ser	Phe

85 90 95
 His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
 100 105 110
 Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115 120 125 130
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
 135 140 145
 Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
 150 155 160
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
 165 170 175
 Arg Gln Leu
 180

<210> 535
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 535
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
 25 30 35
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 536
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 536
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
 -40 -35 -30
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
 -25 -20 -15
 Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
 -10 -5 1 5

09078360.101501

Lys	Ser	Ser	Gln	Ala	Ala	Arg	Lys	Asp	Asp	Phe	Leu	Arg	Ser	Leu	Ser
			10					15					20		
Asp	Gly	Asp	Ser	Gly	Thr	Ser	Glu	His	Ile	Ser	Ala	Val	Val	Thr	Ser
		25					30					35			
Pro	Arg	Ile	Ser	Cys	His	Gly	Ala	Ala	Ile	Pro	Thr	Ala	Arg	Ala	Leu
		40				45					50				
Cys	Leu	Gly	Cys	Ser	Cys	Cys	Thr	Glu	Arg	Leu	Leu	Leu	Pro	Pro	Pro
55					60					65					70
Ser	Leu	Leu	Ser	Leu	Glu	Ala	Pro	Ala	Ser	Thr					
				75					80						

<210> 537
 <211> 346
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 537

Met	Ala	Met	Ala	Gln	Lys	Leu	Ser	His	Leu	Leu	Pro	Ser	Leu	Arg	Gln
				-15					-10					-5	
Val	Ile	Gln	Glu	Pro	Gln	Leu	Ser	Leu	Gln	Pro	Glu	Pro	Val	Phe	Thr
		1				5					10				
Val	Asp	Arg	Ala	Glu	Val	Pro	Pro	Leu	Phe	Trp	Lys	Pro	Tyr	Ile	Tyr
	15					20					25				
Ala	Gly	Tyr	Arg	Pro	Leu	His	Gln	Thr	Trp	Arg	Phe	Tyr	Phe	Arg	Thr
30					35					40					45
Leu	Phe	Gln	Gln	His	Asn	Glu	Ala	Val	Asn	Val	Trp	Thr	His	Leu	Leu
				50					55					60	
Ala	Ala	Leu	Val	Leu	Leu	Leu	Arg	Leu	Ala	Leu	Phe	Val	Glu	Thr	Val
			65					70					75		
Asp	Phe	Trp	Gly	Asp	Pro	His	Ala	Leu	Pro	Leu	Phe	Ile	Ile	Val	Leu
		80					85					90			
Ala	Ser	Phe	Thr	Tyr	Leu	Ser	Leu	Ser	Ala	Leu	Ala	His	Leu	Leu	Gln
	95					100				105					
Ala	Lys	Ser	Glu	Phe	Trp	His	Tyr	Ser	Phe	Phe	Phe	Leu	Asp	Tyr	Val
110					115					120				125	
Gly	Val	Ala	Val	Tyr	Gln	Phe	Gly	Ser	Ala	Leu	Ala	His	Phe	Tyr	Tyr
				130					135					140	
Ala	Ile	Glu	Pro	Ala	Trp	His	Ala	Gln	Val	Gln	Ala	Val	Phe	Leu	Pro
				145				150					155		
Met	Ala	Ala	Phe	Leu	Ala	Trp	Leu	Ser	Cys	Ile	Gly	Ser	Cys	Tyr	Asn
		160					165					170			
Lys	Tyr	Ile	Gln	Lys	Pro	Gly	Leu	Leu	Gly	Arg	Thr	Cys	Gln	Glu	Val
	175					180					185				
Pro	Ser	Val	Leu	Ala	Tyr	Ala	Leu	Asp	Ile	Ser	Pro	Val	Val	His	Arg
190					195					200					205
Ile	Phe	Val	Ser	Ser	Asp	Pro	Thr	Thr	Asp	Asp	Pro	Ala	Leu	Leu	Tyr
				210					215					220	
His	Lys	Cys	Gln	Val	Val	Phe	Phe	Leu	Leu	Ala	Ala	Ala	Phe	Phe	Ser
			225					230					235		
Thr	Phe	Met	Pro	Glu	Arg	Trp	Phe	Pro	Gly	Ser	Cys	His	Val	Phe	Gly
		240					245					250			
Gln	Gly	His	Gln	Leu	Phe	His	Ile	Phe	Leu	Val	Leu	Cys	Thr	Leu	Ala
	255					260					265				
Gln	Leu	Glu	Ala	Val	Ala	Leu	Asp	Tyr	Glu	Ala	Arg	Arg	Pro	Ile	Tyr
270					275					280					285
Glu	Pro	Leu	His	Thr	His	Trp	Pro	His	Asn	Phe	Ser	Gly	Leu	Phe	Leu
				290					295					300	

09978360 101501

Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
 305 310 315
 Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
 320 325

<210> 538
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 538
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
 30 35 40
 Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
 45 50 55 60
 Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
 65 70 75
 Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
 80 85 90
 Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
 95 100 105
 Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
 110 115 120
 Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
 125 130 135 140
 Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
 145 150 155
 His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu
 160 165 170
 Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys
 175 180 185
 Pro Lys
 190

<210> 539
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 539
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr

09978360.101501

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 541
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
-40 -35 -30
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
-25 -20 -15 -10
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
-5 1 5
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
10 15 20
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
25 30

<210> 542
<211> 73
<212> PRT
<213> Homo sapiens

<400> 542
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
1 5 10 15
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
20 25 30
Lys Lys Phe Leu Glu Ser Asp Asp Lys Met Val Lys Lys Ile Ala
35 40 45
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
50 55 60
Asn Leu Leu Glu Val Cys Lys Lys Lys
65 70

<210> 543
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 543
Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
-15 -10 -5
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
1 5 10 15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
20 25 30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
35 40 45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
50 55 60
Lys Asn
65

<210> 544
<211> 119

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56...-1

<400> 544
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys Lys
60

<210> 545
<211> 54
<212> PRT
<213> Homo sapiens

<400> 545
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

<210> 546
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 546
Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
-10 -5 1
Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
5 10 15
Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
20 25 30
Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
35 40 45 50
Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
55 60 65
Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met

<400> 549

Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
1 5 10 15
Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
20 25 30
Phe Phe Gln Ile
35

<210> 550

<211> 307

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 550

Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
-10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
40 45 50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
55 60 65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
70 75 80
Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
85 90 95
Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu
100 105 110 115
Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
120 125 130
Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
135 140 145
Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
150 155 160
Trp Gln Arg Arg Asp Tyr Leu Leu Val Met Glu Gly Thr Asp Asp
165 170 175
Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
180 185 190 195
Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
200 205 210
Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
215 220 225
Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
230 235 240
Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
245 250 255
Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
260 265 270 275
Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
280 285 290
Lys Lys Lys

<210> 551

<211> 106

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32...-1

<400> 551
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65 70

<210> 552
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19...-1

<400> 552
Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 1 5 10
Gln Leu Ser Asp Lys Val His Asn Asp Ile
15 20

<210> 553
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 553
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
30 35 40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg

Gly	Ser	Gln	Glu	Asp	Phe	Thr	Gln	Val	Trp	Asn	Thr	Thr	Met	Lys	Gly
55						60					65				
Leu	Lys	Cys	Arg	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser	Pro
70					75					80					85
Tyr	Phe	Lys	Met	His	Lys	Pro	Val	Thr	Met	Lys	Lys	Lys	Lys		
				90					95						

<210> 556
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -115..-1

<400> 556																
Met	Arg	Trp	Ser	Cys	Glu	His	Leu	Val	Met	Val	Trp	Ile	Asn	Ala	Phe	
-115					-110					-105					-100	
Val	Met	Leu	Thr	Thr	Gln	Leu	Leu	Pro	Ser	Lys	Tyr	Cys	Asp	Leu	Leu	
			-95						-90					-85		
His	Lys	Ser	Ala	Ala	His	Leu	Gly	Lys	Trp	Gln	Lys	Leu	Glu	His	Gly	
		-80					-75						-70			
Ser	Tyr	Ser	Asn	Ala	Pro	Gln	His	Ile	Trp	Ser	Glu	Asn	Thr	Ile	Trp	
		-65				-60					-55					
Pro	Gln	Gly	Val	Leu	Val	Arg	His	Ser	Arg	Cys	Leu	Tyr	Arg	Ala	Met	
-50					-45					-40						
Gly	Pro	Tyr	Asn	Val	Ala	Val	Pro	Ser	Asp	Val	Ser	His	Ala	Arg	Phe	
-35				-30					-25					-20		
Tyr	Phe	Leu	Phe	His	Arg	Pro	Leu	Arg	Leu	Leu	Asn	Leu	Leu	Ile	Leu	
			-15					-10						-5		
Ile	Glu	Gly	Gly	Val	Val	Phe	Tyr	Gln	Leu	Tyr	Ser	Leu	Leu	Arg	Ser	
		1				5					10					
Glu	Lys	Trp	Asn	His	Thr	Leu	Ser	Met	Ala	Leu	Ile	Leu	Phe	Cys	Asn	
15					20					25						
Tyr	Tyr	Val	Leu	Phe	Lys	Leu	Leu	Arg	Asp	Arg	Ile	Val	Leu	Gly	Arg	
30				35					40					45		
Ala	Tyr	Ser	Tyr	Pro	Leu	Asn	Ser	Tyr	Glu	Leu	Lys	Ala	Asn			
				50					55							

<210> 557
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 557																
Met	Pro	Ser	Val	Asn	Ser	Ala	Gly	Leu	Cys	Val	Leu	Gln	Leu	Thr	Thr	
-20				-15					-10					-5		
Ala	Val	Thr	Ser	Ala	Phe	Leu	Leu	Ala	Lys	Val	Asn	Pro	Phe	Glu	Xaa	
			1				5					10				
Phe	Leu	Ser	Arg	Gly	Phe	Trp	Leu	Cys	Ala	Ala	His	His	Phe	Ile	His	
	15					20					25					
Pro	Cys	Leu	Asp													
30																

<210> 558
 <211> 193

0978360.10404

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 558
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
 -20 -15 -10
Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
 -5 1 5
Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
10 15 20 25
Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
 30 35 40
Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
 45 50 55
Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
 60 65 70
Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
75 80 85
Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
90 95 100 105
Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
 110 115 120
Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
 125 130 135
Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
140 145 150
Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
155 160 165
Asn
170

<210> 559
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 559
Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 -10 -5 1
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
5 10 15
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
20 25 30
Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
35 40 45 50
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 55 60 65
Phe Gly

<210> 560
<211> 198
<212> PRT

00973360.10504

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 560

```
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
-20 -15 -10
Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
-5 1 5 10
Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
15 20 25
Leu Asn Gly Val Tyr Arg Thr Thr Gly Arg Leu Thr Lys Ala Arg
30 35 40
Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
45 50 55
Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
60 65 70 75
Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu Gln Ala Xaa Ala Thr
80 85 90
Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
95 100 105
Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa Ala Trp Leu Gly Pro
110 115 120
Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro Pro Xaa Lys Gln Asn
125 130 135
His Ile Leu Trp Ala Leu Thr Gly His Val Xaa Arg Gln Xaa Arg Glu
140 145 150 155
Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile Gln Glu Lys Leu His
160 165 170
Thr Ala Ala Leu Pro Ala
175
```

<210> 561

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 561

```
Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
-55 -50 -45 -40
Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
-35 -30 -25
Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
-20 -15 -10
Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
-5 1 5
Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
10 15 20 25
Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
30 35 40
Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
45 50 55
Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
60 65 70
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
```

75 80 85
 Pro Phe Ala Arg Asp Ala Val Lys Xaa Cys Phe Ala Val Cys Leu Ala
 90 95 100 105

<210> 562
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 562
 Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
 -15 -10 -5
 Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
 1 5 10
 Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
 15 20 25 30
 Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
 35 40 45
 Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
 50 55 60
 Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
 65 70 75
 Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 80 85 90

<210> 563
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 563
 Met Ile Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu
 -20 -15 -10
 Phe Pro Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp
 -5 1 5 10
 Leu Tyr Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser
 15 20 25
 Gln Lys Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
 30 35 40

<210> 564
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 564
 Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
 -15 -10 -5 1
 Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn

0093360101501

<210> 565
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 565
 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 -20 -15 -10
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
 -5 1 5 10
 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 15 20 25
 Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 30 35 40
 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 45 50 55
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys
 60 65 70 75
 Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
 80 85 90
 Pro Ser Thr Xaa Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu
 95 100 105
 Val Phe Met Arg Met Thr Pro Ser Met Met Asn Thr Pro Ser Gly
 110 115 120
 Asn Xaa Gly Cys Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser
 125 130 135
 Ser Ser Pro Val Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile
 140 145 150 155
 Ile Ala Gly Glu Ser Ile Arg Asn Arg Ser
 160 165

<210> 566
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 566
 Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
 -25 -20 -15
 Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys Arg Pro Val Leu Gln Asn
 -10 -5 1 5
 Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser Leu Glu Val Pro Thr Gly
 10 15 20
 Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly Pro Gly Leu Xaa Gly Ala
 25 30 35
 Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu Met Gly Arg Gln Arg Thr
 40 45 50
 Arg Lys Val Lys Gly Pro Ala Trp Xaa His Thr Ala Asn Gln Glu Leu
 55 60 65 70
 Asn Arg Met Arg Ser Leu Ser Ser Gly Ser Val Pro Val Gly His Leu
 75 80 85

Glu Gly Gly Thr Val Lys Leu Gln Lys Asp Thr Gly Leu His Ser Cys
 90 95 100
 Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr Pro Ala Ser Val Leu Ala
 105 110 115
 Asp Ala Cys Pro Gly Phe His Asp Val Xaa Val Gln Xaa Ala Leu Phe
 120 125 130
 Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys Thr His Phe Cys Leu Ser
 135 140 145 150
 Ile Xaa Leu

<210> 567
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 567
 Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
 -55 -50 -45 -40
 Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
 -35 -30 -25
 Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
 -20 -15 -10
 Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
 -5 1 5
 Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
 10 15 20 25
 Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
 30 35 40
 Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
 45 50 55
 Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
 60 65 70
 Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
 75 80 85
 Pro Gly Cys Tyr Arg Tyr
 90 95

<210> 568
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 568
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 -30 -25 -20
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
 -15 -10 -5 1
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 5 10 15
 Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu
 20 25 30
 Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln Ala Ser

```

      35              40              45
Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro Ala Ala
50              55              60              65
Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
              70              75              80
Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
      85              90              95
Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
      100              105              110
Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu Gly Pro
      115              120              125
Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe Glu Asp
130              135              140              145
Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
              150              155              160
Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
      165              170              175
Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
      180              185              190
Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
      195              200              205

```

<210> 569
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -100..-1

```

<400> 569
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100              -95              -90              -85
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
              -80              -75              -70
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
              -65              -60              -55
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
              -50              -45              -40
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
      -35              -30              -25
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20              -15              -10              -5
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
              1              5              10
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
      15              20              25
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
      30              35              40
Gly Tyr Leu Met Gly
45

```

<210> 570
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 570

Met	Pro	Phe	His	Phe	Pro	Phe	Leu	Gly	Phe	Val	Cys	Leu	His	Leu	His
			-45						-40					-35	
Leu	Thr	Pro	Cys	Leu	Thr	Val	Pro	Arg	Arg	Pro	Leu	Phe	Leu	Leu	Leu
			-30					-25					-20		
His	Leu	Cys	Pro	His	Leu	Pro	Phe	Leu	Leu	Leu	Leu	Ser	Cys	Val	Gly
			-15				-10					-5			
Xaa	Xaa	Pro	Ser	Cys	Leu	Pro	Ser	Ser	Ser	Thr	Cys	Val	Ser	Leu	His
	1				5					10					15
Phe	Phe	Ile	Pro	Asp											
				20											

<210> 571

<211> 241

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30...-1

<400> 571

Met	Gly	Thr	Ala	Ser	Arg	Ser	Asn	Ile	Ala	Arg	His	Leu	Gln	Thr	Asn
-30					-25					-20					-15
Leu	Ile	Leu	Phe	Cys	Val	Gly	Ala	Val	Gly	Ala	Cys	Thr	Leu	Ser	Val
				-10					-5					1	
Thr	Gln	Pro	Trp	Tyr	Leu	Glu	Val	Asp	Tyr	Thr	His	Glu	Ala	Val	Thr
		5					10					15			
Ile	Lys	Cys	Thr	Phe	Ser	Ala	Thr	Gly	Cys	Pro	Ser	Glu	Gln	Pro	Thr
	20					25					30				
Cys	Leu	Trp	Phe	Arg	Tyr	Gly	Ala	His	Gln	Pro	Glu	Asn	Leu	Cys	Leu
35					40					45					50
Asp	Gly	Cys	Lys	Ser	Glu	Ala	Xaa	Lys	Phe	Thr	Val	Arg	Glu	Ala	Leu
				55					60					65	
Lys	Glu	Asn	Gln	Val	Ser	Leu	Thr	Val	Asn	Arg	Val	Thr	Ser	Asn	Asp
			70					75					80		
Ser	Ala	Ile	Tyr	Ile	Cys	Gly	Ile	Ala	Phe	Pro	Ser	Val	Pro	Glu	Ala
		85					90					95			
Arg	Ala	Lys	Gln	Thr	Gly	Gly	Thr	Thr	Leu	Val	Val	Arg	Glu	Ile	
	100					105				110					
Lys	Leu	Leu	Ser	Lys	Glu	Leu	Arg	Ser	Phe	Leu	Thr	Ala	Leu	Val	Ser
115					120					125					130
Leu	Leu	Ser	Val	Tyr	Val	Thr	Gly	Val	Cys	Val	Ala	Phe	Ile	Leu	Leu
				135					140					145	
Ser	Lys	Ser	Lys	Ser	Asn	Pro	Leu	Arg	Asn	Lys	Glu	Ile	Lys	Glu	Asp
			150					155					160		
Ser	Gln	Lys	Lys	Lys	Ser	Ala	Arg	Ile	Phe	Gln	Glu	Ile	Ala	Gln	
		165					170				175				
Glu	Leu	Tyr	His	Lys	Arg	His	Val	Glu	Thr	Asn	Gln	Gln	Ser	Glu	Lys
	180					185					190				
Asp	Asn	Asn	Thr	Tyr	Glu	Asn	Arg	Arg	Val	Leu	Ser	Asn	Tyr	Glu	Arg
195					200					205					210
Pro															

<210> 572

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
<222> -30...-1

<400> 572
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys Trp Leu Glu Val Glu
-30 -25 -20 -15
Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn Ala Ser Ala Ile Ser
-10 -5 1
Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp Arg Arg Glu Ser
5 10 15

<210> 573
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 573
Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
-25 -20 -15
Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
-10 -5 1
Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
5 10 15 20
Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa
25 30 35
Ser

<210> 574
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 574
Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
-20 -15 -10
Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
-5 1 5
Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
10 15 20
Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
25 30 35 40
Trp Gly Gln Gly Thr His Ser Ser Leu
45

<210> 575
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 575

Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
-15 -10 -5
Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
1 5 10
Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
15 20 25 30
Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
35 40

<210> 576

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -93...-1

<400> 576

Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
-90 -85 -80
Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val
-75 -70 -65
Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
-60 -55 -50
Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
-45 -40 -35 -30
Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
-25 -20 -15
Val Leu Leu Leu Arg Gln Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu
-10 -5 1
Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu
5 10 15
Gln Xaa Ala Glu Phe Glu Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys
20 25 30 35
Pro Ile Leu Xaa Val Thr Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly
40 45 50
Gly Thr Ala Lys Leu Leu Asn Lys Val Ile Cys Ile Ile Leu Arg Asn
55 60 65
Gly Lys Ser Leu Ile Leu Ser Cys His Cys Leu Gly Trp Arg Asn Lys
70 75 80
Ser Gly Arg Phe Val Ser Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
85 90 95

<210> 577

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -72...-1

<400> 577

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
-70 -65 -60
Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
-55 -50 -45
Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
-40 -35 -30 -25

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 580
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
-20 -15 -10
Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
-5 1 5 10
Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
15 20 25
Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg Ser Leu Asn Gln Glu
30 35 40
Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr Ser Ile Thr
45 50 55

<210> 581
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 581
Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu Pro Leu Ser
-25 -20 -15
Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser
-10 -5 1
Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val Pro Glu Pro
5 10 15 20
Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg
25 30 35
Thr

<210> 582
<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 582
Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu Glu Leu Thr
-25 -20 -15
Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr Asn Lys Phe
-10 -5 1 5
Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile Phe Ile Gly
10 15 20
Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu Ser Lys Asn
25 30 35
Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile Leu Val His
40 45 50
Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly Asp Ala Pro
55 60 65

bioRxiv preprint doi: <https://doi.org/10.1101/096660>; this version posted October 10, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile Lys Ser Ser
70 75 80 85
Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu Gly Asn Ser
90 95 100
Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu Tyr Ser Glu
105 110 115
Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln Ser Ile Cys
120 125 130
Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu His Trp Gln
135 140 145
Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile Ser Phe Phe
150 155 160 165
Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly Ser Asp Tyr
170 175 180
Arg Ser Ile

<210> 583
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -80..-1

<400> 583
Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
-80 -75 -70 -65
Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
-60 -55 -50
Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
-45 -40 -35
Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
-30 -25 -20
Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
-15 -10 -5
Thr Ser Thr Pro Ser Ala Lys Ile Gln Ser Leu Gln Ile Asp Leu Pro
1 5 10 15
Gly Gly Trp Arg Leu Ala Thr Asp Arg Ile Phe Thr Leu Ser Pro Val
20 25 30
Pro Met Asp Xaa Pro Leu Ile Leu His Gln Leu
35 40

<210> 584
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 584
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
-25 -20 -15
Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
-10 -5 1 5
Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
10 15 20
Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp Val Leu

25 30 35
 Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp Ser His
 40 45 50
 Ala His Trp Xaa Ser Xaa
 55 60

<210> 585
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 585
 Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
 -30 -25 -20
 Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
 -15 -10 -5 1
 Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 5 10 15
 Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 20 25 30
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 35 40 45
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
 50 55 60 65
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 70 75 80
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser His Val Ser
 85 90 95
 Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
 100 105 110
 Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp Asn Trp Glu
 115 120 125
 Pro Asn
 130

<210> 586
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 586
 Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
 -35 -30 -25
 Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
 -20 -15 -10
 Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
 -5 1 5 10
 Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Xaa Gln
 15 20 25
 Xaa Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Gly
 30 35 40
 Gly Phe Ser Phe Cys Gln Xaa Arg Leu Asn Lys Arg Lys Glu Tyr Met
 45 50 55

09978360 101501

Val Arg
60

<210> 587
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 587
Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu
-15 -10 -5 1
Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
5 10 15
Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
20 25 30
Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
35 40 45
Asp Phe Ser Ser Phe Thr
50 55

<210> 588
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45...-1

<400> 588
Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
-45 -40 -35 -30
Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
-25 -20 -15
Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
-10 -5 1
Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
5 10 15

<210> 589
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22...-1

<400> 589
Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
-20 -15 -10
Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
-5 1 5 10
Asn Pro Phe Leu Trp Lys Leu
15

<210> 590

TEST OF "09E32650"

<211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 590
 Met Ala Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala
 -20 -15 -10
 Phe Pro Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly
 -5 1 5
 Lys Pro Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg
 10 15 20 25
 Ile Trp Pro

<210> 591
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 591
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Xaa Xaa Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 592
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 592
 Met Asp Glu Tyr Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly
 -30 -25 -20
 Gln Met Phe Thr Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys
 -15 -10 -5
 Gln Arg Phe Phe Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser
 1 5 10 15
 Thr Val Thr Pro Ser Trp Arg Leu Cys Leu Val Ser
 20 25

<210> 593

1097360 1097360

<211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -79...-1

<400> 593
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 -75 -70 -65
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 -45 -40 -35
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 -15 -10 -5 1
 Pro Ser Ser Lys Ala Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa
 5 10 15
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 20 25 30
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa
 35 40 45
 Arg His Xaa Gln Xaa His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 50 55 60 65
 Cys Thr Xaa Cys Gly Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln
 70 75 80
 His Tyr Ile Arg His Ala Arg Gly Gly Leu
 85 90

<210> 594
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<400> 594
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45
 Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe

09978360 "101501

Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met
40 45 50
Leu

<210> 597
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 597
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
-20 -15 -10
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
-5 1 5 10
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
15 20 25
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
30 35 40
Leu Arg Met
45

<210> 598
<211> 332
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32...-1

<400> 598
Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp
-30 -25 -20
Thr Arg Gln Leu Pro Leu Leu Thr Ser Ala Leu His Gly Leu Gln Gln
-15 -10 -5
Gln His Pro Ala Phe Ser Gly Val Ala Arg Leu Ala Lys Arg Trp Val
1 5 10 15
Arg Ala Gln Leu Leu Gly Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu
20 25 30
Val Ala Ala Ala Leu Phe Leu His Pro Glu Pro Phe Thr Pro Pro Ser
35 40 45
Ser Pro Gln Val Gly Phe Leu Arg Phe Leu Phe Leu Val Ser Thr Phe
50 55 60
Asp Trp Lys Asn Asn Pro Leu Phe Val Asn Leu Asn Asn Glu Leu Thr
65 70 75 80
Val Glu Glu Gln Val Glu Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala
85 90 95
Gln Leu Pro Val Met Val Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser
100 105 110
Val Trp Thr Gln Asp Gly Pro Ser Ala Gln Ile Leu Gln Gln Leu Val
115 120 125
Val Leu Ala Ala Glu Xaa Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp
130 135 140
Pro Arg Gly Pro Gly Asp Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp
145 150 155 160
Ile Tyr Asp Val Leu Ile Arg Leu Ser Pro Arg His Ile Pro Arg His

00978360 10501

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 601
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 -15 -10 -5
 Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser
 1 5 10 15
 Asp Ser Asp Glu Leu Ala Ser Gly Xaa Phe Val Phe Pro Tyr Pro Tyr
 20 25 30
 Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
 35 40 45
 Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
 50 55 60
 Leu Pro Ser Glu Lys
 65

<210> 602
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 602
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 -15 -10 -5
 Gly Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser
 1 5 10 15
 Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
 20 25 30
 Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
 35 40 45
 Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
 50 55 60
 Leu Pro Ser Glu Lys
 65

<210> 603
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 603
 Met Thr Cys Arg Gly Ser Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser
 -25 -20 -15
 Glu Leu Ser Leu Leu Pro Ser Ser Leu Trp Val Leu Ala Thr Ser Ser
 -10 -5 1
 Pro Thr Ile Thr Ile Ala Leu Ala Met Ala Ala Gly Asn Leu Cys Pro
 5 10 15
 Leu Pro Ser Ser Xaa Arg Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln
 20 25 30 35
 Gln Xaa Ala Leu Leu

<210> 604
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<400> 604
 Met Val Pro Trp Pro Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile
 -55 -50 -45
 Ser Arg Phe Pro Phe Leu Pro Thr His Asp Pro Pro Thr Pro Ala His
 -40 -35 -30 -25
 Trp Ser Pro Ala Ser His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu
 -20 -15 -10
 Thr Leu Ala Leu Leu Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys
 -5 1 5
 Lys Leu Ala Gly Gln Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu
 10 15 20
 Pro Leu Thr Leu Trp Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr
 25 30 35 40
 Val Ala Gln Lys Lys Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro
 45 50 55
 Val Pro Ser Trp Val Gln Phe Phe Leu Gly
 60 65

<210> 605
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 605
 Met Ala Cys Glu Thr His Gly Val Leu Val Pro Ala His Leu Ser Gly
 -30 -25 -20 -15
 Leu Ile Thr Cys Leu Leu Ala Phe Trp Val Pro Ala Ser Cys Ile Gln
 -10 -5 1
 Arg Cys Ser Gly Ser Pro Leu Pro Leu
 5 10

<210> 606
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 606
 Met Ala Pro His Thr Ala Ser Phe Gly Val Cys Pro Leu Leu Ser Val
 -35 -30 -25
 Thr Arg Val Val Ala Thr Glu His Trp Leu Phe Leu Ala Ser Leu Ser
 -20 -15 -10 -5
 Gly Ile Lys Thr Tyr Gln Ser Tyr Ile Ser Val Phe Cys Lys Val Thr

00973360-10504

Ser Ala Leu Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa
80 85 90 95
Lys Ile Val Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys
100 105 110
Lys His Cys Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu
115 120 125
Val Ser

<210> 609
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69...-1

<400> 609
Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
-65 -60 -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
-50 -45 -40
Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
-35 -30 -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
-20 -15 -10
Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
-5 1 5 10
Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Val Xaa
15 20 25
Lys Xaa Ser Glu Glu Gly Arg Met Gly Gln Xaa Gly Glu Glu Xaa Xaa
30 35 40
Asn Ser Leu Asn Phe Pro Xaa Ala Ser Leu Leu Xaa Leu Ile Cys Gln
45 50 55
Xaa Gln Gly Phe Asn Gly Glu Ser Cys Ser Pro Val Gly
60 65 70

<210> 610
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69...-1

<400> 610
Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
-65 -60 -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
-50 -45 -40
Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Xaa Lys Val Ile
-35 -30 -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
-20 -15 -10
Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
-5 1 5 10
Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
15 20 25
Ile Ser Gly Ser Leu Ser Ile Ala Thr Lys Lys Arg Leu Thr Asn Leu

<210> 613
 <211> 144
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58..-1

<400> 613
 Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
 -55 -50 -45
 Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
 -40 -35 -30
 Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
 -25 -20 -15
 Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
 -10 -5 1 5
 Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
 10 15 20
 Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser Ala
 25 30 35
 Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu Asp
 40 45 50
 Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn Leu
 55 60 65 70
 Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg Ser
 75 80 85

<210> 614
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 614
 Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
 -15 -10 -5
 Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
 1 5 10 15
 Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
 20 25 30
 Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser
 35 40 45
 Glu Ser Pro Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro
 50 55 60
 Val Pro Pro Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg
 65 70 75 80
 Ala Trp Gly Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala
 85 90 95
 Leu Gly Ser Gly Glu His Pro Xaa Xaa
 100 105

<210> 615
 <211> 162
 <212> PRT
 <213> Homo sapiens

09973360.101501

<222> -15...-1

<400> 617

Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
-15 -10 -5 1
Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
5 10 15
Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
20 25 30
Val Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile
35 40 45
Gln Val Pro Arg Arg Ala Gly
50 55

<210> 618

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 618

Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
-20 -15 -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
-5 1 5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
10 15 20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25 30 35 40
Arg Cys Glu Thr Phe Val Phe Ser Ser Cys Asn Gly Asn Leu Asn Asn
45 50 55
Phe Lys Leu Lys Ile Glu Arg Glu Val Xaa Cys Val Ala Lys Tyr Lys
60 65 70
Pro Pro Arg
75

<210> 619

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 619

Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
-25 -20 -15 -10
Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
-5 1 5
Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Gln Arg Phe Phe Ala
10 15 20
Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
25 30 35
Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
40 45 50 55
Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
60 65 70

09073360 101501

Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser
			75					80					85		
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser
		90					95					100			
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Xaa	Ser	Ala	Glu	Val
	105					110					115				
Ser	Pro	Thr	Thr	Asp	Asp	Leu	Pro	His	Leu	Thr	Pro	Leu	His	Ser	Asp
120					125					130					135
Arg	Thr	Pro	Asp	Leu	Pro	Ala	Leu	Ala							
					140										

<210> 620
 <211> 167
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76...-1

<400> 620															
Met	Gly	Asp	Tyr	Leu	Leu	Arg	Gly	Tyr	Arg	Met	Leu	Gly	Glu	Thr	Cys
	-75					-70					-65				
Ala	Asp	Cys	Gly	Thr	Ile	Leu	Leu	Gln	Asp	Lys	Gln	Arg	Lys	Ile	Tyr
-60					-55					-50					-45
Cys	Val	Ala	Cys	Gln	Glu	Leu	Asp	Ser	Asp	Val	Asp	Lys	Asp	Asn	Pro
				-40					-35					-30	
Ala	Leu	Asn	Ala	Gln	Ala	Ala	Leu	Ser	Gln	Ala	Arg	Glu	His	Gln	Leu
			-25					-20					-15		
Ala	Ser	Ala	Ser	Glu	Leu	Pro	Leu	Gly	Ser	Arg	Pro	Ala	Pro	Gln	Pro
		-10					-5					1			
Pro	Val	Pro	Arg	Pro	Glu	His	Cys	Glu	Gly	Ala	Ala	Ala	Gly	Leu	Lys
5					10					15					20
Ala	Ala	Gln	Gly	Pro	Pro	Ala	Pro	Ala	Val	Pro	Pro	Asn	Thr	Xaa	Val
				25					30					35	
Met	Ala	Cys	Thr	Gln	Thr	Ala	Leu	Leu	Gln	Lys	Leu	Thr	Trp	Ala	Ser
			40					45					50		
Ala	Glu	Leu	Gly	Ser	Xaa	Thr	Ser	Xaa	Gly	Lys	Xaa	Ala	Ser	Ser	Cys
	55						60					65			
Val	Ala	Leu	Ser	Ala	His	Val	Arg	Arg	Pro	Cys	Ala	Ala	Cys	Ser	Ser
	70					75					80				
Tyr	Ser	Thr	Lys	Arg	Ser	Pro									
85					90										

<210> 621
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 621															
Met	Ile	Leu	Cys	Phe	Leu	Leu	Pro	His	His	Arg	Leu	Gln	Glu	Ala	Arg
-15					-10					-5					1
Gln	Ile	Gln	Val	Leu	Lys	Met	Leu	Pro	Arg	Glu	Lys	Leu	Arg	Arg	Arg
		5						10					15		
Glu	Glu	Arg	Lys	Gln	Ile	Asn	Gly	Lys	Lys	Xaa	Arg	Thr	Lys	Tyr	Glu
		20				25					30				
Thr	Pro	Arg	Lys	Xaa	Xaa	Gly	Lys	Lys	Gly	Gly	Asn	Xaa	Xaa	Xaa	Xaa

35
Xaa Leu Ser Lys Arg Asp
50 55

40

45

<210> 622
<211> 381
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33...-1

<400> 622
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
-30 -25 -20
Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
-15 -10 -5
Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
1 5 10 15
Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
20 25 30
Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
35 40 45
Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
50 55 60
Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys Gly Glu Thr Met
65 70 75
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
80 85 90 95
Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr
100 105 110
Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu Asn Leu Xaa Gln
115 120 125
Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr
130 135 140
Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu
145 150 155
Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile
160 165 170 175
Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg Phe Leu Ile Gly
180 185 190
Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly
195 200 205
Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala
210 215 220
Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp
225 230 235
Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr
240 245 250 255
Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
260 265 270
Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
275 280 285
Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile Xaa Glu Glu Val
290 295 300
Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
305 310 315
Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
320 325 330 335
Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu

00978360.101501

<210> 623
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 623
 Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
 -10 -5 1
 Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr
 5 10 15
 Val Tyr Pro Thr Ser Ala Gly
 20 25

<210> 624
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 624
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 -35 -30 -25
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 -20 -15 -10
 Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met Pro
 -5 1 5 10
 Asp Asn

<210> 625
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 625
 Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
 -25 -20 -15
 Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
 -10 -5 1 5
 Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser Leu Ser Ala Thr
 10 15 20
 Thr Arg Gly
 25

<210> 626
 <211> 242
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 626
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35 40 45 50
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 55 60 65
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 70 75 80
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 85 90 95
 Pro Xaa Glu Gly Xaa Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 100 105 110
 Glu Lys Glu Ala Leu Val Pro Xaa Gln Lys Ala Thr Asp Ser Phe His
 115 120 125 130
 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
 135 140 145
 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Xaa Glu
 150 155 160
 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
 165 170 175
 His Lys Asp Xaa Leu Xaa Xaa Gly Thr Glu Ser Ser Ser His Ser Arg
 180 185 190
 Leu Ser Pro Arg Lys Xaa His Leu Leu Tyr Ile Leu Xaa Pro Ser Arg
 195 200 205 210
 Gln Leu

<210> 627
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60..-1

<400> 627
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu
 25 30 35

09978360 "101501

Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
40 45 50
Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe
55 60 65
Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
70 75 80
Pro Glu Phe His Ile Glu Ile Leu Ser Ile
85 90

<210> 628
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -61...-1

<400> 628
Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr
-60 -55 -50
Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro
-45 -40 -35 -30
Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala
-25 -20 -15
Leu Leu Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg
-10 -5 1
Pro Asp Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro
5 10 15
His Pro Cys Ala Thr Tyr Pro Pro Xaa
20 25

<210> 629
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26...-1

<400> 629
Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
-25 -20 -15
Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
-10 -5 1 5
Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
10 15 20
Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
25 30 35
Phe Asp Leu Asp Met Asp His Thr Ile
40 45

<210> 630
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34...-1

0097360 "10501

<400> 630

[illegible]

<210> 631

<211> 121

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<221> SIGNAL

<222> -38..-1

<400> 631

[illegible]

$\langle 210 \rangle$ 632

<211> 166

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<221> SIGNAL

<222> -37..-1

<400> 632

Met	Ser	Thr	Val	Gly	Leu	Phe	His	Phe	Pro	Thr	Pro	Leu	Thr	Arg	Ile
		-35					-30					-25			
Cys	Pro	Ala	Pro	Trp	Gly	Leu	Arg	Leu	Trp	Glu	Lys	Leu	Thr	Leu	Leu
	-20					-15					-10				
Ser	Pro	Gly	Ile	Ala	Val	Thr	Pro	Val	Gln	Met	Ala	Gly	Lys	Lys	Asp
	-5				1			5						10	
Tyr	Pro	Ala	Leu	Leu	Ser	Leu	Asp	Glu	Asn	Glu	Leu	Glu	Glu	Gln	Phe
			15					20					25		
Val	Lys	Gly	His	Gly	Pro	Gly	Gly	Gln	Ala	Thr	Asn	Lys	Thr	Ser	Asn
		30					35					40			
Cys	Val	Val	Leu	Lys	Xaa	Ile	Pro	Ser	Gly	Ile	Val	Val	Lys	Cys	His
	45					50					55				
Gln	Thr	Arg	Ser	Val	Asp	Gln	Asn	Arg	Lys	Leu	Ala	Arg	Lys	Ile	Leu

60 65 70 75
 Gln Glu Lys Val Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His
 80 85 90
 Lys Glu Lys Arg Glu Ala Ala Lys Lys Lys Glu Glu Arg Lys Lys Arg
 95 100 105
 Ala Lys Glu Thr Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu
 110 115 120
 Ser Ser Lys Lys Val His
 125

<210> 633
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 633
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
 105 110 115
 Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
 135 140 145 150
 Arg Asn Trp Glu

<210> 634
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -64...-1

<400> 634
 Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
 -60 -55 -50
 Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
 -45 -40 -35
 Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val
 -30 -25 -20

093350 101501

Arg Thr Phe Leu Phe Ile Val Val Cys Val Ile Cys Val Thr Leu Asn
 -15 -10 -5
 Phe Pro Arg Phe Tyr Phe Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly
 1 5 10 15
 Thr Pro Pro Ile Gly Val His Ile Pro Ser Pro
 20 25

<210> 635
 <211> 257
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 635
 Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
 -20 -15 -10
 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
 -5 1 5
 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
 10 15 20 25
 Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
 30 35 40
 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 45 50 55
 Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
 60 65 70
 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
 75 80 85
 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg
 90 95 100 105
 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
 110 115 120
 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
 125 130 135
 Asn His Glu Ala Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa
 140 145 150
 Leu Glu Xaa Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
 155 160 165
 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val
 170 175 180 185
 Ser Pro Xaa Asn Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro
 190 195 200
 Xaa Xaa Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly
 205 210 215
 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa
 220 225 230
 Xaa

<210> 636
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 636

```

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
-60          -55          -50          -45
Cys Ser Gly Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
          -40          -35          -30
Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
          -25          -20          -15
Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
          -10          -5          1
Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala Pro
5          10          15          20
Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg Ala
          25          30          35
Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa Thr
          40          45          50
Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile Val
          55          60          65
Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa Phe
          70          75          80
Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val Leu
85          90          95          100
Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr His
          105          110          115
Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro Trp
          120          125          130
Glu

```

<210> 637

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 637

```

Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg
          -25          -20          -15
Phe Leu Ser Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser
          -10          -5          1
Trp Asp Val Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile
5          10          15          20
Arg Ala Val Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys
          25          30          35
Val Glu Phe Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val
          40          45          50
Tyr Ser Leu Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu
          55          60          65
Ala Glu Arg Lys Ser Pro Glu Ile Ser Trp Gly
          70          75

```

<210> 638

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<210> 641
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 641
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu
 25 30 35
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn
 40 45 50 55
 Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85
 Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr Gly Thr Phe Glu
 90 95 100

<210> 642
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 642
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Xaa
 -10 -5 1
 Xaa Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
 70 75 80
 Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
 85 90 95
 Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val
 100 105 110
 Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
 115 120 125 130
 Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
 135 140 145

099830.04504

Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
 150 155 160
 Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
 165 170 175
 Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
 180 185 190
 Val Lys Cys Lys Phe Leu Tyr Asn
 195 200

<210> 643
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 643
 Met Thr Phe Arg His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met
 -20 -15 -10
 Ala Thr Cys Thr Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys
 -5 1 5 10
 Ser Leu Thr Ser Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu
 15 20 25
 Ile Lys Phe Gly Tyr Asp Arg Lys Ser Thr Ile Lys Ser
 30 35 40

<210> 644
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 644
 Met Phe Leu Lys Ser Gly Ala Gly Leu Ser Ser Cys Leu Leu Pro Leu
 -15 -10 -5
 Cys Trp Leu Glu Arg Lys Asp His Gly Arg Arg Pro Ser Xaa His Pro
 1 5 10
 Gly Arg
 15

<210> 645
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 645
 Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
 -50 -45 -40
 Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
 -35 -30 -25
 Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
 -20 -15 -10

"09E6660" 09E6660

Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
 -5 1 5 10
 Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
 15 20 25
 Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
 30 35 40
 Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
 45 50 55
 Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
 60 65 70
 Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
 75 80 85 90
 Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
 95 100 105
 Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
 110 115 120
 Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
 125 130 135
 Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
 140 145 150
 Ile Ile Arg Lys Cys Phe Ile
 155 160

<210> 646
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 646
 Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
 -15 -10 -5
 Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10

<210> 647
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 647
 Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
 -20 -15 -10
 Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
 -5 1 5
 Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
 10 15 20
 Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
 25 30 35 40
 Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
 45 50 55
 Tyr Trp Asp Asn Leu
 60

<210> 648
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 648
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 649
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 649
 Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
 -40 -35 -30
 Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
 -25 -20 -15
 Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Thr Asn Thr Ala Val
 -10 -5 1 5
 Lys His Ser Ile Gln Lys Asn Cys Met Xaa Leu Val Leu Gly Lys Leu
 10 15 20
 Leu Ser Gln

<210> 650
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 650
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
 -15 -10 -5 1
 Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
 5 10 15
 Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
 20 25 30
 Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr Ser Ser Ala
 35 40 45

<210> 651
 <211> 179

09978350 101501

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -58...-1

<400> 651
Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
 -55 -50 -45
Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
 -40 -35 -30
Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
 -25 -20 -15
Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
 -10 -5 1 5
Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
 10 15 20
Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile
 25 30 35
Tyr Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa
 40 45 50
Xaa Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser
55 60 65 70
His Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro
 75 80 85
Thr Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys
 90 95 100
Xaa Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly
 105 110 115
Gln Val Asn
 120

<210> 652
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -71...-1

<400> 652
Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
 -70 -65 -60
Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55 -50 -45 -40
Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
 -35 -30 -25
Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu Leu
 -20 -15 -10
Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His Gln
 -5 1 5
Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr Trp
10 15 20 25
Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu His
 30 35 40
Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu Ala
 45 50 55
Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro Asp
 60 65 70

09978360 101501

Gln	Ile	Ile	Cys	Pro	Asp	Glu	Glu	Gly	Thr	Glu	Gly	Thr	Ile	Ser	Leu
75						80				85					
Trp	Ser	Ile	Ile	Ser	Lys	Val	Arg	Ile	Glu	Ala	Cys	Met	Trp	Gly	Ile
90					95				100						105
Gly	Thr	Ala	Ile	Gly	Glu	Leu	Pro	Pro	Tyr	Phe	Met	Ala	Arg	Ala	Ala
				110					115						120
Arg	Leu	Ser	Gly	Ala	Glu	Pro	Asp	Asp	Glu	Glu	Tyr	Gln	Glu	Phe	Glu
			125					130					135		
Glu	Met	Leu	Glu	His	Ala	Glu	Ser	Ala	Gln	Val	Arg	Thr	Val	Gly	Ile
		140					145					150			
Glu	Asn	Arg	Thr	Leu	Tyr	Phe	Phe	Leu	Lys	Arg	Leu	Leu	Arg		
	155						160					165			

<210> 653
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 653															
Met	Glu	Arg	Gln	Ser	Arg	Val	Met	Ser	Glu	Lys	Asp	Glu	Tyr	Gln	Phe
	-35					-30					-25				
Gln	His	Gln	Gly	Ala	Val	Glu	Leu	Leu	Val	Phe	Asn	Phe	Leu	Leu	Ile
	-20					-15				-10					
Leu	Thr	Ile	Leu	Thr	Ile	Trp	Leu	Phe	Lys	Asn	His	Arg	Phe	Arg	Phe
-5					1				5					10	
Leu	His	Glu	Thr	Gly	Gly	Ala	Met	Val	Tyr	Gly	Leu	Xaa	Met	Gly	Leu
		15						20				25			
Ile	Leu	Xaa	Tyr	Ala	Thr	Ala	Pro	Thr	Asp	Ile	Glu	Ser	Gly	Xaa	Val
	30					35					40				
Tyr	Asp	Cys	Val	Lys	Leu	Thr	Phe	Ser	Pro	Ser	Thr	Leu	Leu	Val	Asn
	45					50					55				
Ile	Thr	Asp	Gln	Val	Tyr	Glu	Tyr	Lys	Tyr	Lys	Arg	Glu	Ile	Ser	Gln
60					65					70				75	
His	Xaa	Ile	Asn	Pro	His	Xaa	Gly	Asn	Ala	Ile	Leu	Glu	Lys	Met	Thr
			80					85						90	
Phe	Asp	Pro	Xaa	Ile	Phe	Phe	Asn	Val	Leu	Leu	Pro	Pro	Ile	Ile	Phe
		95						100					105		
His	Ala	Gly	Tyr	Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly
		110					115					120			
Ser	Ile	Leu	Thr	Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val
	125						130					135			
Ile	Gly														
140															

<210> 654
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 654															
Met	Ser	Met	Gln	Phe	Leu	Phe	Lys	Met	Val	Ala	Leu	Cys	Cys	Cys	Leu
	-20					-15					-10				
Trp	Lys	Ile	Ser	Gly	Cys	Glu	Glu	Val	Pro	Leu	Thr	Tyr	Asn	Leu	Leu

<222> -18..-1

<400> 657

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu	Val
		-15						-10					-5		
Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	His	Ser
	1				5						10				
Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	Leu	Cys	Gly
15				20						25					30
Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Leu
			35					40						45	
Lys	Pro	Arg	Tyr	Ile	Xaa	His	Leu	Gly	Gln	His	Asn	Leu	Gln	Lys	Glu
		50					55					60			
Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	Glu	Ser	Phe	Pro	His	Pro
	65					70					75				
Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	Asp	Xaa	Xaa	Asn	Asp	Ile	Met
	80				85					90					
Leu	Val	Xaa	Met	Xaa	Ser	Pro	Val	Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro
95				100					105						110
Leu	Thr	Leu	Ser	Ser	Arg	Cys	Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile
			115					120						125	
Ser	Gly	Trp	Gly	Ser	Thr	Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr
		130					135						140		
Leu	Arg	Cys	Ala	Asn	Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn
	145				150						155				
Ala	Tyr	Pro	Gly	Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln
	160			165						170					
Glu	Gly	Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
175				180					185						190
Cys	Asn	Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys
		195					200						205		
Ala	Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val
		210					215						220		
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
	225						230								

<210> 658

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 658

Met	Ala	Ala	Ser	Thr	Ser	Met	Val	Pro	Val	Ala	Val	Thr	Ala	Ala	Val
	-20					-15					-10				
Ala	Pro	Val	Leu	Ser	Ile	Asn	Ser	Asp	Phe	Ser	Asp	Leu	Arg	Glu	Ile
-5				1					5					10	
Lys	Lys	Gln	Leu	Leu	Leu	Ile	Ala	Gly	Leu	Thr	Arg	Glu	Arg	Gly	Leu
		15					20					25			
Leu	His	Ser	Ser	Lys	Trp	Ser	Ala	Glu	Leu	Ala	Phe	Ser	Leu	Pro	Ala
	30					35					40				
Leu	Pro	Leu	Ala	Glu	Leu	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Glu	Glu	Asp
	45				50						55				
Ala	Gln	Asp	Met	Asp	Ala	Tyr	Thr	Leu	Ala	Lys	Ala	Tyr	Phe	Asp	Val
60				65					70						75
Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys	Asn	Ala	Arg
			80					85					90		
Lys	Ala	Tyr	Phe	Leu	Tyr	Met	Tyr	Ser	Arg	Tyr	Leu	Val	Arg	Ala	Ile

<210> 663
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 663
 Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
 -15 -10 -5
 Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
 1 5 10 15
 Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys Lys
 20 25 30
 Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser Ala
 35 40 45
 Thr

<210> 664
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 664
 Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
 -55 -50 -45 -40
 Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
 -35 -30 -25
 Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 -5 1 5
 Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
 10 15 20 25
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Xaa
 30 35 40
 Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu Gly Arg
 45 50 55
 Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln Gly Trp
 60 65 70
 Ala Leu
 75

<210> 665
 <211> 209
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -84...-1

0093360.101501

<400> 665

Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu
 -80 -75 -70
 Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr
 -65 -60 -55
 Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly
 -50 -45 -40
 Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu
 -35 -30 -25
 Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu
 -20 -15 -10 -5
 Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr
 1 5 10
 Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly
 15 20 25
 Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val
 30 35 40
 Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala Ala Leu His
 45 50 55 60
 Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Xaa Val Xaa
 65 70 75
 Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg
 80 85 90
 Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr
 95 100 105
 Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser
 110 115 120
 His
 125

<210> 666

<211> 36

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 666

Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
 -15 -10 -5
 Ala His Pro Pro Gln Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp
 1 5 10 15
 Val Gly Ile Cys

<210> 667

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29...-1

<400> 667

Met Met Ser Ser Glu Leu Arg Arg Asn Pro His Phe Leu Lys Ser Asn
 -25 -20 -15
 Leu Phe Leu Gln Leu Leu Val Ser His Glu Ile Val Cys Ala Thr Glu
 -10 -5 1

Thr Val Thr Thr Asn Phe Leu Arg His Glu Lys Ala
 5 10 15

<210> 668
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -52...-1

<400> 668
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 -50 -45 -40
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 -35 -30 -25
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 -20 -15 -10 -5
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
 1 5 10
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
 15 20 25
 Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp Ser Trp
 30 35 40
 Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val Arg Arg
 45 50 55 60
 His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu Asp Pro
 65 70 75
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
 80 85 90
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala Xaa Xaa
 95 100 105
 Thr Arg Ser
 110

<210> 669
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 669
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
 -30 -25 -20
 Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
 -15 -10 -5 1
 Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys Gly Xaa Asn Thr
 5 10 15

<210> 670
 <211> 218
 <212> PRT
 <213> Homo sapiens

<220>

093301010

<221> SIGNAL
 <222> -50...-1

<400> 670

Met	His	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys
-50					-45					-40					-35
Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala
				-30					-25						-20
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly
			-15					-10					-5		
Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	
	1				5				10						
Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Lys	Lys	Tyr	Ala	Val	Ser	Ser
15				20					25						30
Arg	His	Asn	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Xaa	Lys	Gln
			35					40						45	
Xaa	Leu	Lys	Val	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Xaa	Gln	Asp	Leu	Lys
			50				55						60		
Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Lys	Gly	Ser	Glu	Asn	Ser
	65					70						75			
Gln	Pro	Glu	Glu	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Xaa	Gly	Gly	Asp
	80				85						90				
Arg	Lys	Val	Glu	Xaa	Xaa	Met	Lys	Lys	His	Gly	Ser	Xaa	His	Met	Gly
95				100						105					110
Phe	Pro	Xaa	Asn	Leu	Xaa	Asn	Gly	Ala	Thr	Ala	Asp	Asn	Gly	Asp	Asp
			115					120						125	
Gly	Leu	Ile	Pro	Pro	Xaa	Lys	Xaa	Xaa	Thr	Pro	Glu	Ser	Xaa	Gln	Phe
			130				135						140		
Pro	Asp	Thr	Glu	Asn	Glu	Gln	Tyr	His	Arg	Asp	Phe	Ser	Gly	His	Pro
	145					150						155			
Xaa	Phe	Pro	Thr	Thr	Leu	Pro	Ile	Lys	Gln						
	160					165									

<210> 671
 <211> 216
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 671

Met	Val	Cys	Val	Leu	Val	Leu	Ala	Ala	Ala	Ala	Gly	Ala	Val	Ala	Val
-15					-10					-5					1
Phe	Leu	Ile	Leu	Arg	Ile	Trp	Val	Val	Leu	Arg	Ser	Met	Asp	Val	Thr
		5				10						15			
Pro	Arg	Glu	Ser	Leu	Ser	Ile	Leu	Val	Val	Ala	Gly	Ser	Gly	Gly	His
	20					25						30			
Thr	Thr	Glu	Ile	Leu	Arg	Leu	Leu	Gly	Ser	Leu	Ser	Asn	Ala	Tyr	Ser
	35				40					45					
Pro	Arg	His	Tyr	Val	Ile	Ala	Asp	Thr	Asp	Glu	Met	Ser	Ala	Asn	Lys
50				55						60					65
Ile	Asn	Ser	Phe	Glu	Leu	Xaa	Arg	Xaa	Asp	Arg	Xaa	Pro	Ser	Asn	Met
			70					75						80	
Xaa	Thr	Lys	Tyr	Tyr	Ile	His	Arg	Ile	Pro	Xaa	Ser	Arg	Glu	Val	Gln
		85					90						95		
Gln	Ser	Trp	Pro	Ser	Thr	Val	Xaa	Thr	Thr	Leu	His	Ser	Met	Trp	Leu
	100					105						110			
Ser	Xaa	Pro	Leu	Ile	His	Arg	Val	Lys	Pro	Xaa	Leu	Val	Leu	Cys	Asn
	115					120					125				

00978360.10501

[illegible]

```
<220>
<221> SIGNAL
<222> -29..-1
```

[illegible]

```
<220>
<221> SIGNAL
<222> -56..-1
```

<400> 675

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
 -55 -50 -45
 Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Asn Pro Ser
 -40 -35 -30 -25
 Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
 -20 -15 -10
 Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly
 -5 1 5
 Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala Gly Pro
 10 15 20
 Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly Pro Leu
 25 30 35 40
 Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser Cys Gly
 45 50 55
 Ala His Pro Lys Val Leu Lys Val Ala Leu
 60 65

<210> 676
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 676
 Met Leu Xaa Leu Ser Arg Ala Thr Lys Xaa Gly Arg Ala Arg Trp Leu
 -25 -20 -15
 Met Pro Val Ile Pro Ala Leu Gln Glu Ala Xaa Ala Gly Gly Ser Arg
 -10 -5 1
 Gly Gln Glu Phe Glu Thr Ser Leu Ala Asn Met Glu Thr Glu Ala Gly
 5 10 15 20
 Glu Leu Leu Lys Pro Arg Arg Arg Arg Leu Gln
 25 30

<210> 677
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 677
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

<210> 678
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 678
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

<210> 679
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 679
 Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
 -25 -20 -15 -10
 Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
 -5 1 5
 Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
 10 15 20
 Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 25 30 35
 Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 40 45 50 55
 Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
 60 65 70
 Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
 75 80

<210> 680
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 680
 Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp

09978360 "101501

```

-15          -10          -5          1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
      5          10          15
Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20          25          30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35          40          45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Gly Asn
50          55          60          65
Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu Leu Leu Gln Ser Cys
      70          75          80
Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met Ile Ile Asp Asn Arg
      85          90          95
Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp Thr Xaa His Val Ala
      100          105          110
Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly Ile Asn Leu Val Val
      115          120          125
Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser Asn His Ile Ala Leu
130          135          140          145
Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile Cys Lys Pro Cys Gly
      150          155          160
Thr Gly Gln Asp Phe Lys Glu
      165

```

<210> 681
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 681
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15          -10          -5          1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
      5          10          15
Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20          25          30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35          40          45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
50          55          60          65
Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu Thr Ser Glu Pro Leu
      70          75          80
Xaa Ala

```

<210> 682
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -57...-1

```

<400> 682
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile Asn
      -55          -50          -45

```


Met	Leu	Lys	Lys	Tyr	Ser	His	His	Arg	Asn	Ile	Ala	Thr	Tyr	Tyr	Gly
-40						-35					-30				
Ala	Phe	Ile	Lys	Lys	Asn	Pro	Pro	Gly	Met	Asp	Asp	Gln	Leu	Trp	Leu
-25					-20					-15					-10
Val	Met	Glu	Phe	Cys	Gly	Ala	Gly	Ser	Val	Thr	Asp	Leu	Ile	Lys	Asn
			-5					1				5			
Thr	Lys	Gly	Asn	Thr	Leu	Lys	Glu	Glu	Trp	Ile	Ala	Tyr	Ile	Cys	Xaa
	10						15				20				
Glu	Ile	Leu	Arg	Gly	Leu	Xaa	His	Leu	His	Gln	His	Lys	Val	Ile	His
	25					30				35					
Arg	Xaa	Ile	Lys	Gly	Gln	Asn	Val	Leu	Leu	Thr	Glu	Asn	Ala	Glu	Val
40					45					50					55
Lys	Leu	Val	Asp	Phe	Gly	Xaa	Xaa	Ala	Gln	Leu	Asp	Arg	Thr	Val	Gly
			60						65					70	
Arg	Xaa	Asn	Thr	Phe	Ile	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Xaa	Val
			75					80				85			
Ile	Ala	Cys	Asp	Glu	Asn	Pro	Xaa	Ala	Thr	Tyr	Asp	Phe	Lys	Xaa	Asp
	90					95						100			
Leu	Trp	Ser	Leu	Gly	Ile	Thr	Ala	Ile	Glu	Met	Ala	Glu	Gly	Leu	Pro
	105					110					115				
Leu	Ser	Val	Thr	Cys	Thr	Pro									
120					125										

<210> 683
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400>	683														
Met	Phe	Leu	Thr	Ala	Leu	Leu	Trp	Arg	Gly	Arg	Ile	Pro	Gly	Arg	Gln
				-10					-5					1	
Trp	Ile	Gly	Lys	His	Arg	Arg	Pro	Arg	Phe	Val	Ser	Leu	Arg	Ala	Lys
	5					10					15				
Gln	Asn	Met	Ile	Arg	Arg	Leu	Glu	Ile	Glu	Ala	Glu	Asn	His	Tyr	Trp
	20					25					30				
Leu	Ser	Met	Pro	Tyr	Met	Thr	Arg	Glu	Gln	Glu	Arg	Gly	His	Ala	Ala
35					40				45						50
Leu	Arg	Arg	Arg	Glu	Ala	Phe	Glu	Ala	Ile	Lys	Ala	Ala	Ala	Thr	Ser
				55					60					65	
Lys	Phe	Pro	Pro	His	Arg	Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Asn
				70				75					80		
Xaa	His	Gln	Glu	Met	Val	Leu	Ile	Leu	Ser	Arg	His	Pro	Trp	Ile	Leu
	85					90					95				
Trp	Ile	Thr	Glu	Leu	Thr	Ile	Phe	Thr	Trp	Ser	Gly	Leu	Lys	Asn	Cys
	100					105					110				
Ser	Leu	Cys	Glu	Asn	Glu	Leu	Trp	Thr	Ser	Leu	Tyr				
115					120					125					

<210> 684
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

0097360 101501

<400> 684

Met	Ala	Ala	Leu	Val	Thr	Val	Leu	Phe	Thr	Gly	Val	Arg	Arg	Leu	His
				-10					-5					1	
Cys	Ser	Ala	Xaa	Leu	Gly	Arg	Ala	Ala	Ser	Gly	Xaa	Tyr	Ser	Arg	Asn
	5						10					15			
Trp	Leu	Pro	Thr	Pro	Pro	Ala	Thr	Gly	Pro	Leu	Pro	Ser	Ser	Gln	Thr
	20					25					30				
Gly	His	Met	Arg	Met	Ala	Ala	Leu	Leu	Pro	Gln					
35					40					45					

<210> 685

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 685

Met	Gly	Pro	Tyr	Asn	Val	Ala	Val	Pro	Ser	Asp	Val	Ser	His	Ala	Arg
	-35					-30					-25				
Phe	Tyr	Phe	Leu	Phe	His	Arg	Pro	Leu	Arg	Leu	Leu	Asn	Leu	Leu	Ile
	-20				-15					-10					-5
Leu	Ile	Glu	Gly	Ser	Val	Val	Phe	Tyr	Gln	Leu	Tyr	Ser	Leu	Leu	Arg
				1				5					10		
Ser	Glu	Lys	Trp	Asn	His	Thr	Leu	Ser	Met	Ala	Leu	Ile	Leu	Phe	Cys
	15					20					25				
Asn	Tyr	Tyr	Val	Leu	Phe	Lys	Leu	Leu	Arg	Asp	Arg	Xaa	Xaa	Leu	Gly
	30					35				40					
Arg	Ala	Tyr	Ser	Tyr	Pro	Leu	Asn	Ser	Tyr	Glu	Leu	Lys	Ala	Asn	Xaa
45					50					55					60
Ala	Ala	Ser	Xaa	Gln											
					65										

<210> 686

<211> 341

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 686

Met	Arg	Lys	Val	Val	Leu	Ile	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Leu
-55					-50					-45					-40
Ala	Leu	Cys	Lys	Arg	Leu	Leu	Ala	Glu	Asp	Asp	Glu	Leu	His	Leu	Cys
				-35					-30					-25	
Leu	Ala	Cys	Arg	Asn	Met	Ser	Lys	Ala	Glu	Ala	Val	Cys	Ala	Ala	Leu
			-20					-15					-10		
Leu	Ala	Ser	His	Pro	Thr	Ala	Glu	Val	Thr	Ile	Val	Gln	Val	Asp	Val
		-5				1					5				
Ser	Asn	Leu	Gln	Ser	Phe	Phe	Arg	Ala	Ser	Lys	Glu	Leu	Lys	Gln	Arg
10					15				20					25	
Phe	Gln	Arg	Leu	Asp	Cys	Ile	Tyr	Leu	Asn	Ala	Gly	Ile	Met	Pro	Asn
				30					35					40	
Pro	Gln	Leu	Asn	Ile	Lys	Ala	Leu	Phe	Gly	Leu	Phe	Ser	Arg	Lys	
		45					50				55				
Val	Ile	His	Met	Phe	Ser	Thr	Ala	Glu	Gly	Leu	Leu	Thr	Gln	Gly	Asp
		60					65					70			

Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn Val Phe
 75 80 85
 Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys His Ser
 90 95 100 105
 Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala Arg Lys
 110 115 120
 Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys Glu Pro
 125 130 135
 Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala Leu Asn
 140 145 150
 Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys Pro Gly
 155 160 165
 Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe Ile Trp
 170 175 180 185
 Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala Asn Ala
 190 195 200
 Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp Leu Phe
 205 210 215
 His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu Ser Ala
 220 225 230
 Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met Asp Leu
 235 240 245
 Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Glu Leu Glu
 250 255 260 265
 Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala Arg Leu
 270 275 280
 Ser Gly Ser Cys Leu
 285

<210> 687
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 687
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile
 -10 -5 1 5
 Leu Gln Xaa Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys
 25 30 35
 Gly Asp Gly Gly Ser Gly Ser Lys Gly Arg Pro Xaa Xaa Gln Thr Glu
 40 45 50
 Xaa Phe Leu Cys Ile Ser Lys Pro Ser Ser Phe Leu
 55 60 65

<210> 688
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

09073360 101501

<222> -26...-1

<400> 688

Met	Glu	Glu	Ile	Ser	Ser	Pro	Leu	Val	Glu	Phe	Val	Lys	Val	Leu	Cys
-25						-20					-15				
Thr	Asn	Gln	Val	Leu	Ile	Thr	Ala	Arg	Ala	Val	Pro	Thr	Lys	Lys	Ala
-10					-5					1				5	
Ser	Val	Arg	Cys	Val	Glu	Lys	Arg	Phe	Trp	Ile	Pro	Lys	Thr	Thr	Ser
		10						15					20		
Lys	His	Leu	Ser	Arg	Cys	Ile	Asp	Gly	Ile	Ser	Gly	Phe	Leu	Asn	Asp
	25						30					35			
Phe	Thr	Phe	Cys	Leu	Glu	Phe	Ser	Arg	His	Arg	Cys	Gln	Leu	Thr	Glu
40						45					50				

<210> 689

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44...-1

<400> 689

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys	Ile
				-40					-35					-30	
Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala	Gly	Ile
		-25						-20					-15		
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	Val	Val	Tyr
	-10					-5						1			
Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	Cys	Gly	Val	Phe
5				10					15					20	
Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	Ser	Asn	Ala	Gln	Val
			25					30						35	
Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	Gly	Arg	Thr	Gly	Ala	Arg
		40					45						50		
Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	Met	Phe	Gly	Ser	Leu	Ile	Ala
	55					60						65			
Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val
	70					75					80				
Tyr	Pro	Gly	Leu	Ala	Val	Phe	Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser
85				90					95						100
Thr	Leu	Ile	Tyr	Lys	Phe	Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr		
			105						110						

<210> 690

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 690

Met	Asn	Trp	Glu	Leu	Leu	Leu	Trp	Leu	Leu	Val	Leu	Cys	Ala	Leu	Leu
	-25						-20						-15		
Leu	Leu	Leu	Val	Gln	Leu	Leu	Arg	Phe	Leu	Arg	Ala	Asp	Gly	Asp	Leu
	-10						-5					1			
Thr	Leu	Leu	Trp	Ala	Glu	Trp	Gln	Gly	Arg	Arg	Pro	Glu	Trp	Glu	Leu
5					10					15				20	

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
25 30 35
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
40 45 50
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
55 60 65
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
70 75 80
Thr Asp Thr Gly Ser His Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly
85 90 95 100
Ile Trp

<210> 691
<211> 199
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -62...-1

<400> 691
Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
-60 -55 -50
Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
-45 -40 -35
Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
-30 -25 -20 -15
Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
-10 -5 1
Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu
5 10 15
Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro
20 25 30
Val Gln Ser Asn Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys
35 40 45 50
Thr Ile Gly Asn Asn Gly Asn Gln Ser His Lys Met Thr Thr Ser Arg
55 60 65
Cys Val Arg Leu Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val
70 75 80
Trp Ile Ser Glu Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr
85 90 95
Met Pro Thr Trp Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg
100 105 110
Ile Glu Asn Phe Lys Ser Gly Val Asp Ala Xaa Ser Ser Tyr Phe Lys
115 120 125 130
Ile Phe Lys Thr Lys His Asp
135

<210> 692
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25...-1

<400> 692
Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu

05973360.101501

-25					-20					-15					-10
Ser	Val	Met	Ala	Ala	Leu	Thr	Phe	Gly	Cys	Phe	Ile	Xaa	Thr	Ala	Phe
				-5					1				5		
Lys	Asp	Arg	Ser	Val	Pro	Val	Arg	Leu	His	Val	Ser	Arg	Ile	Met	Leu
		10					15					20			
Lys	Asn	Val	Glu	Asp	Phe	Thr	Gly	Pro	Arg	Glu	Arg	Ser	Asp	Leu	Gly
	25					30					35				
Phe	Ile	Thr	Phe	Asp	Ile	Thr	Ala	Asp	Leu	Glu	Asn	Ile	Phe	Asp	Trp
40				45						50				55	
Asn	Val	Lys	Gln	Leu	Phe	Leu	Tyr	Leu	Ser	Ala	Glu	Tyr	Ser	Thr	Lys
			60					65					70		
Asn	Asn	Ala	Leu	Asn	Gln	Xaa	Val	Leu	Trp	Asp	Lys	Ile	Val	Leu	Arg
		75						80					85		
Gly	Asp	Asn	Pro	Lys	Leu	Leu	Leu	Lys	Asp	Met	Lys	Thr	Lys	Tyr	Phe
	90					95						100			
Phe	Phe	Asp	Asp	Gly	Asn	Gly	Leu	Xaa	Gly	Asn	Arg	Asn	Val	Thr	Leu
	105					110					115				
Thr	Leu	Ser	Trp	Asn	Val	Val	Pro	Asn	Ala	Gly	Ile	Leu	Pro	Leu	Val
120				125						130				135	
Thr	Gly	Ser	Gly	His	Val	Ser	Val	Pro	Phe	Pro	Asp	Thr	Tyr	Glu	Ile
			140					145						150	
Thr	Lys	Ser	Tyr												
		155													

<210> 693
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 693

Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala	Met	Met	Leu
			-10				-5					1			
Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	Glu	Pro	Pro
	5				10					15					
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu
20				25					30					35	
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile
			40					45					50		
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu
	55					60						65			
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	Gly	Pro	Cys
	70				75					80					
Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg
	85				90					95					
Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly	Leu
100				105					110					115	
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
			120					125					130		
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
		135				140						145			
Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
	150					155				160					
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp	
	165				170					175					
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180				185					190					195	
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu

009330.10501

<400> 696
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
-30 -25 -20
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
-15 -10 -5
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1 5 10 15
Thr Phe Ala His
20

<210> 697
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -97..-1

<400> 697
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
-95 -90 -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
-80 -75 -70
Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
-65 -60 -55 -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
-45 -40 -35
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
-30 -25 -20
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
-15 -10 -5
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
1 5 10 15
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
20 25

<210> 698
<211> 230
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 698
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
-20 -15 -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
-5 1 5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
10 15 20
Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
25 30 35 40
Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
45 50 55
Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
60 65 70
Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg

09978360 101501

75	80	85
Ala Lys Asp Arg Val	Ala Val Ala Gly Gly Val	Phe Phe Ile Leu Gly
90	95	100
Gly Leu Leu Gly Phe	Ile Pro Val Ala Trp Asn	Leu His Gly Ile Leu
105	110	115
Arg Asp Phe Tyr Ser	Pro Leu Val Pro Asp	Ser Met Lys Phe Glu Ile
125	130	135
Gly Glu Ala Leu Tyr	Leu Gly Ile Ile Ser	Ser Ser Leu Phe Ser Leu Ile
140	145	150
Ala Gly Ile Ile Leu	Cys Phe Ser Cys Ser	Ser Gln Arg Asn Arg Ser
155	160	165
Asn Tyr Tyr Asp Ala	Tyr Gln Ala Gln Pro	Leu Ala Thr Arg Ser Ser
170	175	180
Pro Arg Pro Gly Gln	Pro Pro Lys Val Lys	Ser Glu Phe Asn Ser Tyr
185	190	195
Ser Leu Thr Gly Tyr	Val	200
205		

<210> 699
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 699
Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
-30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Ile Ala Gly Gly Ser Phe Gly
-15 -10 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
20 25 30
Ser Glu Tyr Glu Gly Ser Ile Cys
35 40

<210> 700
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 700
Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
-30 -25 -20
Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
-15 -10 -5
Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
1 5 10 15
Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
20 25 30
Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
35 40 45
Asp Pro Lys Arg Lys Thr Lys Cys
50 55

<210> 701
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 701
 Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 702
 <211> 267
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 702
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
 45 50 55
 Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
 60 65 70 75
 Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
 80 85 90
 Gln Lys Thr Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr
 95 100 105
 Phe Gly Met Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr
 110 115 120
 Gln Met Gln Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu
 125 130 135
 Leu Leu Val Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys
 140 145 150 155
 Ser Ser Val Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys
 160 165 170
 Leu His Trp Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr

			175					180				185			
Thr	Ala	Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu
		190					195					200			
Thr	Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
	205					210					215				
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn
220					225					230					235
Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg					
				240					245						

<210> 703
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 703
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 704
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46...-1

<400> 704
 Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile
 -45 -40 -35
 Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys
 -30 -25 -20 -15
 Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu
 -10 -5 1
 Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu
 5 10 15
 Lys Tyr His Trp Pro
 20

<210> 705
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

00978360 101501

<400> 705

```

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
-25 -20 -15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
-10 -5 1
Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
5 10 15 20
Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
25 30 35
Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
40 45 50
Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Tyr
55 60 65
Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
70 75 80
Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe
85 90 95 100
Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys
105 110 115
Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val
120 125 130
Val Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu
135 140 145
Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg
150 155 160
Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn
165 170 175 180
Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu
185 190 195
Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys
200 205 210
Tyr Trp Gly Lys Phe Tyr Met Pro Lys Arg Val
215 220

```

<210> 706

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 706

```

Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
-45 -40 -35
Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
-30 -25 -20
Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
-15 -10 -5
Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
1 5 10 15
Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
20 25 30
Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
35 40 45
Glu Val Leu
50

```

<210> 707

<211> 81

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31...-1

<400> 707
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
-30 -25 -20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15 -10 -5 1
Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
5 10 15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
20 25 30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
35 40 45
Leu
50

<210> 708
<211> 150
<212> PRT
<213> Homo sapiens

<400> 708
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
1 5 10 15
Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
20 25 30
Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
35 40 45
Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
50 55 60
Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
65 70 75 80
Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
85 90 95
Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
100 105 110
Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His
115 120 125
Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser
130 135 140
Val Ser Thr Lys Lys Lys
145 150

<210> 709
<211> 273
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45...-1

<400> 709
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
-45 -40 -35 -30
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg

09978360.10504


```

      95              100              105
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
110              115              120              125
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
              130              135              140
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
              145              150              155
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
              160              165              170
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
              175              180              185
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
190              195              200              205
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
              210              215              220
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
              225              230              235
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
              240              245              250
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys
              255              260              265
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met
270              275              280              285
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg
              290              295              300
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser
              305              310              315
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg
              320              325              330
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu
              335              340              345
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln
350              355              360              365
Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
              370

```

<210> 712
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

```

<400> 712
Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
              -10              -5              1
Thr Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val
              5              10              15
Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
20              25              30              35
Asp Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
              40              45              50
Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
              55              60              65
Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
              70              75              80
Ile Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
              85              90              95
Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp

```


Ile Ser His Asp Glu Leu
160

<210> 718

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 718

Met	Pro	Ala	Gly	Val	Pro	Met	Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala
-25					-20					-15					-10
Ser	Leu	Leu	Ala	Met	Cys	Ala	Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr
			-5						1			5			
Arg	Pro	Asp	Leu	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu
		10					15					20			
Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val
	25					30					35				
Ser	Gln	Gln	Glu	Glu	Leu	Lys									
40					45										

<210> 719

<211> 73

<212> PRT

<213> Homo sapiens

<400> 719

Met	Arg	Ile	Arg	Met	Thr	Asp	Gly	Arg	Thr	Leu	Val	Gly	Cys	Phe	Leu
1				5					10					15	
Cys	Thr	Asp	Arg	Asp	Cys	Asn	Val	Ile	Leu	Gly	Ser	Ala	Gln	Glu	Phe
			20					25					30		
Leu	Lys	Pro	Ser	Asp	Ser	Phe	Ser	Ala	Gly	Glu	Pro	Arg	Val	Leu	Gly
		35				40					45				
Leu	Ala	Met	Val	Pro	Gly	His	His	Ile	Val	Ser	Ile	Glu	Val	Gln	Arg
	50					55					60				
Glu	Ser	Leu	Thr	Gly	Pro	Pro	Tyr	Leu							
65					70										

<210> 720

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -150...-1

<220>

<221> UNSURE

<222> -67

<223> Xaa = any one of the twenty amino acids

<400> 720

Met	Ala	Glu	Thr	Lys	Asp	Thr	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
-150					-145					-140					-135
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
				-130					-125					-120	
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Gly	Ile	Gly	Phe	Pro	Lys	Pro	Glu	Leu
			-115					-110						-105	

Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly
 -100 -95 -90
 Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly Trp
 -85 -80 -75
 Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu
 -70 -65 -60 -55
 Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg
 -50 -45 -40
 Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr
 -35 -30 -25
 Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys
 -20 -15 -10
 Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser
 -5 1 5 10
 His Arg Ala Arg Gln Arg Lys Thr Ala
 15

<210> 721
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 721
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
 30 35 40
 Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 45 50

<210> 722
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 722
 Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
 -50 -45 -40
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -35 -30 -25
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
 -20 -15 -10
 Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
 -5 1 5 10
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
 15 20 25
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
 30 35 40

09978360 101501

<210> 723
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 723
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
 30 35 40
 Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
 45 50 55
 Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys
 60 65 70

<210> 724
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 724
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 20 25 30
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 35 40 45
 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 50 55 60
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70

<210> 725
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 725
 Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
 1 5 10 15
 Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
 20 25 30
 Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
 35 40 45
 Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
 50 55 60
 Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln

099360 "09EB" 0660

<212> PRT
<213> Homo sapiens

<400> 730
Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu
1 5 10 15
Cys Pro Ala Glu Leu Phe Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly
20 25 30
Pro Gly Leu Asp Ile Leu Arg Cys Val Leu Ser Pro Trp Ala Ser His
35 40 45
Phe Pro Ser Leu Ser Leu Gly Val Phe Asn Leu
50 55

<210> 731
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 731
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 732
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -94...-1

<400> 732
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-90 -85 -80
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-75 -70 -65
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
-60 -55 -50
Val Leu Phe Asn Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
-45 -40 -35
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
-30 -25 -20 -15
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
-10 -5 1
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
5 10 15
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
20 25 30
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
35 40 45 50
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

Arg Arg

55 60 65

<210> 733
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68...-1

<400> 733
 Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
 -65 -60 -55
 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
 -50 -45 -40
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
 -35 -30 -25
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
 -20 -15 -10 -5
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
 1 5 10
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
 15 20 25
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
 30 35 40
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
 45 50 55 60
 His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
 65 70 75
 Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 80 85

<210> 734
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 734
 Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu His Gly
 1 5 10 15
 Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala Leu Leu
 20 25 30
 Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn Ile Thr
 35 40 45
 Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His
 50 55 60
 Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr
 65 70 75 80
 Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His
 85 90 95
 Leu Gly Asn

<210> 735
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

09978360.101501

<222> -24...-1

<400> 735

```
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
      -20                      -15                      -10
Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
      -5                      1                      5
Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
      10                      15
```

<210> 736

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 736

```
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
      -20                      -15                      -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
      -5                      1                      5                      10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
      15                      20                      25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
      30                      35                      40
Val Leu Cys Gln Lys
      45
```

<210> 737

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 737

```
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
      -15                      -10                      -5
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
      1                      5                      10
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
      15                      20                      25                      30
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
      35                      40                      45
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50                      55                      60
```

<210> 738

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

0993360 10161

Met	Ser	Asp	Ser	Leu	Val	Val	Cys	Glu	Val	Asp	Pro	Glu	Leu	Thr	Glu
1			5					10					15		
Lys	Leu	Arg	Lys	Phe	Arg	Phe	Arg	Lys	Glu	Thr	Asp	Asn	Ala	Ala	Ile
		20						25				30			
Ile	Met	Lys	Val	Asp	Lys	Asp	Arg	Gln	Met	Val	Val	Leu	Glu	Glu	Glu
	35						40					45			
Phe	Arg	Asn	Ile	Ser	Pro	Glu	Glu	Leu	Lys	Met	Glu	Leu	Pro	Glu	Arg
	50					55					60				
Gln	Pro	Arg	Phe	Val	Val	Tyr	Ser	Tyr	Lys	Tyr	Val	Arg	Asp	Asp	Gly
65					70					75					80
Arg	Val	Ser	Tyr	Pro	Leu	Cys	Phe	Ile	Phe	Ser	Ser	Pro	Val	Gly	Cys
			85						90					95	
Lys	Pro	Glu	Gln	Met	Met	Tyr	Ala	Gly	Ser	Lys	Asn	Arg	Leu	Val	
		100					105					110			
Gln	Thr	Ala	Glu	Leu	Thr	Lys	Val	Phe	Glu	Ile	Arg	Thr	Thr	Asp	Asp
		115					120					125			
Leu	Thr	Glu	Ala	Trp	Leu	Gln	Glu	Lys	Leu	Ser	Phe	Phe	Arg		
	130					135					140				

<210> 741
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Thr	Leu	Ala	Leu	Leu	
		-20					-15				-10				
Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	Gly	Lys
	-5					1				5					10
Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	Gly	Leu	Arg
			15						20					25	
Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	Val	Lys	Leu	Gly
		30						35					40		
Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	Gly	Asn	Thr	Gln	Glu
		45				50						55			
Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	Lys	Val	Phe	Val	Ala	Phe
	60					65					70				
Gln	Thr	Phe	Leu	Arg	Gly	Met	Val	Met	Tyr	Thr	Ser	Lys	Asp	Arg	Tyr
75				80						85					90
Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser
			95						100					105	
Gln	Glu	Gly	Gln	Val	Leu	Val	Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu
		110					115						120		
Gly	Ile	Lys	Ser	Ile	Gly	Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro
	125						130					135			
Thr	Thr	Glu	Pro	Pro	Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val
	140					145					150				
Gly	Arg														
155															

<210> 742
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

09978360.10501

<222> -19..-1

<400> 742

```
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
      -15                      -10                      -5
Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
      1                      5                      10
Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
      15                      20                      25
Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
      30                      35                      40                      45
Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
      50                      55                      60
Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
      65                      70
```

<210> 743

<211> 125

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 743

```
Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
      -15                      -10                      -5                      1
Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
      5                      10                      15
Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
      20                      25                      30
Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile
      35                      40                      45
Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe
      50                      55                      60                      65
Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly
      70                      75                      80
Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly
      85                      90                      95
Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser
      100                      105                      110
```

<210> 744

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 744

```
Met Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr
      -30                      -25                      -20
Phe Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu
      -15                      -10                      -5
Leu Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn
      1                      5                      10
Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr
      15                      20                      25                      30
```

Thr	Ile	Val	Ser	Val	Arg	Leu	Phe	Gln	Asp	Gly	Glu	Lys	Arg	Leu	Ala
			35					40						45	
Val	Leu	Arg	Leu	Phe	Trp	Val	Leu	Thr	Val	Leu	Ser	Leu	Lys	Phe	Val
			50					55					60		
Phe	Glu	Met	Leu	Leu	Cys	Gln	Lys	Leu	Ala	Glu	Gln	Thr	Arg	Glu	Leu
		65				70						75			
Trp	Phe	Gly	Leu	Ile	Thr	Ser	Pro	Leu	Phe	Ile	Leu	Leu	Gln	Leu	Leu
	80					85					90				
Met	Ile	Arg	Ala	Cys	Arg	Val	Asn								
95						100									

<210> 745
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -53...-1

<400>	745														
Met	Ala	Asp	Pro	Asp	Pro	Arg	Tyr	Pro	Arg	Ser	Ser	Ile	Glu	Asp	Asp
		-50						-45					-40		
Phe	Asn	Tyr	Gly	Ser	Ser	Val	Ala	Ser	Ala	Thr	Val	His	Ile	Arg	Met
		-35					-30					-25			
Ala	Phe	Leu	Arg	Lys	Val	Tyr	Ser	Ile	Leu	Ser	Leu	Gln	Val	Leu	Leu
	-20					-15					-10				
Thr	Thr	Val	Thr	Ser	Thr	Val	Phe	Leu	Tyr	Phe	Glu	Ser	Val	Arg	Thr
-5					1				5					10	
Phe	Val	His	Glu	Ser	Pro	Ala	Leu	Ile	Leu	Leu	Phe	Ala	Leu	Gly	Ser
		15						20					25		
Leu	Gly	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Asn	Arg	His	Lys	Tyr	Pro	Leu
	30						35					40			
Asn	Leu	Tyr	Leu	Leu	Phe	Gly	Phe	Thr	Leu	Leu	Glu	Ala	Leu	Thr	Val
	45					50					55				
Ala	Val	Val	Val	Thr	Phe	Tyr	Asp	Val	Tyr	Ile	Ile	Leu	Gln	Ala	Phe
60					65					70				75	
Ile	Leu	Thr	Thr	Thr	Val	Phe	Phe	Gly	Leu	Thr	Val	Tyr	Thr	Leu	Gln
				80					85					90	
Ser	Lys	Lys	Asp	Phe	Ser	Lys	Phe	Gly	Ala	Gly	Leu	Phe	Ala	Leu	Leu
			95					100					105		
Trp	Ile	Leu	Cys	Leu	Ser	Gly	Phe	Leu	Lys	Phe	Phe	Leu	Tyr	Ser	Glu
		110					115					120			
Ile	Met	Glu	Leu	Val	Leu	Ala	Ala	Ala	Gly	Ala	Leu	Leu	Phe	Cys	Gly
	125					130					135				
Phe	Ile	Ile	Tyr	Asp	Thr	His	Ser	Leu	Met	His	Lys	Leu	Ser	Pro	Glu
140					145					150				155	
Glu	Tyr	Val	Leu	Ala	Ala	Ile	Ser	Leu	Tyr	Leu	Asp	Ile	Ile	Asn	Leu
				160						165				170	
Phe	Leu	His	Leu	Leu	Arg	Phe	Leu	Glu	Ala	Val	Asn	Lys	Lys		
			175					180					185		

<210> 746
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -71...-1

0928360 101501

<400> 746
Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
-70 -65 -60
Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
-55 -50 -45 -40
Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
-35 -30 -25
Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
-20 -15 -10
Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
-5 1 5
Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
10 15 20 25
Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
30 35

<210> 747
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84...-1

<400> 747
Met Ser Gly Gly Pro Glu Ala Arg Pro Pro Met Leu Val Glu Gly Gly
-80 -75 -70
Gly Pro Glu Ser Leu Gln Lys Ala Pro Cys Thr Arg Gly Pro Pro Ser
-65 -60 -55
His Pro Val Pro Pro Ala Leu Ala Phe Thr Val Gly Asn Gly Ser Gly
-50 -45 -40
Pro Gly Val Arg Cys Pro Arg Asn Met Ala Glu Gly His Pro Gly Pro
-35 -30 -25
Glu Arg Arg Gln Ser Gln Gln Gly Leu Phe Arg Ala Ala Trp Leu Pro
-20 -15 -10 -5
Gly Ser Arg Pro Ser Pro Leu Phe Cys Val Cys Ser Val Thr Ser Pro
1 5 10
Gly Trp Asp Val Pro Gln Val His Arg Val Glu Val Gly His Gly Arg
15 20 25
Arg Gln Glu Thr His Pro Val Arg Arg Arg Ala
30 35

<210> 748
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49...-1

<400> 748
Met Pro Arg Gly Arg Arg Leu Gly Met Val Phe Ala Pro Pro Arg Pro
-45 -40 -35
Gly Gln Arg Gln Ala Gly Ala Pro Trp Val Pro Glu Arg Arg Lys Arg
-30 -25 -20
Arg Pro Asp Gly Asp Thr Phe Leu Leu Ser Phe Leu Ser Thr Thr Trp
-15 -10 -5
Leu Lys Thr Trp Arg Ser Gln Gln Tyr Lys Glu Ser Lys Ser Arg Ser
1 5 10 15

Cys Ala Arg Glu Gln Met Asn Ser Ser Ser Cys
 20 25

<210> 749
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 749
 Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile Ser Gln
 -40 -35 -30 -25
 Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala Leu
 -20 -15 -10
 Phe Val Ala Phe Leu Leu Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser
 -5 1 5
 Gln Lys His Thr Arg Leu Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu
 10 15 20
 Asn Asp Val Gln His Gly Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu
 25 30 35 40

<210> 750
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 750
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
 -45 -40 -35
 Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
 -30 -25 -20
 His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
 -15 -10 -5
 Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
 1 5 10 15
 Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 20 25 30
 Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
 35 40 45
 Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 50 55 60
 Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
 65 70 75
 Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
 80 85 90 95
 Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
 100 105 110
 Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
 115 120 125
 Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
 130 135 140
 Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
 145 150 155
 Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp

099803660

160 165 170 175
 Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 180 185 190
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
 195 200 205
 His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
 210 215 220
 Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
 225 230 235
 Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
 240 245 250 255
 Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
 260 265 270
 Thr Pro Trp Cys Thr Phe Ser
 275

<210> 751
 <211> 235
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 751
 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe
 -20 -15 -10 -5
 Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile
 1 5 10
 Pro Asp Ala Pro Leu Ser Ser Ala Tyr Ser Ile Arg Ser Ile Gly
 15 20 25
 Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
 30 35 40
 His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
 45 50 55 60
 Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
 65 70 75
 Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
 80 85 90
 Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
 95 100 105
 Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
 110 115 120
 Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
 125 130 135 140
 Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
 145 150 155
 Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
 160 165 170
 Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
 175 180 185
 His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
 190 195 200
 Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
 205 210 215

<210> 752
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 754

Met	Thr	Lys	Leu	Ala	Gln	Trp	Leu	Trp	Gly	Leu	Ala	Ile	Leu	Gly	Ser	-20	-15	-10
Thr	Trp	Val	Ala	Leu	Thr	Thr	Gly	Ala	Leu	Gly	Leu	Glu	Leu	Pro	Leu	-5	1	5
Ser	Cys	Gln	Glu	Val	Leu	Trp	Pro	Leu	Pro	Ala	Tyr	Leu	Leu	Val	Ser	10	15	20
Ala	Gly	Cys	Tyr	Ala	Leu	Gly	Thr	Val	Gly	Tyr	Arg	Val	Ala	Thr	Phe	25	30	35
His	Asp	Cys	Glu	Asp	Ala	Ala	Arg	Glu	Leu	Gln	Ser	Gln	Ile	Gln	Glu	45	50	55
Ala	Arg	Ala	Asp	Leu	Ala	Arg	Arg	Gly	Leu	Arg	Phe					60	65	

<210> 755
 <211> 425
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 755

Met	Ala	Ser	Ser	Ser	Pro	Asp	Ser	Pro	Cys	Ser	Cys	Asp	Cys	Phe	Val	-20	-15	-10
Ser	Val	Pro	Pro	Ala	Ser	Ala	Ile	Pro	Ala	Val	Ile	Phe	Ala	Lys	Asn	-5	1	5
Ser	Asp	Arg	Pro	Arg	Asp	Glu	Val	Gln	Glu	Val	Val	Phe	Val	Pro	Ala	10	15	20
Gly	Thr	His	Thr	Pro	Gly	Ser	Arg	Leu	Gln	Cys	Thr	Tyr	Ile	Glu	Val	30	35	40
Glu	Gln	Val	Ser	Lys	Thr	His	Ala	Val	Ile	Leu	Ser	Arg	Pro	Ser	Trp	45	50	55
Leu	Trp	Gly	Ala	Glu	Met	Gly	Ala	Asn	Glu	His	Gly	Val	Cys	Ile	Gly	60	65	70
Asn	Glu	Ala	Val	Trp	Thr	Lys	Glu	Pro	Val	Gly	Glu	Gly	Glu	Ala	Leu	75	80	85
Leu	Gly	Met	Asp	Leu	Leu	Arg	Leu	Ala	Leu	Glu	Arg	Ser	Ser	Ser	Ala	90	95	100
Gln	Glu	Ala	Leu	His	Val	Ile	Thr	Gly	Leu	Leu	Glu	His	Tyr	Gly	Gln	110	115	120
Gly	Gly	Asn	Cys	Leu	Glu	Asp	Ala	Ala	Pro	Phe	Ser	Tyr	His	Ser	Thr	125	130	135
Phe	Leu	Leu	Ala	Asp	Arg	Thr	Glu	Ala	Trp	Val	Leu	Glu	Thr	Ala	Gly	140	145	150
Arg	Leu	Trp	Ala	Ala	Gln	Arg	Ile	Gln	Glu	Gly	Ala	Arg	Asn	Ile	Ser	155	160	165
Asn	Gln	Leu	Ser	Ile	Gly	Thr	Asp	Ile	Ser	Ala	Gln	His	Pro	Glu	Leu	170	175	180
Arg	Thr	His	Ala	Gln	Ala	Lys	Gly	Trp	Trp	Asp	Gly	Gln	Gly	Ala	Phe	190	195	200
Asp	Phe	Ala	Gln	Ile	Phe	Ser	Leu	Thr	Gln	Gln	Pro	Val	Arg	Met	Glu	205	210	215
Ala	Ala	Lys	Ala	Arg	Phe	Gln	Ala	Gly	Arg	Glu	Leu	Leu	Arg	Gln	Arg	220	225	230
Gln	Gly	Gly	Ile	Thr	Ala	Glu	Val	Met	Met	Gly	Ile	Leu	Arg	Asp	Lys			

09978360.101501

235		240		245
Glu Ser Gly Ile Cys Met Asp Ser Gly Gly Phe Arg Thr Thr Ala Ser				
250		255		260
Met Val Ser Val Leu Pro Gln Asp Pro Thr Gln Pro Cys Val His Phe				
	270		275	280
Leu Thr Ala Thr Pro Asp Pro Ser Arg Ser Val Phe Lys Pro Phe Ile				
	285		290	295
Phe Gly Val Gly Val Ala Gln Ala Pro Gln Val Leu Ser Pro Thr Phe				
	300		305	310
Gly Ala Gln Asp Pro Val Arg Thr Leu Pro Arg Phe Gln Thr Gln Val				
	315		320	325
Asp Arg Arg His Thr Leu Tyr Arg Gly His Gln Ala Ala Leu Gly Leu				
330		335		340
Met Glu Arg Asp Gln Asp Arg Gly Gln Gln Leu Gln Gln Lys Gln Gln				
	350		355	360
Asp Leu Glu Gln Glu Gly Leu Glu Ala Thr Gln Gly Leu Leu Ala Gly				
	365		370	375
Glu Trp Ala Pro Pro Leu Trp Glu Leu Gly Ser Leu Phe Gln Ala Phe				
	380		385	390
Val Lys Arg Glu Ser Gln Ala Tyr Ala				
395		400		

<210> 756
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -62...-1

<400> 756
Met Ala Ile Phe Trp Ile Val His Ala His Phe Trp Ser Pro Leu Pro
-60 -55 -50
Pro Arg Leu Pro His Gly Arg Cys Cys Cys Leu Lys Ala Pro Leu Pro
-45 -40 -35
Pro Asp Val Gly Pro Leu Gln Val Ala Pro His Leu Phe Ser Val Pro
-30 -25 -20 -15
Leu His Ile Leu Thr Val Pro Leu Leu Glu Pro Ala Arg Cys Ser Gly
-10 -5 1
Ile Leu Val Phe Phe Leu His Gln Pro Val Ser Ser Leu Ser Phe Cys
5 10 15
Tyr Phe Ile Gly Gly Trp Cys
20 25

<210> 757
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -100...-1

<400> 757
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100 -95 -90 -85
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55

09978360 10160

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50 -45 -40
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35 -30 -25
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20 -15 -10 -5
Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
1 5 10
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
15 20 25
Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
30 35 40
Gly Tyr Leu Met Gly
45

<210> 758
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35...-1

<400> 758
Met Ala Asn Asn Thr Thr Ser Leu Gly Ser Pro Trp Pro Glu Asn Phe
-35 -30 -25 -20
Trp Glu Asp Leu Ile Met Ser Phe Thr Val Ser Met Ala Ile Gly Leu
-15 -10 -5
Val Leu Gly Gly Phe Ile Trp Ala Val Phe Ile Cys Leu Ser Arg Arg
1 5 10
Arg Arg Ala Ser Ala Pro Ile Ser Gln Trp Ser Ser Arg Arg Ser
15 20 25
Arg Ser Ser Tyr Thr His Gly Leu Asn Arg Thr Gly Phe Tyr Arg His
30 35 40 45
Ser Gly Cys Glu Arg Arg Ser Asn Leu Ser Leu Ala Ser Leu Thr Phe
50 55 60
Gln Arg Gln Ala Ser Leu Glu Gln Ala Asn Ser Phe Pro Arg Lys Ser
65 70 75
Ser Phe Arg Ala Ser Thr Phe His Pro Phe Leu Gln Cys Pro Pro Leu
80 85 90
Pro Val Glu Thr Glu Ser Gln Leu Val Thr Leu Pro Ser Ser Asn Ile
95 100 105
Ser Pro Thr Ile Ser Thr Ser His Ser Leu Ser Arg Pro Asp Tyr Trp
110 115 120 125
Ser Ser Asn Ser Leu Arg Val Gly Leu Ser Thr Pro Pro Pro Pro Ala
130 135 140
Tyr Glu Ser Ile Ile Lys Ala Phe Pro Asp Ser
145 150

<210> 759
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26...-1

<400> 759
Met Ala Thr Ala Ala Gly Ala Thr Tyr Phe Gln Arg Gly Ser Leu Phe

-25 -20 -15
 Trp Phe Thr Val Ile Thr Leu Ser Phe Gly Tyr Tyr Thr Trp Val Val
 -10 -5 1 5
 Phe Trp Pro Gln Ser Ile Pro Tyr Gln Asn Leu Gly Pro Leu Gly Pro
 10 15 20
 Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys Asn Gly
 25 30 35
 Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr Ala Ile
 40 45 50
 Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln Leu Leu
 55 60 65 70
 Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Thr Ile Leu
 75 80 85
 Ile Ala Tyr Lys Arg Lys Arg Gln Lys Gln Thr
 90 95

<210> 760
 <211> 153
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -102...-1

<400> 760
 Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
 -100 -95 -90
 Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
 -85 -80 -75
 Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
 -70 -65 -60 -55
 Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
 -50 -45 -40
 Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
 -35 -30 -25
 Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
 -20 -15 -10
 Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
 -5 1 5 10
 Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr
 15 20 25
 Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro
 30 35 40
 Ser Lys Ile Gln Leu Pro Glu Asp Glu
 45 50

<210> 761
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 761
 Leu Pro Val Ser Thr Arg Ile Ile Asn His Ile Tyr Ser Phe Pro Ser
 1 5 10 15
 Val Asp Leu Trp Ile Val Cys Ile Phe Thr Val Ser Val Ser His Leu
 20 25 30
 Phe Glu Lys Gly Thr Leu Tyr Gly Tyr Phe Tyr Val Ile Asn Ser Ser
 35 40 45
 Ile Asn Leu Cys Val Asn Asp Cys Leu Pro Val Met Asp Ser Ile Ser
 50 55 60

0097860.10101
 105101 09E82660

Leu Ser Pro Leu Phe Leu Ser His
65 70

<210> 762
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 762
Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20 -15 -10 -5
Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
1 5 10
Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
15 20 25
Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
30 35 40
Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
45 50 55 60
Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
65 70 75
Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
80 85 90
Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile
95 100 105
Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Thr Gly Arg
110 115 120
Tyr Ser Asn Arg Leu Tyr Ala Tyr Glu Pro Ala Asp Thr Ala Leu Leu
125 130 135 140
Leu Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr Glu Leu
145 150 155

<210> 763
<211> 303
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 763
Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
-20 -15 -10 -5
Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
1 5 10
Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
15 20 25
Cys Gln Leu Pro Gly Leu Phe Ser Tyr Ala Gln His Ile Ala Ser Ile
30 35 40
Asp Gly Arg Arg Gly Leu Phe Thr Gly Leu Thr Pro Arg Leu Cys Ser
45 50 55 60
Gly Val Leu Gly Thr Val Val His Gly Lys Val Leu Gln His Tyr Gln
65 70 75
Glu Ser Asp Lys Gly Glu Glu Leu Gly Pro Gly Asn Val Gln Lys Glu
80 85 90
Val Ser Ser Ser Phe Asp His Val Ile Lys Glu Thr Thr Arg Glu Met

Gly Phe Lys Asn Lys Thr Val Leu Asn Lys Arg Cys Lys Asp Cys Tyr
 30 35 40
 Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
 45 50 55 60
 Arg His Lys Gln Arg Gln Met
 65

<210> 768
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -74...-1

<400> 768
 Met Pro Tyr Ala Phe Thr Ser Pro Cys Pro Cys Ser Phe Val Ser Leu
 -70 -65 -60
 Pro Glu Ile Ser Phe Tyr Phe Thr Lys Leu Leu Leu Ile Leu Lys Ala
 -55 -50 -45
 Leu Pro Glu Ser Pro Phe Leu Leu Ala Ser Ser Pro Leu Pro Pro Leu
 -40 -35 -30
 Pro Thr Thr Leu Arg Lys Phe Ile Pro Pro Pro Ser Leu Ile Ser Cys
 -25 -20 -15
 Thr Cys Leu Leu Leu Tyr Leu Thr His Cys Ile Leu Gly Ile Cys Phe
 -10 -5 1 5
 Ala Tyr Pro Phe Ile Leu
 10

<210> 769
 <211> 395
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -310...-1

<400> 769
 Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp Leu Glu Pro Pro
 -310 -305 -300 -295
 Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
 -290 -285 -280
 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
 -275 -270 -265
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
 -260 -255 -250
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
 -245 -240 -235
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
 -230 -225 -220 -215
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
 -210 -205 -200
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
 -195 -190 -185
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
 -180 -175 -170
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
 -165 -160 -155
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val

09978350 104501

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 773
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -99...-1

<400> 773
 Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
 -95 -90 -85
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
 -80 -75 -70
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
 -65 -60 -55
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
 -50 -45 -40
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
 -35 -30 -25 -20
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
 -15 -10 -5
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
 1 5 10
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
 15 20 25
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
 30 35 40 45
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
 50 55 60
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
 65 70 75
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
 80 85 90
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
 95 100 105
 Leu Gln
 110

<210> 774
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -67...-1

<400> 774
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala
 -65 -60 -55
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 -50 -45 -40
 Thr Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg
 -35 -30 -25 -20
 Asp Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Ser Leu Phe Met
 -15 -10 -5
 Gly Phe Gly Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val

0992360 0992360 0992360

1

5

10

<210> 775
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 775
 Met Ala Val Trp Pro Glu Val Ser Gln Asn Arg Leu Thr Arg Gly Leu
 1 5 10 15
 Leu Leu Pro Asn Tyr Gln Leu Arg Gly Ser Val Pro Lys Arg Glu Lys
 20 25 30
 Arg Pro Lys Arg Lys His Gln His Leu Phe Thr Pro Ser Glu Arg His
 35 40 45
 Ser Val Cys Leu Asp Cys Leu Leu Glu Ile Ser Leu Ser Gly Lys Gln
 50 55 60
 Trp Arg Asn Val Ile Ser Phe Asn Cys Phe Cys Thr Thr Lys Thr Leu
 65 70 75 80
 Phe Trp Val Asn

<210> 776
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 776
 Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr
 -20 -15 -10 -5
 Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp
 1 5 10
 Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe
 15 20 25
 Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Cys Lys Phe
 30 35 40
 Asn Gln Gln Gln Arg Thr Gly Glu Pro Asp Glu Glu Gly Thr Phe
 45 50 55 60
 Arg Ser Ser Ile Arg Arg Leu Ser Thr Arg Arg Arg
 65 70

<210> 777
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 777
 Met Leu Thr Leu Leu Gly Leu Ser Leu Ile Leu Ala Gly Leu Ile Val
 -10 -5 1
 Gly Gly Ala Cys Ile Tyr Lys His Phe Met Pro Lys Ser Thr Ile Tyr
 5 10 15
 Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
 20 25 30
 Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile

"09EBZ660" 104601

35					40					45					50
Arg	Glu	Asp	Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe
				55					60					65	
Ser	Asp	Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met
			70					75					80		
Thr	Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
		85					90					95			
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Glu	Asn	Leu	Val	Glu	Leu	Phe	Gly
	100					105					110				
Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val	Arg	Glu
	115				120					125					130
Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn	Leu	Gly	Ile
				135					140					145	
Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe	Arg	Leu	Arg	Arg
			150					155					160		
Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala	Ile	Asp	Lys	Cys	Trp
		165					170					175			
Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile	Val	Glu	Thr	Lys	Ile	Cys
	180					185					190				
Gln	Glu														
195															

<210> 778
 <211> 205
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -139..-1

<400> 778															
Met	Ala	Pro	Thr	Arg	Lys	Asp	Lys	Leu	Leu	Gln	Phe	Tyr	Pro	Ser	Leu
				-135				-130						-125	
Glu	Asp	Pro	Ala	Ser	Ser	Arg	Tyr	Gln	Asn	Phe	Ser	Lys	Gly	Ser	Arg
			-120					-115					-110		
His	Gly	Ser	Glu	Glu	Ala	Tyr	Ile	Asp	Pro	Ile	Ala	Met	Glu	Tyr	Tyr
		-105					-100					-95			
Asn	Trp	Gly	Arg	Phe	Ser	Lys	Pro	Pro	Glu	Gly	Glu	Ala	Lys	Asp	Lys
	-90					-85					-80				
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Val	Gly	Ala	Gln	Gly	Arg	Ser	His	Thr
	-75			-70					-65					-60	
Ser	Arg	Gln	Glu	Arg	Arg	Leu	Gly	Leu	Gly	Ser	Asp	Asp	Asp	Ala	Asn
				-55				-50						-45	
Ser	Tyr	Glu	Asn	Val	Leu	Ile	Cys	Lys	Gln	Lys	Thr	Thr	Glu	Thr	Gly
			-40					-35					-30		
Ala	Gln	Gln	Glu	Asp	Val	Gly	Gly	Leu	Cys	Arg	Gly	Asp	Leu	Ser	Leu
	-25					-20					-15				
Ser	Leu	Ala	Leu	Lys	Thr	Gly	Pro	Thr	Ser	Gly	Leu	Cys	Pro	Ser	Ala
	-10				-5					1				5	
Ser	Pro	Glu	Glu	Asp	Gly	Glu	Ser	Glu	Asp	Tyr	Gln	Asn	Ser	Ala	Ser
			10					15					20		
Ile	His	Gln	Trp	Arg	Glu	Ser	Arg	Lys	Val	Met	Gly	Gln	Leu	Gln	Arg
		25					30					35			
Glu	Ala	Ser	Pro	Gly	Pro	Val	Gly	Ser	Pro	Asp	Glu	Glu	Asp	Gly	Glu
	40					45					50				
Pro	Asp	Tyr	Val	Asn	Gly	Glu	Val	Ala	Ala	Thr	Glu	Ala			
	55					60					65				

<210> 779
 <211> 85

0097360 101501

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17...-1

<400> 779
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
-15 -10 -5
Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser
1 5 10 15
Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
20 25 30
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
35 40 45
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
50 55 60
Leu Pro Ser Glu Lys
65

<210> 780
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51...-1

<400> 780
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val Gly
-50 -45 -40
Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
-35 -30 -25 -20
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
-15 -10 -5
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
1 5 10
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
15 20 25
Pro Gly Pro Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
30 35 40 45
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
50 55 60
Arg Thr Phe

<210> 781
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31...-1

<400> 781
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
-30 -25 -20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15 -10 -5 1

09978360 104501

Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
5 10 15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
20 25 30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
35 40 45
Leu
50

<210> 782
<211> 235
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39...-1

<400> 782
Met Gly Thr Ala Asp Ser Asp Glu Met Ala Pro Glu Ala Pro Gln His
-35 -30 -25
Thr His Ile Asp Val His Ile His Gln Glu Ser Ala Leu Ala Lys Leu
-20 -15 -10
Leu Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg
-5 1 5
Gly Ser Ser Arg Leu Leu Val Ala Ser Trp Val Met Gln Ile Val Leu
10 15 20 25
Gly Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr
30 35 40
Thr Leu Leu Val Thr Ser Gly Ala Ala Ile Trp Thr Gly Ala Val Ala
45 50 55
Val Leu Ala Gly Ala Ala Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr
60 65 70
Tyr Trp Ala Leu Leu Arg Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr
75 80 85
Ala Ile Ala Ala Leu Lys Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr
90 95 100 105
Ser Tyr Tyr Asn Ser Ala Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn
110 115 120
Thr Pro Ala Pro Thr Gln Ser Pro Glu Glu Val Arg Arg Leu His Leu
125 130 135
Cys Thr Ser Phe Met Asp Met Leu Lys Ala Leu Phe Arg Thr Leu Gln
140 145 150
Ala Met Leu Leu Gly Val Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala
155 160 165
Pro Leu Trp Leu Tyr Cys Trp Arg Met Phe Pro Thr Lys Gly Lys Arg
170 175 180 185
Asp Gln Lys Glu Met Leu Glu Val Ser Gly Ile
190 195

<210> 783
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 783
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu

-20 -15 -10
 Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
 -5 1 5 10
 Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
 15 20 25
 Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Ala
 30 35 40

<210> 784
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 784
 Met Gly Leu Ser Ser Ser Glu Gly Asp Ile Pro
 1 5 10

<210> 785
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 785
 Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
 -30 -25 -20
 Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
 -15 -10 -5
 Phe Gly Asp Pro Ala Ser Met Phe Cys Lys Val Phe Asp Leu Leu Val
 1 5 10
 Leu Asn Lys Ile Leu Leu Gly Leu
 15 20

<210> 786
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<220>
 <221> UNSURE
 <222> -5,42,58
 <223> Xaa = any one of the twenty amino acids

<400> 786
 Met Ala Ala Ala Ala Ala Ser Arg Gly Val Gly Ala Lys Leu Gly Leu
 -30 -25 -20
 Arg Glu Ile Arg Ile His Leu Cys Gln Arg Ser Xaa Gly Ser Gln Gly
 -15 -10 -5
 Val Arg Asp Phe Ile Glu Lys Arg Tyr Val Glu Leu Lys Lys Ala Asn
 1 5 10 15
 Pro Asp Leu Pro Ile Leu Ile Arg Glu Cys Ser Asp Val Gln Pro Lys
 20 25 30
 Leu Trp Ala Arg Tyr Ala Phe Gly Gln Xaa Thr Asn Val Pro Leu Asn
 35 40 45

"09E360" 10501

Asn Phe Ser Ala Asp Gln Val Thr Arg Xaa Leu Glu Asn Val Leu Ser
 50 55 60
 Gly Lys Ala
 65

<210> 787
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 49,74,75,88,98,104,112,114,120
 <223> Xaa = any one of the twenty amino acids

<400> 787
 Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
 -25 -20 -15
 Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
 -10 -5 1 5
 Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
 10 15 20
 Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
 25 30 35
 Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Xaa Tyr Leu Val Ile
 40 45 50
 Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
 55 60 65
 Gly Leu Cys Leu Xaa Xaa Lys Leu Gln Arg Cys Leu Pro Phe Lys His
 70 75 80 85
 Lys Leu Xaa Ile Tyr Ile Ser Glu Gly Thr His Ser Xaa Glu Glu Asp
 90 95 100
 Ile Asn Xaa Gln Ile Asn Asp Lys Glu Arg Xaa Ala Xaa Ala Met Glu
 105 110 115
 Asn Pro Xaa Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
 120 125 130

<210> 788
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 788
 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
 Pro Leu Ser Asp Val Leu Asn Thr Val His Lys
 30 35

<210> 789

009360.1041

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -77...-1

<220>
<221> UNSURE
<222> -65,31,34
<223> Xaa = any one of the twenty amino acids

<400> 791
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Xaa Gly Gly Tyr
-75 -70 -65
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
-60 -55 -50
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
-45 -40 -35 -30
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
-25 -20 -15
Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
-10 -5 1
Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
5 10 15
Ile Met Lys Asp Val Pro Asp Trp Lys Val Gly Xaa Ser Val Xaa His
20 25 30 35
Thr Thr Arg Trp Val Pro Pro Leu Ile Gly Glu Leu Tyr Gly Leu Arg
40 45 50
Thr Thr Lys Glu Ala Leu His Ala Ser His Gly Phe Met Trp Tyr Thr
55 60 65

<210> 792
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<220>
<221> UNSURE
<222> 48,52,55,59,65
<223> Xaa = any one of the twenty amino acids

<400> 792
Met Glu Thr Gly Arg Leu Leu Ser Leu Ser Ser Leu Pro Leu Val Leu
-15 -10 -5
Leu Gly Trp Glu Tyr Ser Ser Gln Thr Leu Asn Leu Val Pro Ser Thr
1 5 10
Ser Ile Leu Ser Phe Val Pro Phe Ile Pro Leu His Leu Val Leu Phe
15 20 25 30
Ala Leu Trp Tyr Leu Pro Val Pro His His Leu Tyr Pro Gln Gly Leu
35 40 45
Gly Xaa His Ala Xaa Ala Glu Xaa Gly Lys Arg Xaa Glu Gly Gly
50 55 60
Thr Gln Xaa Ala Leu Trp Leu Arg Val Gln Pro Ser Cys Pro Ser Pro
65 70 75
Val Cys Leu Glu Pro Val Pro Pro Arg Ser Arg Phe Leu Leu
80 85 90

0097860-1064
P.D.F. 0903/660

[illegible]

<400> 793															
Met	Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Ala
	-35					-30					-25				
Val	Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe
-20					-15					-10					-5
Thr	Ala	Trp	Phe	Phe	Val	Tyr	Glu	Val	Thr	Ser	Thr	Lys	Tyr	Thr	Arg
				1			5					10			
Asp	Ile	Tyr	Lys	Glu	Leu	Leu	Ile	Ser	Leu	Val	Ala	Ser	Leu	Phe	Met
		15					20					25			
Gly	Phe	Gly	Val	Leu	Phe	Leu	Leu	Leu	Trp	Val	Gly	Ile	Tyr	Val	
	30					35					40				

```
<220>
<221> SIGNAL
<222> -34..-1
```

<400> 794															
Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser
				-30					-25					-20	
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala
			-15					-10					-5		
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr
		1				5					10				
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe
15					20					25					30
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val
				35					40					45	
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser
			50					55					60		
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val
		65					70					75			
Val	Lys	Xaa	His	Ile	Xaa	Thr	Glu	Xaa	Lys	Asp	Phe	Gln	Pro	Tyr	Phe
	80					85					90				
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln
95					100					105					110
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Met	Trp	Tyr
				115					120					125	
Asn	Phe	Phe	Arg	Xaa	Trp	Asn	Gly	Xaa	Phe	Ser	Gly	Asn	Leu	Glu	Gly
			130					135					140		
Xaa	Gly	Phe	Ile	Leu	Gly	Gly	Ile	Phe	Val	Val	Gly	Ser	Xaa	Lys	Ala
		145					150					155			

45 50 55
 Leu Pro Leu Trp Lys Ile His Ala Cys Arg Phe Asn Cys Arg Cys Gln
 60 65 70
 Phe Ala Asp Gly Arg Gln Ser Trp Ser
 75 80

<210> 797
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<220>
 <221> UNSURE
 <222> 32,100
 <223> Xaa = any one of the twenty amino acids

<400> 797
 Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn Ala
 -45 -40 -35
 Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp Lys
 -30 -25 -20
 Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly Gly
 -15 -10 -5
 Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu
 1 5 10 15
 Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Xaa
 20 25 30
 Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser
 35 40 45
 Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp
 50 55 60
 Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln Glu
 65 70 75 80
 Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp Asn Lys
 85 90 95
 Lys Arg Lys Xaa
 100

<210> 798
 <211> 259
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<220>
 <221> UNSURE
 <222> 31,84,88,90,94,100,110,113,117,122,152,153,173,193,194
 <223> Xaa = any one of the twenty amino acids

<400> 798
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
 -20 -15 -10
 Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
 -5 1 5

Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	Asp	Ile	Pro
10					15					20					25
Tyr	Gln	Glu	Ile	Ala	Xaa	Glu	His	Leu	Arg	Ile	Cys	Pro	Gln	Glu	Tyr
				30					35					40	
Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	Ser	Gln	Gln	Ser	Lys
			45					50					55		
Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	Ser	His	Phe	Val	Arg	Thr
		60					65					70			
Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	Asp	Xaa	Phe	Phe	Arg	Xaa	Leu
	75					80					85				
Xaa	Glu	Asn	Ala	Xaa	Lys	Ser	Leu	Asn	Asp	Xaa	Phe	Val	Arg	Thr	Tyr
90					95					100					105
Gly	Met	Leu	Tyr	Xaa	Gln	Asn	Xaa	Glu	Val	Phe	Xaa	Asp	Leu	Phe	Thr
				110					115					120	
Xaa	Leu	Lys	Arg	Tyr	Tyr	Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met
			125					130					135		
Leu	Asn	Asp	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Xaa	Xaa
		140					145					150			
Asn	Pro	Gln	Tyr	His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys
	155					160					165				
Tyr	Thr	Asp	Xaa	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys
170					175					180					185
Ile	Gln	Val	Thr	Arg	Ala	Phe	Xaa	Xaa	Ala	Arg	Thr	Phe	Val	Gln	Gly
				190					195					200	
Leu	Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ile	Glu
			205				210						215		
Asn	Val	Leu	Ser	Phe	Ser	Leu	Val	Phe	Leu	Val	Tyr	Ser	Val	Phe	Lys
		220					225					230			
Thr	Asn	Val													
	235														

<210> 799

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -62..-1

<220>

<221> UNSURE

<222> 37,43

<223> Xaa = any one of the twenty amino acids

<400> 799

Met	Gly	Glu	Ser	Ile	Pro	Leu	Ala	Ala	Pro	Val	Pro	Val	Glu	Gln	Ala
		-60					-55					-50			
Val	Leu	Glu	Thr	Phe	Phe	Ser	His	Leu	Gly	Ile	Phe	Ser	Tyr	Asp	Lys
	-45					-40					-35				
Ala	Lys	Asp	Asn	Val	Glu	Lys	Glu	Arg	Glu	Ala	Asn	Lys	Ser	Ala	Gly
-30					-25				-20					-15	
Gly	Ser	Trp	Leu	Ser	Leu	Leu	Ala	Ala	Leu	Ala	His	Leu	Ala	Ala	Ala
			-10					-5						1	
Glu	Lys	Val	Tyr	His	Ser	Leu	Thr	Tyr	Leu	Gly	Gln	Lys	Leu	Gly	Thr
	5					10					15				
Ser	Ala	Pro	Pro	Pro	Glu	Pro	Leu	Glu	Glu	Glu	Val	Lys	Gly	Val	Tyr
20					25					30					
Ser	Pro	Xaa	Gly	Ser	Gly	Leu	Gly	Xaa	Pro	Ser	Leu	Cys	His	Phe	
35					40				45						

009380 10101

1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--

```
<220>
<221> UNSURE
<222> 56,70,107,110,113,178,181,183,195,200,202,204,230,231,244
<223> Xaa = any one of the twenty amino acids
```

```
<210> 801
<211> 91
<212> PRT
<213> Homo sapiens
```


Ser	Ala	Glu	Asp	Gln	Lys	Ile	His	Arg	Pro	Met	Ala	Pro	Lys	Glu	Ala
	210						215					220			
Pro	Lys	Lys	Leu	Ile	Arg	Tyr	Ile	Asp	Asn	Gln	Val	Val	Ser	Thr	Lys
	225					230					235				
Gly	Glu	Arg	Phe	Lys	Asp	Val	Arg	Asn	Pro	Glu	Ala	Glu	Glu	Met	Lys
240					245					250					255
Ala	Thr	Tyr	Ile	Asn	Leu	Lys	Pro	Ala	Arg	Lys	Tyr	Arg	Phe	His	
				260					265					270	

<210> 803
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<220>
 <221> UNSURE
 <222> 4
 <223> Xaa = any one of the twenty amino acids

<400> 803															
Met	Glu	His	Leu	Thr	His	Ser	Ser	Gln	Lys	Leu	Gln	Ala	Asp	Glu	His
				-45				-40						-35	
Leu	Thr	Lys	Glu	Val	Trp	Ser	Arg	Leu	Leu	Lys	Glu	Lys	Gly	Pro	Ala
			-30				-25						-20		
Gly	Leu	Ile	Leu	Cys	Phe	Leu	Cys	Leu	Tyr	Pro	Ile	Pro	Leu	Cys	Thr
		-15				-10					-5				
Ser	His	Pro	Val	Xaa	Leu	Cys	Ala	His	Pro	Gln	Asp	Val	Tyr	Pro	Val
1				5					10					15	
Val	Val	Arg	Ala	Glu	Ile	His	Ala	Glu	Leu	Tyr	Gln	Glu	Leu	Ala	Tyr
			20					25					30		
Leu	Lys	Thr	Glu	Thr	Glu	Ser	Leu	Ala	His	Leu	Phe	Ala	Leu	Val	Pro
			35				40					45			
Gln	Ala	Lys	Ile	Lys	Asn	Arg	Val								
		50				55									

<210> 804
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<220>
 <221> UNSURE
 <222> -26,-25,-24
 <223> Xaa = any one of the twenty amino acids

<400> 804															
Met	Gly	Leu	Leu	Thr	Phe	Gly	Tyr	Ile	Glu	Xaa	Xaa	Xaa	Lys	Thr	Glu
	-35				-30					-25					
His	Asn	Pro	Asp	His	His	Ser	Cys	Leu	Ala	Val	Ser	Trp	Glu	Ala	Ala
-20				-15					-10					-5	
Gly	Cys	His	Gly	Ala	Gly	Thr	Gln	Gln	Ser	Pro	Leu	Gly	Val	Ala	Gly
			1				5					10			
Pro	Trp	Arg	Pro	Arg	Pro	Pro	Cys	Val	Gly	Ser	Leu	Leu	Ala	Ala	Arg

00978360 101501

Pro Leu Glu Gly Thr Thr Trp Thr His Ser Leu Lys Ala Gln Leu Leu
30 35 40
Ser Leu Pro Phe Trp Val Trp Thr Val Ile Phe Leu Val Pro Tyr Leu
45 50 55
Gln Xaa Phe Leu Phe Leu Tyr Ser Cys Thr Lys Xaa Asp Pro Lys Thr
60 65 70
Val Gly Tyr Cys Xaa Ile Pro Ile Cys Leu Ala Xaa Ile Xaa Asn Arg
75 80 85
His Gln Asp Phe Val Lys Ala Ser Asn Gln Ile Ser Lys Leu Gln Leu
90 95 100 105
Ile Asp Thr

<210> 807
<211> 335
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<220>
<221> UNSURE
<222> 70,139,141,154,156,165
<223> Xaa = any one of the twenty amino acids

<400> 807
Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly
-15 -10 -5
Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn
1 5 10 15
Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
20 25 30
Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
35 40 45
Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met Val
50 55 60
Lys Gly Val Asn Asn Xaa Pro Leu Pro Pro Gly Cys Val Ile Ser Tyr
65 70 75 80
Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser
85 90 95
Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala
100 105 110
Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Trp
115 120 125
Lys Thr Phe Gln Ser Leu Ala Pro Ala Pro Xaa Ile Xaa Cys Phe Lys
130 135 140
Lys Thr Leu Phe Ser Val His Ser Pro Xaa Ile Xaa Leu Ser Arg Asn
145 150 155 160
Asn Glu Val Asp Xaa Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
165 170 175
Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
180 185 190
Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
195 200 205
Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
210 215 220
Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
225 230 235 240
Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser

00978360 "10501

				245					250					255					
Leu	Ile	Arg	Lys	Thr	Arg	Thr	Ile	Leu	Glu	Ala	Lys	Gln	Ala	Lys	Asn				
			260					265					270						
Pro	Ala	Ser	Pro	Tyr	Asn	Leu	Ala	Tyr	Lys	Tyr	Asn	Phe	Glu	Tyr	Ser				
		275					280					285							
Val	Val	Phe	Asn	Met	Val	Leu	Trp	Ile	Met	Ile	Ala	Leu	Ala	Leu	Ala				
	290					295					300								
Val	Ile	Ile	Thr	Ser	Tyr	Asn	Ile	Trp	Asn	Met	Glu	Ser	Trp	Ile					
305					310					315									

<210> 808
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 808																			
Met	Arg	Lys	Val	Val	Leu	Ile	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Leu				
-55					-50					-45					-40				
Ala	Leu	Cys	Lys	Arg	Leu	Leu	Ala	Glu	Asp	Asp	Glu	Leu	His	Leu	Cys				
			-35					-30						-25					
Leu	Ala	Cys	Arg	Asn	Met	Ser	Lys	Ala	Glu	Ala	Val	Cys	Ala	Ala	Leu				
		-20					-15					-10							
Leu	Ala	Ser	His	Pro	Thr	Ala	Glu	Val	Thr	Ile	Val	Gln	Val	Asp	Val				
	-5				1					5									
Ser	Asn	Leu	Gln	Ser	Phe	Phe	Arg	Ala	Ser	Lys	Glu	Leu	Lys	Gln	Arg				
10				15					20						25				
Met	Ile	Ser	Cys																

<210> 809
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 809																			
Met	Glu	Gly	Pro	Arg	Gly	Trp	Leu	Val	Leu	Cys	Val	Leu	Ala	Ile	Ser				
			-15				-10					-5							
Leu	Ala	Ser	Met	Val	Thr	Glu	Asp	Leu	Cys	Arg	Ala	Pro	Asp	Gly	Lys				
	1				5					10									
Lys	Gly	Glu	Ala	Gly	Arg	Pro	Gly	Arg	Arg	Gly	Arg	Pro	Gly	Leu	Lys				
15				20				25						30					
Gly	Glu	Gln	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Ile	Arg	Thr	Gly	Ile	Gln				
			35				40						45						
Gly	Leu	Lys	Gly	Asp	Gln	Gly	Glu	Pro	Gly	Pro	Ser	Gly	Asn	Pro	Gly				
		50				55						60							
Lys	Val	Gly	Tyr	Pro	Gly	Pro	Ser	Gly	Pro	Leu	Gly	Ala	Arg	Gly	Ile				
	65				70					75									
Pro	Gly	Ile	Lys	Gly	Thr	Lys	Gly	Ser	Pro	Gly	Asn	Ile	Lys	Asp	Gln				
	80				85					90									
Pro	Arg	Pro	Ala	Phe	Ser	Ala	Ile	Arg	Arg	Asn	Pro	Pro	Met	Gly	Gly				
95				100						105					110				
Asn	Val	Val	Ile	Phe	Asp	Thr	Val	Ile	Thr	Asn	Gln	Glu	Glu	Pro	Tyr				
			115				120							125					
Gln	Asn	His	Ser	Gly	Arg	Phe	Val	Cys	Thr	Val	Pro	Ala	Thr	Thr	Thr				

09978360.101501

